

Pending Nucleic Acid and Pending Amino Acid database searches generate two sets of results each. The Pending databases have been split into two parts to reduce the amount of time required for their daily updates. This results in more machine time being available for processing searches. Searches run against the Nucleic Acid Pending database produce two sets of results, with the extensions .rnpm and .rnpn. Searches run against the Amino Acid Pending database produce two sets of results, with the extensions .rapm and .rapn.

Because they contain data that is confidential, the results of Pending database searches should not be left in the case .

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Protein Sequence Searches - February 2005

All of the sequence databases on ABSS have recently been updated.

- Please note that the curators of the UniProt database have purged some temporary accession numbers from the most recent version of UniProt. These sequences have been assigned new permanent accession numbers. The new UniProt record may not contain the previous temporary accession number.
- If you encounter an accession number from an older search run against UniProt (results file extension **.rup**) that can no longer be found in the database, the permanent record with the new accession number can be found by searching the old accession number in the UniProt Protein, Archive database (UniPARC) at:

<http://www.pir.uniprot.org/database/archive.shtml>

If you have any questions regarding this information or your results, please contact any STIC searcher.

When submitting sequence search results for scanning into IFW, please include a copy of this attachment to assist any future Examiners or members of the public who may encounter UniProt temporary accession numbers.

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: April 24, 2005, 18:52:43 ; Search time 758 Seconds
(without alignments)
9949.539 Million cell updates/sec

Title: US-10-679-246-1

Perfect score: 1274

Sequence: 1 ttcttttggtggttatgtg.....ctcttcgtagtggaagc 1274

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

N Geneseq_16Dec04:.*
1: Geneseqn1980s:.*
2: Geneseqn1990s:.*
3: Geneseqn2000s:.*
4: Geneseqn2001as:.*
5: Geneseqn2001bs:.*
6: Geneseqn2002as:.*
7: Geneseqn2002bs:.*
8: Geneseqn2003as:.*
9: Geneseqn2003bs:.*
10: Geneseqn2003cs:.*
11: Geneseqn2003ds:.*
12: Geneseqn2004as:.*
13: Geneseqn2004bs:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1274	100.0	1274	4 AAC67281	Human Sia
2	1274	100.0	2824	5 ABV28804	Human pro
3	1274	100.0	2924	5 ABV25468	Human pro
4	1274	100.0	2924	5 ABV22970	Human pro
5	1274	100.0	6107	4 AAL05382	Human rep
6	1274	100.0	6107	4 ABL98246	Human tes
7	1272.4	99.9	2829	11 ADM01584	Human cDN
8	1272.4	99.9	2829	13 ADS34362	POSH prot
9	1249	98.0	4090	10 ADF81981	Leukaemia
10	1104	86.7	2128	13 ADS34361	POSH prot
11	1042.8	81.9	2440	11 ADI31262	Human cDN
12	958	75.2	1540	13 ADS34365	POSH prot
13	958	75.2	2048	13 ADS34360	POSH prot
14	957	75.1	2454	13 ADS34359	POSH prot
15	951.4	74.7	1886	13 ADS34359	POSH prot
16	947	74.3	2034	13 ADS34364	POSH prot
17	928.4	72.9	1884	2 AAT64820	Tumour eu
18	807.8	63.4	1968	6 ABI99429	Mouse isc
19	761.4	59.8	3128	10 ADI40343	Human pur
20	429	33.7	975	13 ADR25256	Breast ca

21	429	33.7	2502	8 ACC50293	Acc50293 Breast ca
22	427.4	33.5	2240	8 ACC50292	Acc50292 Breast ca
23	427.4	33.5	2240	12 ADP13401	Adp13401 Renal cel
24	427.4	33.5	2240	13 ADR14122	Adr14122 Human NF-
25	427.4	33.5	2240	13 ADP54830	Adp54830 Human NF-
26	425.8	33.4	2198	6 ABI99430	Abi99430 Mouse isc
27	379	29.7	1535	3 AAC98856	Aac98856 Human pan
28	354	27.8	4647	4 ABL15923	Abli15923 Drosophil
29	354	27.8	8418	4 ABL15922	Abli15922 Drosophil
30	354	27.8	12029	4 ABL15508	Abli15508 Drosophil
31	293.8	23.1	360	8 ABX44846	Abx44846 Bovine ES
32	268	21.0	466	4 AAI87326	Aai87326 Human pro
33	191.6	15.0	405	5 ABV38421	Abv38421 Human pro
34	188.2	14.8	426	5 ABV18678	Abv18678 Human pro
35	183.4	14.4	473	5 ABV48461	Abv48461 Human pro
36	183	14.4	277	5 ABV08519	Abv08519 Human pro
37	178	14.0	3349	4 ABL21784	Abli21784 Drosophil
38	161	12.6	257	10 ACA55799	ACA55799 Human sig
39	161	12.6	257	12 ADI55595	Adi55595 Human pol
40	160.2	12.6	411	5 ABV13828	Abv13828 Human pro
41	156.8	12.3	441	5 ABV34940	Abv34940 Human pro
42	145.6	11.4	388	2 AAQ60440	Aaq60440 Human bra
43	139	10.9	417	5 ABV43789	Abv43789 Human pro
44	122.6	9.6	2363	4 ABL21782	Abli21782 Drosophil
45	112	8.8	438	5 ABV04659	Abv04659 Human pro

ALIGNMENTS

RESULT 1

AAC67281
ID AAC67281 standard; cDNA; 1274 BP.

XX AAC67281;

DT 09-APR-2001 (first entry)

XX Human Siah-1alpha coding sequence SEQ ID NO: 1.

Human; protein degradation; siah-mediated degradation protein; SMDP;
SCF-complex protein; SCP; siah-1alpha; siah-1 interacting protein; SIP;
Skpl-associated F-box protein; SAF-1; SAF-2; SAF; cancer; cell division;
Skpl-associated destruction-box protein; inflammatory disease; ss.

XX Homo sapiens.

XX WO200077207-A2.

XX 21-DEC-2000.

XX 09-JUN-2000; 2000WO-US015873.

XX 11-JUN-1999; 99US-00330517.

XX (BURN-) BURNHAM INST.

XX Reed JC, Matsuzawa S;

XX WPI; 2001-071273/08.

XX P-PSDB; AAB35157.

Siah-Mediated Degradation Protein, useful for drug screening, for therapeutic applications and for functional genomics.

Claim 5; Page 95-97; 121pp; English.

The present invention provides the protein and coding sequences of several siah-mediated degradation proteins and SCF-complex proteins. These are designated Siah-1alpha, Siah-1 interacting protein (SIP), which encodes two proteins due to alternative splicing (SIP-L and SIP-S), Skpl-associated F-box protein-alpha and beta and -2 (SAF-1alpha, SAF-1beta and SAF-2) and Skpl-associated destruction-box protein (SAD). The

CC of a test compound to inhibit prostate cancer in a patient; (d) assessing
CC the efficacy of a therapy for inhibiting prostate cancer in a patient;
CC (e) selecting a composition for inhibiting prostate cancer in a patient;
CC (f) assessing the prostate cell carcinogenic potential of a compound; (g)
CC determining whether prostate cancer has metastasized in a patient; (h)
CC assessing the aggressiveness or indolence of prostate cancer in a patient
CC ; (i) is also useful as a pharmacodynamic or pharmacogenomic marker
XX

SQ Sequence 2924 BP; 871 A; 562 C; 562 G; 925 T; 0 U; 4 Other;

Query Match 100.0%; Score 1274; DB 5; Length 2924;
Best Local Similarity 100.0%; Pred. No. 1.7e-303;
Matches 1274; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTTCTTTAGTGTGTTAAGTCCATTTTCTATTTTATTTAGCATTTTATTTCTATGTAGTCTAT 60
DB TTTCTTTAGTGTGTTAAGTCCATTTTCTATTTTATTTAGCATTTTATTTCTATGTAGTCTAT 539
QY 61 CCAAGACGATTAAAGGAGTTCACATGTTTCCGGAACATTTGAAAGAGAGCTTATC 120
DB CCAAGACGATTAAAGGAGTTCACATGTTTCCGGAACATTTGAAAGAGAGCTTATC 599
QY 121 CAGTGTACAGATCCCTAATAAGTGCACTTCAGTGTAAATTTTATTTTATATATCTTTT 180
DB CAGTGTACAGATCCCTAATAAGTGCACTTCAGTGTAAATTTTATTTTATATATCTTTT 659
QY 181 TTAATCTATTTTCT 240
DB TTAATCTATTTTCT 719
QY 241 TATGCGATGTAAACATTTATTAAGTAAGTCATGGTTATTAATTTTCTCTCTCTCTCT 300
DB TATGCGATGTAAACATTTATTAAGTAAGTCATGGTTATTAATTTTCTCTCTCTCTCTCT 779
QY 301 CCTTATGTATTTATTTTTCAGAAATGAGCGTTCAGATGCTACAGCATTTACTACCGGTACC 360
DB CCTTATGTATTTATTTTTCAGAAATGAGCGTTCAGATGCTACAGCATTTACTACCGGTACC 839
QY 361 TCGAAGTGTCCACCATCCAGAGGGTCTGCGCTGACTGGCACAACCTCATCCAACT 420
DB TCGAAGTGTCCACCATCCAGAGGGTCTGCGCTGACTGGCACAACCTCATCCAACT 899
QY 421 GACTTGGCGAGTCTTTTGGAGTGTCCAGTCTGCTGTTTGGACTATGTGTACGGCCCATCTT 480
DB GACTTGGCGAGTCTTTTGGAGTGTCCAGTCTGCTGTTTGGACTATGTGTACGGCCCATCTT 959
QY 481 CAATGTACAGTGGCCATCTGTTTGTAGCAACTGTCGCCCAAGCTCACATGTTGTCCA 540
DB CAATGTACAGTGGCCATCTGTTTGTAGCAACTGTCGCCCAAGCTCACATGTTGTCCA 1019
QY 541 ACTTGGCGGGCCCTTTGGGATCCATTTCCCAACTTGGCTATGGAGAAAGTGGCTAATTC 600
DB ACTTGGCGGGCCCTTTGGGATCCATTTCCCAACTTGGCTATGGAGAAAGTGGCTAATTC 1079
QY 601 GTACTTTTCCCTGTAAATATGCGTCTTCTGGATGGAATAACTCTGCGCACACACAGAA 660
DB GTACTTTTCCCTGTAAATATGCGTCTTCTGGATGGAATAACTCTGCGCACACACAGAA 1139
QY 661 AAAGCAGACCATGAAGAGCTCTGTGAGTTTAGCCCTTATTCCTGCGCGCCCTGGTCT 720
DB AAAGCAGACCATGAAGAGCTCTGTGAGTTTAGCCCTTATTCCTGCGCGCCCTGGTCT 1199
QY 721 TCCTGTAAATGCAAGGCTCTCTGATGCTGTAATGCCCCCATCTGATGATCAGCATTAAG 780
DB TCCTGTAAATGCAAGGCTCTCTGATGCTGTAATGCCCCCATCTGATGATCAGCATTAAG 1259
QY 781 TCCATTACACCCCTACAGGAGAGATATAGTTTTTCTTGGCTACAGACATTAATCTTCT 840
DB TCCATTACACCCCTACAGGAGAGATATAGTTTTTCTTGGCTACAGACATTAATCTTCT 1319
QY 841 GGTGCTGTGATGGGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 900
DB GGTGCTGTGATGGGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1379

QY 901 GAGAAACAGGAAAAATACGATGGTCCAGCAGTCTTCGCAATCTGTACAGCTGTAGGA 960
DB GAGAAACAGGAAAAATACGATGGTCCAGCAGTCTTCGCAATCTGTACAGCTGTAGGA 1439
QY 961 ACACCGCAGCAGCTGAAATTTTCTTACCGACTTGACCTAAATGCTCATAGCGCAGCA 1020
DB ACACCGCAGCAGCTGAAATTTTCTTACCGACTTGACCTAAATGCTCATAGCGCAGCA 1499
QY 1021 TTGACTTTGGGAAGCGACTCTCTCGATCTATTCTATGAAGGAATTTGCAACAGCCATTATGAAT 1080
DB TTGACTTTGGGAAGCGACTCTCTCGATCTATTCTATGAAGGAATTTGCAACAGCCATTATGAAT 1559
QY 1081 AGCGACTGTCTAGTCTTTTGACACCGCAGCATTTGACAGCTTTTTCAGAAAAATGCAATTTA 1140
DB AGCGACTGTCTAGTCTTTTGACACCGCAGCATTTGACAGCTTTTTCAGAAAAATGCAATTTA 1619
QY 1141 GGCATCAATGTAACTATTTCCATGTTTGAATGGCAATCAAACTTTTCTGCGCAGTCT 1200
DB GGCATCAATGTAACTATTTCCATGTTTGAATGGCAATCAAACTTTTCTGCGCAGTCT 1679
QY 1201 TTAAAACTTTCAGTTTTCACAGAAAAATAAGGCACCCCATCTGCTGCCAACCTTAAACTCTTT 1260
DB TTAAAACTTTCAGTTTTCACAGAAAAATAAGGCACCCCATCTGCTGCCAACCTTAAACTCTTT 1739
QY 1261 CGGTAGTGGGAAGC 1274
DB CGGTAGTGGGAAGC 1753
RESULT 3
ABV25468
ID ABV25468 standard; cDNA; 2924 BP.
XX
AC ABV25468;
XX
DT 16-SEP-2002 (first entry)
XX
DE Human prostate expression marker cDNA 25459.
XX
KW Human; prostate cancer; cytostatic; carcinogen; pharmacodynamic marker;
KW pharmacogenomic marker; gene; ss.
XX
OS Homo sapiens.
XX
PN WO200160860-A2.
XX
PD 23-AUG-2001.
XX
PF 20-FEB-2001; 2001WO-US005171.
XX
PR 17-FEB-2000; 2000US-0183319P.
PR 16-MAR-2000; 2000US-0189862P.
PR 25-MAY-2000; 2000US-0207454P.
PR 09-JUN-2000; 2000US-0211314P.
PR 18-JUL-2000; 2000US-0219007P.
PR 13-DEC-2000; 2000US-0255281P.
XX
XX (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
PA
XX Schlegel R, Endege WO, Monahan JE;
PI
XX WPI; 2001-662795/76.
DR
XX
XX Novel isolated nucleic acid molecule associated with cancerous state of
PT prostate cells and correlating with presence of prostate cancer, useful
PT for detecting presence of prostate cancer, stage of prostate cancer.
XX
PS Claim 1; Page 5054-5055; 11750pp; English.
XX
CC The invention relates to an isolated nucleic acid molecule (I) comprising
CC a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the
CC specification or its complement. (I) is useful for: (a) assessing whether

CC a patient is afflicted with prostate cancer; (b) monitoring the
CC progression of prostate cancer in a patient; (c) assessing the efficacy
CC of a test compound to inhibit prostate cancer in a patient; (d) assessing
CC the efficacy of a therapy for inhibiting prostate cancer in a patient;
CC (e) selecting a composition for inhibiting prostate cancer in a patient;
CC (f) assessing the prostate cell carcinogenic potential of a compound; (g)
CC determining whether prostate cancer has metastasized in a patient; (h)
CC assessing the aggressiveness or indolence of prostate cancer in a patient
CC ; (i) is also useful as a pharmacodynamic or pharmacogenomic marker
XX
SQ Sequence 2924 BP; 871 A; 562 C; 562 G; 925 T; 0 U; 4 Other;
Query Match 100.0%; Score 1274; DB 5; Length 2924;
Best Local Similarity 100.0%; Pred. No. 1.7e-303;
Matches 1274; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TTTCTTTAGTGTGTTATGTCCTATTTCTATTATTTAGCAATTTATTTCTATAGTCTAT 60
DB 480 TTTCTTTAGTGTGTTATGTCCTATTTCTATTATTTAGCAATTTATTTCTATAGTCTAT 539
QY 61 CCAAGACGATTAAAGGAGTTCACATGTTTCCGGAACATTTGAAAGAGAGCTTATC 120
DB 540 CCAAGACGATTAAAGGAGTTCACATGTTTCCGGAACATTTGAAAGAGAGCTTATC 599
QY 121 CAGGTACAGATCCTAATAAGTGCAATTCAGTGTAAATTTTATTTTATATATCTTTT 180
DB 600 CAGGTACAGATCCTAATAAGTGCAATTCAGTGTAAATTTTATTTTATATCTTTT 659
QY 181 TTAATCCTATTTTCTCTCTTTCTCTCAGTAAATTTTGTATGAAACTTTAAAGGACT 240
DB 660 TTAATCCTATTTTCTCTCTTTCTCTCAGTAAATTTTGTATGAAACTTTAAAGGACT 719
QY 241 TATGGCATGTAACATTTATTAAGTAAGTCAATGTTTATTTTCTCTCTCTCTCT 300
DB 720 TATGGCATGTAACATTTATTAAGTAAGTCAATGTTTATTTTCTCTCTCTCTCT 779
QY 301 CCTATGATTTATTTTTCAGAAATGAGCGTTCAGATGCTACAGCAATTTACCTACCGTACC 360
DB 780 CCTATGATTTATTTTTCAGAAATGAGCGTTCAGATGCTACAGCAATTTACCTACCGTACC 839
QY 361 TCGAAGTGTCCATCCAGAGGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 420
DB 840 TCGAAGTGTCCATCCAGAGGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 899
QY 421 GACTTGGCAGTCTTTTGTAGTCTCAGTCTGCTTGTGCTGCTGCTGCTGCTGCTGCT 480
DB 900 GACTTGGCAGTCTTTTGTAGTCTCAGTCTGCTTGTGCTGCTGCTGCTGCTGCTGCT 959
QY 481 CAATGTGAGAGTGGCCATCTTTTGTAGCAATGCTGCTGCTGCTGCTGCTGCTGCTGCT 540
DB 960 CAATGTGAGAGTGGCCATCTTTTGTAGCAATGCTGCTGCTGCTGCTGCTGCTGCT 1019
QY 541 ACTTGGCGGGGCTTTGGGATCATTGCAACTTGGCTATGAGAAAGTGGCTAATTTCA 600
DB 1020 ACTTGGCGGGGCTTTGGGATCATTGCAACTTGGCTATGAGAAAGTGGCTAATTTCA 1079
QY 601 GTACTTTTCCCTGTAATATGCTTCTCTGATGTGAAATACTCTGCGCACACACAGAA 660
DB 1080 GTACTTTTCCCTGTAATATGCTTCTCTGATGTGAAATACTCTGCGCACACACAGAA 1139
QY 661 AAAGCAGACCATGAAGAGCTCTGTGAGTTAGGCTTTATTCCTGCTGCTGCTGCTGCT 720
DB 1140 AAAGCAGACCATGAAGAGCTCTGTGAGTTAGGCTTTATTCCTGCTGCTGCTGCTGCT 1199
QY 721 TCTGTAATAGGAGGCTCTGTGATGCTGTAATGCCCATCTGTATGATCAGCATAGAA 780
DB 1200 TCTGTAATAGGAGGCTCTGTGATGCTGTAATGCCCATCTGTATGATCAGCATAGAA 1259
QY 781 TCCATTACAACCCCTACAGGAGAGGATATAGTTTCTTCTGCTACAGACATTAATCTTCT 840
DB 1260 TCCATTACAACCCCTACAGGAGAGGATATAGTTTCTTCTGCTACAGACATTAATCTTCT 1319
QY 841 GGTGCTGTGATCGGGTATGATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 900

DB 1320 GGTGCTGTGATCGGGTATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1379
QY 901 GAGAAACAGGAAATACGATGGTACACAGAGTCTTTCGCAATCGTACAGCTGATAGGA 960
DB 1380 GAGAAACAGGAAATACGATGGTACACAGAGTCTTTCGCAATCGTACAGCTGATAGGA 1439
QY 961 ACAGCGAAGCAAGCTGAAATTTTGTCTTACCGACTTCCAGCTTAAATGGTCTATAGCGGACGA 1020
DB 1440 ACAGCGAAGCAAGCTGAAATTTTGTCTTACCGACTTAAATGGTCTATAGCGGACGA 1499
QY 1021 TTGACTTGGGAAGGACTCTCTGATCTATTCATGAAGAAATTCGACAGCCATTTATGAAT 1080
DB 1500 TTGACTTGGGAAGGACTCTCTGATCTATTCATGAAGAAATTCGACAGCCATTTATGAAT 1559
QY 1081 AGCGACTCTCTAGTCTTTTGACACAGCAATTCGACAGCTTTTTCGAGAAATTCGCAATTTA 1140
DB 1560 AGCGACTCTCTAGTCTTTTGACACAGCAATTCGACAGCTTTTTCGAGAAATTCGCAATTTA 1619
QY 1141 GCGATCAATGTAATCTTATTTCCATGTTGAAATGGCAATCAAAATTTTCTGGCCAGTGT 1200
DB 1620 GCGATCAATGTAATCTTATTTCCATGTTGAAATGGCAATCAAAATTTTCTGGCCAGTGT 1679
QY 1201 TTAAACTTTCAGTTTCACAGAAATTAAGGACCCATCTGCTGCAACCTTAAACTCTTT 1260
DB 1680 TTAAACTTTCAGTTTCACAGAAATTAAGGACCCATCTGCTGCAACCTTAAACTCTTT 1739
QY 1261 CGGTAGGTGGAAGC 1274
DB 1740 CGGTAGGTGGAAGC 1753
RESULT 4
ABV22970
ID ABV22970 standard; cDNA; 2924 BP.
XX AC ABV22970;
XX DT 13-SEP-2002 (first entry)
XX DE Human prostate expression marker cDNA 22961.
XX KW Human; prostate cancer; cytostatic; carcinogen; pharmacodynamic marker;
XX OS Homo sapiens.
XX PN WO200160860-A2.
XX PD 23-AUG-2001.
XX PF 20-FEB-2001; 2001WO-US005171.
XX PR 17-FEB-2000; 2000US-0183319P.
XX PR 16-MAR-2000; 2000US-0189862P.
XX PR 25-MAY-2000; 2000US-0207454P.
XX PR 09-JUN-2000; 2000US-0211314P.
XX PR 18-JUL-2000; 2000US-0219007P.
XX PR 13-DEC-2000; 2000US-0255281P.
XX (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
XX PI Schlegel R, Endege WO, Monahan JE;
XX WIPI; 2001-662795/76.
XX Novel isolated nucleic acid molecule associated with cancerous state of
XX prostate cells and correlating with presence of prostate cancer, useful
XX for detecting presence of prostate cancer, stage of prostate cancer.
XX Claim 1; Page 4080-4081; 11750pp; English.
XX The invention relates to an isolated nucleic acid molecule (I) comprising
CC

Query Match	100.0%;	Score 1274;	DB 5;	Length 2924;
Best Local Similarity	100.0%;	Prod. No. 1.7e-303;		
Matches 1274;	Conservative	0;	Mismatches 0;	Indels 0;
Qy	1	TTTTCTTTAGTTGTTTATGGTCCATTTTCTATTTTAGCAATTTATTTATTTCTATGTAGTCTCAT	60	
Db	480	TTTTCTTTAGTTGTTTATGGTCCATTTTCTATTTTAGCAATTTATTTATTTCTATGTAGTCTCAT	539	
Qy	61	CCAAAGACGATTAAGGGAGTTTCCACATGTTTTCCGGAACATTTTGAAGAAGAGAGCTTATC	120	
Db	540	CCAAAGACGATTAAGGGAGTTTCCACATGTTTTCCGGAACATTTTGAAGAAGAGAGCTTATC	599	
Qy	121	CAGTGTACAGATCCTAATAAAGTGCACATTCAGTGTAAATTTTATTTTTTAAATATCTTTTT	180	
Db	600	CAGTGTACAGATCCTAATAAAGTGCACATTCAGTGTAAATTTTATTTTTTAAATATCTTTTT	659	
Qy	181	TTAATCCTATTTTTCTTCTCTTTGCTCAGTAAATTTTGTATGAACCTTTTAAAGGACT	240	
Db	660	TTAATCCTATTTTTCTTCTCTTTGCTCAGTAAATTTTGTATGAACCTTTTAAAGGACT	719	
Qy	241	TATGSCATGTAAACATTAATTTATAAAGTAAGTCATGGTTATAATTTTCTCTCGCT	300	
Db	720	TATGSCATGTAAACATTAATTTATAAAGTAAGTCATGGTTATAATTTTCTCTCGCT	779	
Qy	301	CCTTATGTATTTATTTTCAGAAATGAGCCGTCAGACTGCTACAGCATTAACCTACCGGTACC	360	
Db	780	CCTTATGTATTTATTTTCAGAAATGAGCCGTCAGACTGCTACAGCATTAACCTACCGGTACC	839	
Qy	361	TCGAAGTGTCCACATCCACAGAGGTGCTCGCCCTGACTGGCAACATGCAATCCAACAAT	420	
Db	840	TCGAAGTGTCCACATCCACAGAGGTGCTCGCCCTGACTGGCAACATGCAATCCAACAAT	899	
Qy	421	GACTTGGCGAGTCCTTTTGAGTGTCCAGTCTGCTTTGACTATGTGTACCGCCCAATCTCT	480	
Db	900	GACTTGGCGAGTCCTTTTGAGTGTCCAGTCTGCTTTGACTATGTGTACCGCCCAATCTCT	959	
Qy	481	CAATGTACAGATGGCCATCTTTGTTGTAGCAACTGTGCGCCAAAGCTCACATGTTGTCCA	540	
Db	960	CAATGTACAGATGGCCATCTTTGTTGTAGCAACTGTGCGCCAAAGCTCACATGTTGTCCA	1019	
Qy	541	ACTTGGCGGGGCCCTTTGGGATCCATTCGCAACTTGGCTATGGAGAAAGTGGCTAATTC	600	
Db	1020	ACTTGGCGGGGCCCTTTGGGATCCATTCGCAACTTGGCTATGGAGAAAGTGGCTAATTC	1079	
Qy	601	GTACTTTTCCCTGTAAATATGCGTCTTCTGGATGTGAATAAATCTGCGCACACACAGAA	660	
Db	1080	GTACTTTTCCCTGTAAATATGCGTCTTCTGGATGTGAATAAATCTGCGCACACACAGAA	1139	
Qy	661	AAAGCAGACCATGAAGAGCTCTGTGAGTTTAAAGCCCTAATTCCTGTGCGCTGGCTGGTCT	720	
Db	1140	AAAGCAGACCATGAAGAGCTCTGTGAGTTTAAAGCCCTAATTCCTGTGCGCTGGCTGGTCT	1199	
Qy	721	TCCTGTAAATGGCAGGCTCTCTGGATGCTGTAATGCCCCCATCTGATGCATCAGCATAA	780	
Db	1200	TCCTGTAAATGGCAGGCTCTCTGGATGCTGTAATGCCCCCATCTGATGCATCAGCATAA	1259	
Qy	781	TCCATTAACAACCTTACAGGGAGAGATATAGTTTTTTCTTGCTACAGCATTAATCTTCCT	840	
Db	1260	TCCATTAACAACCTTACAGGGAGAGATATAGTTTTTTCTTGCTACAGCATTAATCTTCCT	1319	

PR	14-AUG-2000;	2000US-0224518P.	PR	08-NOV-2000;	2000US-0246477P.
PR	14-AUG-2000;	2000US-0224519P.	PR	08-NOV-2000;	2000US-0246478P.
PR	14-AUG-2000;	2000US-0225213P.	PR	08-NOV-2000;	2000US-0246523P.
PR	14-AUG-2000;	2000US-0225214P.	PR	08-NOV-2000;	2000US-0246524P.
PR	14-AUG-2000;	2000US-0225266P.	PR	08-NOV-2000;	2000US-0246525P.
PR	14-AUG-2000;	2000US-0225267P.	PR	08-NOV-2000;	2000US-0246526P.
PR	14-AUG-2000;	2000US-0225268P.	PR	08-NOV-2000;	2000US-0246527P.
PR	14-AUG-2000;	2000US-0225270P.	PR	08-NOV-2000;	2000US-0246528P.
PR	14-AUG-2000;	2000US-0225447P.	PR	08-NOV-2000;	2000US-0246532P.
PR	14-AUG-2000;	2000US-0225757P.	PR	08-NOV-2000;	2000US-0246609P.
PR	14-AUG-2000;	2000US-0225758P.	PR	08-NOV-2000;	2000US-0246610P.
PR	14-AUG-2000;	2000US-0225759P.	PR	08-NOV-2000;	2000US-0246611P.
PR	18-AUG-2000;	2000US-0226279P.	PR	08-NOV-2000;	2000US-0246613P.
PR	22-AUG-2000;	2000US-0226681P.	PR	17-NOV-2000;	2000US-0249207P.
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Db	3284	CAGTGTCAGATCCTAATAAGTGCAATTCAGTGTAAATTTTAAATATCTTTTTT	3343
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Qy	361	TCGAAGTGTCACACCATCCAGAGGGTGCCTGCCTGACTGGCAACACTGCATCCAACAAT	420
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Qy	481	CAATGTCAGAGTGGCCATCTTGTGTTGTAGCAACTGTGCGCCCAAGCTCACAATGTTGCCA	540
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Qy	541	ACTTTCGGGGCCCTTTGGGATCCATTTCGCAACTTTGGCTATGGAGAAAGTGGCTTAATTC	600
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Qy	601	GTACTTTTCCCCTGTAAATATGCGTCTTCTGGATGTGAAATAACTCTGCACACACAGAA	660
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Qy	781	TCCATTACAAACCTACAGGAGAGGATATAGTTTTTCTTGCTACAGACATTAATCTTCCCT	840
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Qy	841	GGTGCTGTTGACTGGGTGATGATGCAGTCTGTTTTTGGCTTTTCACTTCATGTTAGTCTTA	900
Db	4004	GGTGCTGTTGACTGGGTGATGATGCAGTCTGTTTTTGGCTTTTCACTTCATGTTAGTCTTA	4063
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Qy	961	ACACGCAAGCAAGCTGAAAAATTTTGTCTTACCGACTTGAGCTAAATGGTCAATAGCGACGA	1020
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Qy	1021	TTGACTTGGGAAGGCACTCTCGATCTATTTTCATGAAGGAATGCGAACAGCCATTTATGAAT	1080
Db	4184	TTGACTTGGGAAGGCACTCTCGATCTATTTTCATGAAGGAATGCGAACAGCCATTTATGAAT	4243
Qy	1081	AGCGAGTCTGTAGTCTTTTGACACGACATTTGCAAGCTTTTTTTCAGAAAAATGCAATTTA	1140
Db	4244	AGCGAGTCTGTAGTCTTTTGACACGACATTTGCAAGCTTTTTTTCAGAAAAATGCAATTTA	4303
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PR 08-DEC-2000; 2000US-0251990P.
PR 11-DEC-2000; 2000US-0254097P.
PR 05-JAN-2001; 2001US-0259678P.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
XX Rosen CA, Barash SC, Ruben SM;
PI WPI; 2001-483232/52.
XX
XX Nucleic acids encoding 973 human testicular antigen polypeptides, useful
XX for preventing, diagnosing and/or treating testicular cancer.
XX
XX Disclosure; SEQ ID NO 2898; 766pp; English.
XX
XX The present invention provides the protein and coding sequences of 973
XX human testicular antigens, and fragments of their genomic sequences. The
XX sequences can be used in the treatment of cardiovascular, urinary system,
XX reproductive system, immune, respiratory, neurological and
XX gastrointestinal disorders, infections, and particularly cancer,
XX especially testicular cancers. The present sequence is a DNA encoding a
XX protein fragment of the invention
XX
XX Sequence 6107 BP; 1636 A; 1200 C; 1285 G; 1986 T; 0 U; 0 Other;
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Query Match 100.0%; Score 1274; DB 4; Length 6107;
Best Local Similarity 100.0%; Pred. No. 2.1e-303;
Matches 1274; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 3224 CCAAGACGATTAAGGAGTCCACATGTTTCCGGAACATTTGAAAGAGAGCTTATC 3283
QY 121 CAGTGTACAGATCCCTAATAAAGTGACATTCAGTGTAAATTTATTTTATTAATCTTTT 180
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Db 3464 CCTATGTATTATTTCAGAAATGAGCGGTGACATGCTACAGCATTACCTACCGGTACC 3523
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Qy 841 GGTGCTGTTGACTGGGTGATGATGAGTCTGTTTTGGCTTTTCACTTCATGTTAGTCTTA 900
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RESULT 7

ADM01584

ID ADM01584 standard; cDNA; 2829 BP.

XX

AC ADM01584;

XX

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DT 20-MAY-2004. (first entry)
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DE Human cDNA of the invention SEQ ID NO:269.
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KW ss; gene; human; gene therapy; diagnostic marker; pharmaceutical.
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OS Homo sapiens.
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PN BP1347046-A1.
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PD 24-SEP-2003.
XX
PF 12-APR-2002; 2002EP-00008400.
XX
PR 22-MAR-2002; 2002JP-00137785.
XX
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
XX
PI Isogai T, Sugiyama T, Otsuki T, Wakamatsu A, Sato H, Ishii S;
PI Yamamoto J, Isono Y, Hio Y, Otsuka K, Nagai K, Irie R, Tamechika I;
PI Seki N, Yoshikawa T, Otsuka M, Nagahari K, Masuho Y;
XX
WPI: 2003-723558/69.
DR P-PSDB; ADM04027.
XX
PT New polynucleotides and polypeptides are useful in gene therapy, for
PT developing a diagnostic marker or medicines for regulating their
PT expression and activity, or as a target of gene therapy.
XX
PS Claim 1; SEQ ID NO 269; 305pp; English.
XX
CC The invention relates to a novel human polynucleotide and the encoded
CC polypeptide. A polynucleotide of the invention ADM06202-ADM06773 is useful
CC therapy. An oligonucleotide of the invention ADM06202-ADM06773 is useful
CC as a primer for synthesizing the polynucleotide or as a probe for
CC detecting the polynucleotide. The polynucleotides ADM01316-ADM03758 are
CC useful in gene therapy, for developing a diagnostic marker or medicines
CC for regulating their expression and activity, or as a target of gene
CC therapy. The proteins ADM03759-ADM06201 encoded by the polynucleotides
CC are useful as pharmaceutical agents. The present sequence represents a
CC cDNA sequence of the invention.
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Query Match 99.9%; Score 1272.4; DB 11; Length 2829;
Best Local Similarity 99.9%; Pred. No. 4e-303;
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Db 1914 TCATTTACACCTCAAGGAGAGGATATAGTTTCTTGGCTTACAGACATTAATCTTCT 1973
QY 841 GGTGCTGTTGACTGGGTGATGATGAGTCTGTTTGGCTTTCACCTCATGTTAGTCTTA 900
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QY 901 GAGAAACAGGAAATATACGATGCTACAGAGTCTTTCGCAATCTGACGTGATAGA 960
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Db 2154 TTGACTTGGGAAGCACTCTCGATCTATTTCATGAAGGAATTCACAGCCATTAAT 2213
QY 1081 AGCGACTGTCTAGTCTTTTGACACAGCAATTCGACAGTCTTTTCAGAAAATGCAATTTA 1140
Db 2214 AGCGACTGTCTAGTCTTTTGACACAGCAATTCGACAGTCTTTTCAGAAAATGCAATTTA 2273
QY 1141 GGCATCAATGTAATTTTCCATGTTTGAATGGCAATCAAACTTTCTGGCCAGTGT 1200
Db 2274 GGCATCAATGTAATTTTCCATGTTTGAATGGCAATCAAACTTTCTGGCCAGTGT 2333
QY 1201 TTAACCTTCAGTTTTCAGAAAATAGGCAACCCATCTGTCGCCAATCAAACTTTT 1260
Db 2334 TTAACCTTCAGTTTTCAGAAAATAGGCAACCCATCTGTCGCCAATCAAACTTTT 2393
QY 1261 CGGTAGGTGGAAGC 1274
Db 2394 CGGTAGGTGGAAGC 2407

RESULT 8

AD534362

ID AD534362 standard; DNA; 2829 BP.

XX

AC AD534362;

XX

DT 02-DEC-2004 (first entry)

XX

DE POSH protein associated DNA #116.

XX ds; gene; cytostatic; neurotropic; neuroprotective; antiparkinsonian;
KW anticonvulsant; antiviral; neuroleptic; central nervous system;
KW POSH polypeptide; POSH-associated protein; POSH-AP; HERPUDI1;
KW Ubiquitin ligase; antiviral agent; anti-apoptotic agent;
KW anti-cancer agent; secretory pathway trafficking inhibitor;
KW neurological disorder progression disorder; Alzheimer's disease;
KW Parkinson's disease; Huntington's disease; schizophrenia;
KW Niemann-Pick's disease.
XX Homo sapiens.
OS WO2004078130-A2.
XX 16-SEP-2004.
PD 02-MAR-2004; 2004WO-US006308.
PF 03-MAR-2003; 2003US-0451437P.
XX 05-MAR-2003; 2003US-0452284P.
PR 19-MAR-2003; 2003US-0455760P.
PR 20-MAR-2003; 2003US-0456640P.
PR 03-APR-2003; 2003US-0460526P.
PR 04-APR-2003; 2003US-0460792P.
PR 21-APR-2003; 2003US-0464285P.
PR 09-MAY-2003; 2003US-0469462P.
PR 15-MAY-2003; 2003US-0471378P.
PR 20-MAY-2003; 2003US-0472327P.
PR 30-MAY-2003; 2003US-0474066P.
PR 03-JUN-2003; 2003US-0475825P.
PR 17-JUN-2003; 2003US-0479317P.
PR 19-JUN-2003; 2003US-0480215P.
PR 19-JUN-2003; 2003US-0480376P.
PR 08-AUG-2003; 2003US-0493860P.
PR 28-AUG-2003; 2003US-0498634P.
PR 16-SEP-2003; 2003US-0503931P.
PR 10-NOV-2003; 2003WO-US035712.
PR 05-FEB-2004; 2004WO-US003600.
PR 02-MAR-2004; 2004WO-US049896P.
XX (PROT-) PROTEOLOGICS INC.
XX Taglicht DN, Alroy I, Reiss Y, Yaar L, Ben-Avraham D, Tuvia S;
PI Greener T;
XX WPI; 2004-662346/64.
XX Isolated, purified or recombinant complex, useful for identifying an
PT antiviral, anti-apoptotic or anti-cancer, comprising POSH polypeptide and
PT POSH-associated protein (POSH-AP).
XX Disclosure; SEQ ID NO 126; 374pp; English.
XX The invention relates to an isolated, purified or recombinant complex (I)
CC comprising a POSH polypeptide and a POSH-associated protein (POSH-AP) (a
CC or HERPUDI1 and a Ubiquitin ligase (b). Methods using (I), (a) or (b) are
CC useful for identifying an agent that modulates an activity of a POSH
CC polypeptide or POSH-AP, for identifying an antiviral agent, an anti-
CC apoptotic agent, an anti-cancer agent, an agent that inhibits trafficking
CC of a protein through the secretory pathway, an agent that modulates a POSH
CC progression of a neurological disorder, an agent that modulates a POSH
CC function, an agent that modulates a HERPUDI1 function. The methods can be
CC used for treating a viral infection, for inhibiting an activity of a POSH
CC -AP in a cell, for treating a POSH-associated disease in a subject. The
CC POSH-associated disease is viral infection, POSH-associated cancer or
CC POSH-associated neurological disorder. The methods are useful for
CC POSH-associated neurological disorder. The methods are useful for
CC treating or preventing POSH-associated neurological disorder in a subject
CC e.g. Alzheimer's disease, Parkinson's disease, Huntington's disease,
CC schizophrenia, Niemann-Pick's disease. This sequence corresponds to a
CC nucleic acid of the invention.
XX Sequence 2829 BP; 756 A; 566 C; 553 G; 954 T; 0 U; 0 Other;

Query Match	99.9%;	Score	1272.4;	DB 13;	Length	2829;
Best Local Similarity	99.9%;	Pred. No.	4e-303;			
Matches 1273;	Conservative	0;	Mismatches	1;	Indels	0;
1	T T T C T T T A G T C T T T A T G T G C C A T T T C T A T T T T A G C A T T T A T T A T T C T A T G T A G C T A T C T A T G T A G T C T A T	60				
1134	T T T C T T T A G T G T T A T G G T C C A T T T C T A T T T T A G C A T T T A T T A T T C T A T G T A G C A T T A T T A T T C T A T G T A G T C T A T	1193				
61	C C A A A G A C G A T T A A G G G A G T T C C A C A T G T T T T C C G G A A C A T T T T G A A A G A G A G C T T A T C	120				
1194	C C A A A G A C G A T T A A G G G A G T T C C A C A T G T T T T C C G G A A C A T T T T G A A A G A G A G C T T A T C	1253				
121	C A G T G T A C A G A T C C T A A T A A A G T G C A C A T T C A G T G T A A T T T T T T T T T T T T A A T A T C T T T T	180				
1254	C A G T G T A C A G A T C C T A A T A A A G T G C A C A T T C A G T G T A A T T T T T T T T T T T T T T A A T A T C T T T T	1313				
181	T T A A T C C T A T T T T T C T C C T C T T T T G C T C A G T A A A T T T T G T A T G A A C T T T T A A A G A G A C T	240				
1314	T T A A T C C T A T T T T T C T C C T C T T T T G C T C A G T A A A T T T T G T A T G A A C T T T T A A A A G G A C T	1373				
241	T A T G G C A T G T A A A C A T T A T T A T A A G T A A A G T C A T G G T T A T A A T T A T T T T T C T C T C G C C T	300				
1374	T A T G G C A T G T A A A C A T T A T T A T A A G T A A A G T C A T G G T T A A T T A T T T T T C T C T C G C C T	1433				
301	C C T T A T G T A T T A T T T C A G A A A T A G A C C G T C A G A C T G C T A C A G A T T A C C T A C C G T A C C	360				
1434	C C T T A T G T A T T A T T T C A G A A A T A G A C C G T C A G A C T G C T A C A G A T T A C C T A C C G T A C C	1493				
361	T C G A A G T C C A C C A T C C C A G A G G T G C C T C C C T G A C T G C A C A A C T G C A A T C C A A C A A T	420				
1494	T C G A A G T C C A C C A T C C C A G A G G T G C C T C C C T G A C T G C A C A A C T G C A C A A T C C A A C A A T	1553				
421	G A C T T G G G G A G T C T T T T T T G A G T G T C C A G T C T G C T T T G A C T A T G T T G T T A C C G C C A T T C T T	480				
1554	G A C T T G G G G A G T C T T T T T T G A G T G T C C A G T C T G C T T T G A C T A T G T T G T T A C C G C C A T T C T T	1613				
481	C A A T G T C A G A T G G C C A T C T T T T T T T G A G A A C A T G T G C C C A A A G C T C A C A T G T T G T C C A	540				
1614	C A A T G T C A G A T G G C C A T C T T T T T T T G A G A A C A T G T G C C C A A A G C T C A C A T G T T G T C C A	1673				
541	A C T T G C C G G G C C C T T T G G G A T C C A A T C G C A A C T T G G C T A T G G A A A G T G G C T A A T T C A	600				
1674	A C T T G C C G G G C C C T T T G G G A T C C A A T C G C A A C T T G G C T A T G G A A A G T G G C T A A T T C A	1733				
601	G T A C T T T T C C C C T G T A A A T A T G C G T C T T T C T G A T G T G A A A T A A C T C T G C C A C A C A C A G A A	660				
1734	G T A C T T T T C C C C T G T A A A T A T G C G T C T T C T G A T G T G A A A T A A C T C T G C C A C A C A C A G A A	1793				
661	A A A G C A G A C C A T G A A G A G C T C T G T A G T T A A G G C C T T A T T C C T G C C G T G C C C T G G T G C T	720				
1794	A A A G C A G A C C A T G A A G A G C T C T G T A G T T A A G G C C T T A T T C C T G C C G T G C C C T G G T G C T	1853				
721	T C C T G T A A A T G G C A A G G C T C T C T G A T G C T G T A A T G C C C A T C T G A T G C A T C A G C A T A A G	780				
1854	T C C T G T A A A T G G C A A G G C T C T C T G A T G C T G T A A T G C C C A T C T G A T G C A T C A G C A T A A G	1913				
781	T C C A T T A C A A C C T A C G G A G A G A T A G T T T T T C T T G C T A C A G A C A T T A A T C T T C C T	840				
1914	T C C A T T A C A A C C T A C G G A G A G A T A G T T T T T C T T G C T A C A G A C A T T A A T C T T C C T	1973				
841	G G T G C T G T T G A C T G G G T G A T G A T G C A G T C C T G T T T T T G G C T T T C A C T T C A T G T T A G T C T T A	900				
1974	G G T G C T G T T G A C T G G G T G A T G A T G C A G T C C T G T T T T T G G C T T T C A C T T C A T G T T A G T C T T A	2033				
901	G A G A A A C A G G A A A A T A C A T G T G T C A C A G A G T T C T T C G C A A T C G T A C A G C T G A T A G G A	960				
2034	G A G A A A C A G G A A A A T A C A T G T G T C A C A G A G T T C T T C G C A A T C G T A C A G C T G A T A G G A	2093				
961	A C A C G C A A G A C G C T G A A A A T T T T T G C T T A C C G A C T T G A G C T T A A A T G T C A T A G C G C A G A	1020				
2094	A C A C G C A A G A C G C T G A A A A T T T T T G C T T A C C G A C T T G A G C T T A A A T G T C A T A G C G C A G A	2153				
1021	T T G A C T T G G G A A G C A C T C C T C G A T C T A T T C A T G A A G A A T T G C A A C A G A C C A T T A T G A A T	1080				

Db	2154	TTGACTTTGGGAAGCGACTCTCTCGATCTATTTCATGAGGAAATTGCAACAGCCATTATGAAT	2213
Qy	1081	AGCGACTGCTTAGTCTTTTGACACCCAGCATTTGCACAGCTTTTTCAGAAAAATGGCAATTTTA	1140
Db	2214	AGCGACTGCTTAGTCTTTTGACACCCAGCATTTGCACAGCTTTTTCAGAAAAATGGCAATTTTA	2273
Qy	1141	GGCATCAATGTAACTATTTCATGTGTGTAATGGCAATCAAAACATTTTCTGGCCAGTGT	1200
Db	2274	GGCATCAATGTAACTATTTCATGTGTGTAATGGCAATCAAAACATTTTCTGGCCAGTGT	2333
Qy	1201	TTAAACTTCAGTTTTCAGAAAAATAGGCACCCATCTGTCTGCAACCTTAAACTCTTTT	1260
Db	2334	TTAAACTTCAGTTTTCAGAAAAATAGGCACCCATCTGTCTGCAACCTTAAACTCTTTT	2393
Qy	1261	CGGTAGTGGGAAGC 1274	
Db	2394	CGGTAGTGGGAAGC 2407	
RESULT 9			
ADF81981/c			
ID	ADF81981 standard; DNA; 4090 BP.		
XX	AC		
XX	ADF81981;		
XX	AC		
DT	26-FEB-2004 (first entry)		
XX	Leukaemia-related DNA sequence #2537.		
DE	Leukaemia-related DNA sequence #2537.		
XX	Cytostatic; Gene therapy; leukaemia; ss.		
KW	Unidentified.		
OS	WO2003039443-A2.		
XX	15-MAY-2003.		
PN	04-NOV-2002; 2002WO-EP012303.		
XX	05-NOV-2001; 2001EP-00126244.		
XX	30-APR-2002; 2002EP-00009758.		
PR	(DEKR-) DEUT KREBSFORSCHUNGSZENTRUM.		
XX	(UYLU-) UNIV LUDWIG MAXIMILIANS.		
PA	(HAFE/) HAFERLACH T.		
PA	(SCHO/) SCHOCH C.		
XX	(KERN/) KERN W.		
XX	Haferlach T, Schoch C, Kern W, Kohlmann A, Schnittger S, Dugas M;		
PI	Ells R, Brors B, Mergenthaler S;		
XX	WPI; 2003-505037/47.		
DR	Determining the subtype of leukemia cells and whether a patient sample		
XX	contains leukemia cells or other cells, useful for treating leukemia,		
PT	comprises determining the expression profile of a group of markers in a		
PT	patient sample.		
XX	Disclosure; SEQ ID NO 2537; 2938pp; English.		
PS	The present invention relates to a method (M1) for determining the		
XX	subtype of leukaemia cells and whether a patient sample contains		
CC	leukaemia cells. The method comprises determining the expression profile		
CC	of a group of markers in a patient sample. The method is useful for		
CC	determining the presence of leukaemia cells, its types or subtypes, and		
CC	for the preparation of a medicament for treating leukaemia.		
XX	Sequence 4090 BP; 1233 A; 840 C; 768 G; 1189 T; 0 U; 60 Other;		
XX	Query Match 98.0%; Score 1249; DB 10; Length 4090;		
XX	Best Local Similarity 99.6%; Pred. No. 2.7e-297;		
XX	Matches 1271; Conservative 0; Mismatches 3; Indels 2; Gaps 2;		

CC The invention relates to a composition comprising a plurality of cDNAs
CC for detecting the altered expression of genes in an immunological
CC response. The invention also relates to a method of diagnosing or
CC monitoring the treatment of an immunopathological condition in a sample,
CC comprising obtaining nucleic acids from a sample, contacting the nucleic
CC acids of the sample with an array comprising the plurality of cDNAs under
CC conditions to form one or more hybridisation complexes, detecting the
CC hybridisation complexes and comparing the levels of the detected
CC hybridisation complexes with the level of hybridisation complexes
CC detected in a non-diseased sample, where an altered level of the detected
CC hybridisation complexes correlates with the presence of an
CC immunopathological condition. Also disclosed are an expression profile
CC comprising a microarray and a plurality of detectable complexes and a
CC method for identifying a plurality of polynucleotide probes. The cDNAs
CC are useful as hybridisable array elements in a microarray for monitoring
CC the expression of target polynucleotides. The microarray can be used in
CC the diagnosis of an immunopathology, such as Crohn's disease, asthma,
CC ulcerative colitis, hyperosinophilia, irritable bowel syndrome,
CC osteoarthritis, rheumatoid arthritis or acute monocytic leukaemia, and in
CC identifying agents for the treatment of the diseases. The microarray may
CC also be used in drug discovery and development, toxicological and
CC carcinogenicity studies, forensics or pharmacogenomics. The composition
CC may also be used in purification of a subpopulation of mRNAs, cDNAs or
CC genomic fragments. This sequence represents a human cDNA of the
CC invention. Note: The sequence data for this patent did not form part of
CC the printed specification but was obtained in electronic format directly
CC from USPTO at seqdata.uspto.gov/sequence.html.

XX SQ Sequence 2440 BP; 685 A; 463 C; 472 G; 817 T; 0 U; 3 Other;

Query Match 81.9%; Score 1042.8; DB 11; Length 2440;
Best Local Similarity 99.8%; Pred. No. 1.5e-246;
Matches 1044; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY	229	TTTTAAAGGACCTTATGGCATGTAACATTATTTATTAAGTAAGTCAATGTTATTAATT	288
DB	462	TTTTGGAAGGACCTTATGGCATGTAACATTATTTATTAAGTAAGTCAATGTTATTAATT	521
QY	289	TTTCTCTGCTCTTATGTTATTTATTTTCAAGTAAGTCAATGTTATTAATT	348
DB	522	TTTCTCTGCTCTTATGTTATTTATTTTCAAGTAAGTCAATGTTATTAATT	581
QY	349	CTTACCGGTACCTCGAAGTGTCCACCATCCAGAGGGTGCCTCCCTGAGTGGCAAACT	408
DB	582	CTTACCGGTACCTCGAAGTGTCCACCATCCAGAGGGTGCCTCCCTGAGTGGCAAACT	641
QY	409	GCATCCCAACAATGACTTGGCGAGTCTTTTGTAGTTCAGTCTGCTTGTGATGTTA	468
DB	642	GCATCCCAACAATGACTTGGCGAGTCTTTTGTAGTTCAGTCTGCTTGTGATGTTA	701
QY	469	CCGCCCAATCTTCAATGTCAGAGTGGCCATCTTTGTTAGTCAACTGTCCGCCAAAGCTC	528
DB	702	CCGCCCAATCTTCAATGTCAGAGTGGCCATCTTTGTTAGTCAACTGTCCGCCAAAGCTC	761
QY	529	ACATGTTGTCCAACTTCCCGGGGCCCTTTGGGATCCATTCGCCAACTTGGCTATGGAGAA	588
DB	762	ACATGTTGTCCAACTTCCCGGGGCCCTTTGGGATCCATTCGCCAACTTGGCTATGGAGAA	821
QY	589	GTGGCTAATTCAGTACTTTTCCCTCTTAATATGCGTCTTCTGGATGTGAATACTCTG	648
DB	822	GTGGCTAATTCAGTACTTTTCCCTCTTAATATGCGTCTTCTGGATGTGAATACTCTG	881
QY	649	CCACACAGAAAAGCAGACCATGAGAGCTCTGTGAGTGTAGGCTTATTCCTGTCCG	708
DB	882	CCACACAGAAAAGCAGACCATGAGAGCTCTGTGAGTGTAGGCTTATTCCTGTCCG	941
QY	709	TGCCCTGTGCTCTCTGTAAATGCAAGGCTCTCTGGATGTCTTAATGCCCCATCTGATG	768
DB	942	TGCCCTGTGCTCTCTGTAAATGCAAGGCTCTCTGGATGTCTTAATGCCCCATCTGATG	1001
QY	769	CATCAGCATAGTCCATTTACAACTTACAGGAGGATATAGTTTTCTTGTCTACAGAC	828
DB	1002	CATCAGCATAGTCCATTTACAACTTACAGGAGGATATAGTTTTCTTGTCTACAGAC	1061

QY	829	ATTAAATCTTCTGGTCTGTTGACTGGGTGATGATGAGTCTGCTGTTTGGCTTTCACCTC	888
DB	1062	ATTAAATCTTCTGGTCTGTTGACTGGGTGATGATGAGTCTGCTGTTTGGCTTTCACCTC	1121
QY	889	ATGTTAGTCTTAGAGAAACAGGAAAATAGATGGTCCACGAGTCTTTCGCAATCGTA	948
DB	1122	ATGTTAGTCTTAGAGAAACAGGAAAATAGATGGTCCACGAGTCTTTCGCAATCGTA	1181
QY	949	CAGCTGATAGAAACACCAAGCAGCTGAAAATTTTCTTACCGACTTGAGCTAAATGGT	1008
DB	1182	CAGCTGATAGAAACACCAAGCAGCTGAAAATTTTCTTACCGACTTGAGCTAAATGGT	1241
QY	1009	CATAGGCGACCATTTGACTTTGGGAGCGACTCTCTCGATCTATTATGAAGGAATTCGAACA	1068
DB	1242	CATAGGCGACCATTTGACTTTGGGAGCGACTCTCTCGATCTATTATGAAGGAATTCGAACA	1301
QY	1069	GCCATTATGAATAGCAGTCTGCTAGTCTTTGACACACGAGTTCACAGCTTTTTCGAGAA	1128
DB	1302	GCCATTATGAATAGCAGTCTGCTAGTCTTTGACACACGAGTTCACAGCTTTTTCGAGAA	1361
QY	1129	AATGCAATTTAGCATCAATGTAATTTTCCATGTTGAAATGGCAATCAACATTT	1188
DB	1362	AATGCAATTTAGCATCAATGTAATTTTCCATGTTGAAATGGCAATCAACATTT	1421
QY	1189	TCTGCGCAGTCTTTAAACCTTCAGTTTCACAGAAAATGAAGCACCATCTCTCTGCCAAC	1248
DB	1422	TCTGCGCAGTCTTTAAACCTTCAGTTTCACAGAAAATGAAGCACCATCTCTCTGCCAAC	1481
QY	1249	CTAAACCTTTCGGTAGGTGGAAGC	1274
DB	1482	CTAAACCTTTCGGTAGGTGGAAGC	1507

RESULT 12

ADSS34365
ID ADS34365 standard; DNA; 1540 BP.

XX	AC	ADS34365;
XX	DT	02-DEC-2004 (first entry)
XX	DE	POSH protein associated DNA #119.
XX	KW	ds; gene; cytostatic; neurotropic; neuroprotective; antiparkinsonian;
XX	KW	anticonvulsant; antiviral; neuroleptic; central nervous system;
XX	KW	POSH polypeptide; POSH-associated protein; POSH-AP; HERPUD1;
XX	KW	Ubiquitin ligase; antiviral agent; anti-apoptotic agent;
XX	KW	anti-cancer agent; secretory pathway trafficking inhibitor;
XX	KW	neurological disorder progression disorder; Alzheimer's disease;
XX	KW	Parkinson's disease; Huntington's disease; schizophrenia;
XX	OS	Niemann-Pick's disease.
XX	OS	Homo sapiens.
XX	PN	WO2004078130-A2.
XX	PD	16-SEP-2004.
XX	PF	02-MAR-2004; 2004WO-US006308.
XX	PR	03-MAR-2003; 2003US-0451437P.
XX	PR	05-MAR-2003; 2003US-0452284P.
XX	PR	19-MAR-2003; 2003US-0455760P.
XX	PR	20-MAR-2003; 2003US-0456640P.
XX	PR	03-APR-2003; 2003US-0460526P.
XX	PR	04-APR-2003; 2003US-0460792P.
XX	PR	21-APR-2003; 2003US-0464285P.
XX	PR	09-MAY-2003; 2003US-0469462P.
XX	PR	15-MAY-2003; 2003US-0471378P.
XX	PR	20-MAY-2003; 2003US-0472327P.
XX	PR	30-MAY-2003; 2003US-0474706P.
XX	PR	03-JUN-2003; 2003US-0475825P.

[illegible]

QY	558	GGGATCCATTCCGCAACTTGGCTATATGAGAAAGTGGCTAAATTCAGTACTTTTCCCTCTGTAA	617
Db	696	GGGATCCATTCCGCAACTTGGCTATATGAGAAAGTGGCTAAATTCAGTACTTTTCCCTCTGTAA	755
QY	618	ATATGCGTCTTCTGGATGTGAATTAATCTGCGCACACACAGAAAAGCAGCACCATGAAGA	677
Db	756	ATATGCGTCTTCTGGATGTGAATTAATCTGCGCACACACAGAAAAGCAGCACCATGAAGA	815
QY	678	GCTCTCTGAGTTTAGGCCCTTAATTCCTGTCCGTGCCCTGGTCTTCCTGTTAAATGGCAAGG	737
Db	816	GCTCTGAGTTTAGGCCCTTAATTCCTGTCCGTGCCCTGGTCTTCCTGTTAAATGGCAAGG	875
QY	738	CTCTCTGATGCTGTGAATGCCCCATCTGATGCAATCAGCATPAAGTCCATTACAACCTTACA	797
Db	876	CTCTCTGATGCTGTGAATGCCCCATCTGATGCAATCAGCATPAAGTCCATTACAACCTTACA	935
QY	798	GGGAGAGGATATAGTTTTTCTTCCTACAGACATTAATCTTCCTGGTGTCTTCGACTGGGT	857
Db	936	GGGAGAGGATATAGTTTTTCTTCCTACAGACATTAATCTTCCTGGTGTCTTCGACTGGGT	995
QY	858	GATGATGCAGTCTCTGTTTTGGCTTTCACCTTCACTGTTAGTCTTTAGAGAAAACAGAAAATA	917
Db	996	GATGATGCAGTCTCTGTTTTGGCTTTCACCTTCACTGTTAGTCTTTAGAGAAAACAGAAAATA	1055
QY	918	CGATGCTCACCAGCAGTCTTCCTGCAATCGTACAGCTGATAGGAACACGCAAGCAAGCTGA	977
Db	1056	CGATGCTCACCAGCAGTCTTCCTGCAATCGTACAGCTGATAGGAACACGCAAGCAAGCTGA	1115
QY	978	AAATTTTGGTTACCGACTTTGAGCTAAATGGTCAATAGCGCAGCATTCGACTTGGGAAGCGAC	1037
Db	1116	AAATTTTGGTTACCGACTTTGAGCTAAATGGTCAATAGCGCAGCATTCGACTTGGGAAGCGAC	1175
QY	1038	TCTCTGATCTATTTCATGAAGGAATTGCAACAGCCATTATGAATPAGCGACTGCTAGTCTTT	1097
Db	1176	TCTCTGATCTATTTCATGAAGGAATTGCAACAGCCATTATGAATPAGCGACTGCTAGTCTTT	1235
QY	1098	TGACACCCAGCATTCGACACGCTTTTTCGAGAAATGGCAATTTAGGCATCAATCTAACTAT	1157
Db	1236	TGACACCCAGCATTCGACACGCTTTTTCGAGAAATGGCAATTTAGGCATCAATCTAACTAT	1295
QY	1158	TTCCATGTGTGAAATGGCAATCAAAATTTCTGGCCAGTGTTTAAAACTTCAGTTTCA	1217
Db	1296	TTCCATGTGTGAAATGGCAATCAAAATTTCTGGCCAGTGTTTAAAACTTCAGTTTCA	1355
QY	1218	CAGAAAATPAGGCACCCATCTGTCTGCCAACCTTAAATCTTTTCGGTAGTGTGAAGC	1274
Db	1356	CAGAAAATPAGGCACCCATCTGTCTGCCAACCTTAAATCTTTTCGGTAGTGTGAAGC	1412
RESULT 15			
ADS34363			
ADS34363 standard; DNA; 1886 BP.			
XX	ADS34363;		
XX	02-DEC-2004 (first entry)		
DT	POSH protein associated DNA #117.		
XX	ds; gene; cytostatic; nootropic; neuroprotective; antiparkinsonian;		
XX	anticouplant; antiviral; neuroleptic; central nervous system;		
KW	POSH polypeptide; POSH-associated protein; POSH-AP; HRPUDI;		
KW	Ubiquitin ligase; antiviral agent; anti-apoptotic agent;		
KW	anti-cancer agent; secretory pathway trafficking inhibitor;		
KW	neurological disorder progression disorder; Alzheimer's disease;		
KW	Parkinson's disease; Huntington's disease; schizophrenia;		
XX	Niemann-Pick's disease.		
OS	Homo sapiens.		
XX	WO2004078130-A2.		
PN			
XX			

Mon Apr 25 11:06:39 2005

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XX 02-MAR-2004; 2004WO-US006308.
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XX 03-MAR-2003; 2003US-0451437P.
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XX 10-NOV-2003; 2003WO-US035712.
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XX 05-FEB-2004; 2004WO-US003600.
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XX 02-MAR-2004; 2004US-0549896P.
XX PR
XX (PROF-) PROTEOLOGICS INC.
XX PI
XX Taglicht DN, Alroy I, Reiss Y, Yaar L, Ben-Avraham D, Tuvia S;
XX PI Greener T;
XX WPI; 2004-662346/64.
XX DR
XX Isolated, purified or recombinant complex, useful for identifying an
XX PT antiviral, anti-apoptotic or anti-cancer, comprising POSH polypeptide and
XX PT POSH-associated protein (POSH-AP).
XX PS
XX Disclosure; SEQ ID NO 127; 374bp; English.
XX CC
XX The invention relates to an isolated, purified or recombinant complex (I)
XX CC comprising a POSH polypeptide and a POSH-associated protein (POSH-AP) (a)
XX CC or HERPUDI and a ubiquitin ligase (b). Methods using (I), (a) or (b) are
XX CC useful for identifying an agent that modulates an activity of a POSH
XX CC polypeptide or POSH-AP, for identifying an antiviral agent, an anti-
XX CC apoptotic agent, an anti-cancer agent, an agent that inhibits trafficking
XX CC of a protein through the secretory pathway, an agent that inhibits the
XX CC progression of a neurological disorder, an agent that modulates a POSH
XX CC function, an agent that modulates a HERPUDI function. The methods can be
XX CC used for treating a viral infection, for inhibiting an activity of a POSH
XX CC -AP in a cell, for treating a POSH-associated disease in a subject. The
XX CC POSH-associated disease is viral infection, POSH-associated cancer or
XX CC POSH-associated neurological disorder. The methods are useful for
XX CC treating or preventing POSH-associated neurological disorder in a subject
XX CC e.g. Alzheimer's disease, Parkinson's disease, Huntington's disease,
XX CC schizophrenia, Niemann-Pick's disease. This sequence corresponds to a
XX CC nucleic acid of the invention.
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Search completed: April 24, 2005, 20:02:09
Job time : 767 secs

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3	1274	100.0	2924	6	CQ491092	CQ491092 Sequence
4	1274	100.0	2924	6	CQ493590	CQ493590 Sequence
5	1274	100.0	2924	6	CQ496955	CQ496955 Sequence
6	1274	100.0	31705	9	HS400626	AJ400626 Homo sapi
7	1274	100.0	173304	9	AC023818	AC023818 Homo sapi
8	1272.4	99.9	2829	6	AX833145	AX833145 Sequence
9	1272.4	99.9	2829	6	AK094663	AK094663 Homo sapi
10	1270.8	99.7	2972	9	HS8807215	EX647084 Homo sapi
c 11	1249	98.0	4090	6	AX780380	AX780380 Sequence
c 12	1104	86.7	2128	9	AX056031	AX056031 Homo sapi
13	1042.8	81.9	2440	6	AR380043	AR380043 Sequence
14	958	75.2	1540	9	BC035562	BC035562 Homo sapi
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16	958	75.2	2048	9	HSU76247	U76247 Human hSIAM
17	957	75.1	2454	9	BC042550	BC042550 Homo sapi
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VERSION	AX058082.1	GI:12310662				
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SOURCE	Homo sapiens					
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REFERENCE	1. Reed, J.C. and Matsuzawa, S.I.					
AUTHORS	Nucleic acid encoding proteins involved in protein degradation,					
TITLE	products and methods related thereto					
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RESULT 3
LOCUS CO491092
DEFINITION Sequence 22959 from Patent WO0160860.
ACCESSION CO491092
VERSION CO491092.1 GI:41456711
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS Schlegel, R., Endege, W.O. and Monahan, J.E.
TITLE Genes differentially expressed in human prostate cancer and their use
JOURNAL Patent: WO 0160860-A 22959 23-AUG-2001;
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LOCUS CO493590 2924 bp DNA linear PAT 30-JAN-2004
DEFINITION Sequence 25457 from Patent WO0160860.
ACCESSION CO493590
VERSION CO493590.1 GI:41459209
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Schlegel, R., Endege, W.O. and Monahan, J.E.
TITLE Genes differentially expressed in human prostate cancer and their use
JOURNAL Patent: WO 0160860-A 25457 23-AUG-2001;
Millennium Predictive Medicine, Inc. (US)
FEATURES
source Location/Qualifiers
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Query Match 100.0%; Score 1274; DB 6; Length 2924;
Best Local Similarity 100.0%; Pred. NO. 5.9e-271; Mismatches 0; Indels 0; Gaps 0;
Matches 1274; Conservative 0;

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RESULT 5
LOCUS CO496955 2924 bp DNA linear PAT 30-JAN-2004
DEFINITION Sequence 28822 from Patent WO0160860.
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ACCESSION CQ496955
VERSION CQ496955.1 GI:41462591
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS Schlegel, R., Endege, W.O. and Monahan, J.E.
TITLE Genes differentially expressed in human prostate cancer and their use
JOURNAL Patent: WO 0160860-A 28822 23-AUG-2001;
Millennium Predictive Medicine, Inc. (US)
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Best Local Similarity 100.0%; Pred. No. 5.9e-271;
Matches 1274; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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RESULT 6
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LOCUS Homo sapiens SIAH1 gene, exons 1-2.
DEFINITION Homo sapiens SIAH1 gene, exons 1-2.
ACCESSION AJ400626
VERSION AJ400626.1 GI:13539602
KEYWORDS siah1 gene.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Medhioub, M., Muchardt, C., Tubacher, E., Giudicelli, C.,
Hors-Cayla, M.C. and Thomas, G.
TITLE Down regulation of the TATA-less and GC-rich SIAH1 promoter by TP53
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 31705)
AUTHORS Medhioub, M.
TITLE Direct Submission
JOURNAL Submitted (11-APR-2000) Medhioub M., Fondation Jean DAUSSET. CEPH,
27, rue Juliette Dodu, Paris 75010, FRANCE
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DEFINITION      AC023818
ACCESSION      AC023818.5      GI:40556309
VERSION      HTG.
KEYWORDS      Homo sapiens (human)
SOURCE      Homo sapiens
ORGANISM      Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE      1 (bases 1 to 173304)
AUTHORS      DOE Joint Genome Institute, Stanford Human Genome Center and Los
TITLE      Alamos National Laboratory.
JOURNAL      Direct Submission
REFERENCE      2 (bases 1 to 173304)
AUTHORS      DOE Joint Genome Institute.
TITLE      Direct Submission
JOURNAL      Submitted (18-FEB-2000) Production Sequencing Facility, DOE Joint
REFERENCE      3 (bases 1 to 173304)
AUTHORS      DOE Joint Genome Institute.
TITLE      Direct Submission
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JOURNAL Submitted (03-MAY-2002) Production Sequencing Facility, DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
REFERENCE 4 (bases 1 to 173304)
AUTHORS Alamos National Genome Institute, Stanford Human Genome Center and Los Alamos National Laboratory.
TITLE Direct Submission
JOURNAL Submitted (03-JAN-2004) DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
COMMENT On Jan 3, 2004 this sequence version replaced gi:20429291.
Draft Sequence Produced by DOE Joint Genome Institute
www.jgi.doe.gov
Finishing Completed at Stanford Human Genome Center and Los Alamos National Laboratory
www.shgc.stanford.edu
Quality: Phrap Quality >=40 100% of Sequence;
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Best Local Similarity 100.0%; Pred. No. 4,7e-271;
Matches 1274; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 8
AX833145
LOCUS AX833145 2829 bp DNA linear PAT 15-DEC-2003
DEFINITION Sequence 269 from Patent EPI347046.
ACCESSION AX833145
VERSION AX833145.1 GI:39919280
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Isogai, T., Sugiyama, T., Otsuki, T., Wakamatsu, A., Sato, H., Ishii, S., Yamamoto, J. I., Isono, Y., Hio, Y., Otsuka, K., Nagai, K., Irie, R., Tamechika, I., Seki, N., Yoshikawa, T., Otsuka, M., Nagahari, K. and Masuno, Y.
TITLE Full-length cDNA sequences
JOURNAL Patent: EP 1347046-A 269 24-SEP-2003;
RESEARCH Association for Biotechnology (JP)
FEATURES
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Best Local Similarity 99.9%; Pred. No. 1.3e-270;

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121	Qy	CAGTGTACAGATCCCTAATAAGTGACATTCAGTGTAAATTTTATTTTAAATATCTTTT	180					
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181	Qy	TTAATCCTATTTTCTTCCTCTTTTGGCTCAGTAAATTTTGTATGAACTTTAAAAGGACT	240					
1344	Db	TTAATCCTATTTTCTTCCTCTTTTGGCTCAGTAAATTTTGTATGAACTTTAAAAGGACT	1373					
241	Qy	TATGGCATGTAAACATTTATTAATAAGTAAGTCATGGTTATAATTAATTTTCTCCCTGCCT	300					
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301	Qy	CCCTTATGTAATTTATTTTCAGAAATAGCCGTCAGACTGTCTACAGCATTTACCTACCGGTACC	360					
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Nagahari, K., Masuho, Y., Nagai, K. and Isogai, T.
NEDO human cDNA sequencing project
Unpublished
3 (bases 1 to 2829)
Isogai, T. and Yamamoto, J.
Direct Submission
Submitted (04-JUL-2002) Takao Isogai, FLJ Project (HRI Team); 2-6-7
Kazusa-Kamatari, Kisarazu, Chiba 292-0812, Japan
(E-mail: genomics@hri.co.jp, Tel: 81-438-52-3975, Fax: 81-438-52-3986)
NEDO human cDNA sequencing project supported by Ministry of
Economy, Trade and Industry of Japan; cDNA full insert sequencing:
Research Association for Biotechnology (RAB); cDNA library
construction: Helix Research Institute (HRI) (supported by Japan
Key Technology Center etc.); 5'- & 3'-end one pass sequencing: RAB,
HRI, and Biotechnology Center, National Institute of Technology and
Evaluation; clone selection for full insert sequencing: HRI and
RAB; annotation: HRI and RAB.
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ORIGIN
Query Match 99.9%; Score 1272.4; DB 9; Length 2829;
Best Local Similarity 99.9%; Pred. No. 1.3e-270;
Matches 1273; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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RESULT 10
HSM807215
LOCUS
DEFINITION
HSM807215 Homo sapiens mRNA; cDNA DKFZp686L1897 (from clone DKFZp686L1897); complete cds.
ACCESSION
BX647064
VERSION
BX647064.1 GI:34366097
KEYWORDS
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 2972)
AUTHORS
Koehler, K., Beyer, A., Mewes, H.W., Weil, B., Amid, C., Oeanger, A.,
Fobo, G., Han, M. and Wiemann, S.
CONSTRM
The German Human cDNA Consortium
DIRECT
Submitted (26-AUG-2003) MIPS, Ingolstaedter Landstr.1, D-85764
JOURNAL
Neuberberg, GERMANY
COMMENT
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;
Sequenced by BMFZ (Biomedical Research Center at the
Heinrich-Heine-University, Duesseeldorf/Germany) within the cDNA
sequencing consortium of the German Genome Project. This clone
(DKFZp686L1897) is available at the RZPD in Berlin. Please contact

the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
Berlin-Charlottenburg, GERMANY; Email: clone@rzd.de Further
information about the clone and the sequencing project is available
at <http://mips.gsf.de/proj/cDNA/>.

FEATURES

Location/Qualifiers
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polyA_site

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Best Local Similarity 99.8%; Pred. No. 3e-270;
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RESULT 11

AX780380/c
LOCUS 4090 bp DNA linear PAT 14-JUL-2003
DEFINITION Sequence 2537 from Patent WO03039443.
ACCESSION AX780380
VERSION AX780380.1 GI:32697374

KEYWORDS

Source

ORGANISM

Homo sapiens (human)

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1

Haferlach, T.; Schoch, C.; Kern, W.; Kohlmann, A.; Schnittger, S.,

Dugas, M.; Ellis, R.; Brors, B. and Mergenthaler, S.

Novel genetic markers for leukemias

Patent: WO 03039443-A 2537 15-MAY-2003;

Deutsches Krebsforschungszentrum (DKFZ);

Ludwig-Maximilians-Universitaet Muenchen (LMU);

Haferlach, Torsten,

PD Dr. Dr. (DE) ; Schoch, Claudia (DE) ; Kern, Wolfgang (DE)

FEATURES

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Query Match 98.0%; Score 1249; DB 6; Length 4090;
Best Local Similarity 99.6%; Pred. No. 1.9e-265;
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VERSION AK056051.1 GI:16551141
KEYWORDS oligo capping; fis (full insert sequence).
SOURCE Homo sapiens
ORGANISM Homo sapiens (human)

REFERENCE
1 Ota, T., Suzuki, Y., Nishikawa, T., Otsuki, T., Sugiyama, T., Irie, R., Wakamatsu, A., Hayashi, K., Sato, H., Nagai, K., Kimura, K., Makita, H., Sekine, M., Ohyashi, M., Nishi, T., Shibahara, T., Tanaka, T., Ishii, S., Yamamoto, J., Saito, K., Kawai, Y., Isono, Y., Nakamura, Y., Nagahari, K., Murakami, K., Yasuda, T., Iwayanagi, T., Wagatsuma, M., Shiratori, A., Sudo, H., Hosoiri, T., Kaku, Y., Kodaira, H., Kondo, H., Sugawara, M., Takahashi, M., Kanda, K., Yokoi, T., Furuya, T., Kikkawa, E., Omura, Y., Abe, K., Kamihara, K., Katsuta, N., Sato, K., Tanikawa, M., Yamazaki, M., Ninomiya, K., Ishibashi, T., Yamashita, H., Murakawa, K., Fujimori, K., Tanai, H., Kimata, M., Watanabe, M., Hiraoka, S., Chiba, Y., Ishida, S., Ono, Y., Takiguchi, S., Watanabe, S., Yosida, M., Hotuta, T., Kusano, J., Kanehori, K., Takahashi-Fujii, A., Hara, H., Tanase, T., Nomura, Y., Togiya, S., Komai, F., Hara, R., Takeuchi, K., Arita, M., Imose, N., Musashino, K., Yuuki, H., Oshima, A., Sasaki, N., Aotsuka, S., Yoshioka, Y., Matsunawa, H., Ichihara, T., Shiohata, N., Sano, S., Moriya, S., Momiyama, H., Satoh, N., Takami, S., Terashima, Y., Suzuki, O., Nakagawa, S., Senoh, A., Mizoguchi, H., Goto, Y., Shimizu, P., Wakebe, H., Hishigaki, H., Watanabe, T., Sugiyama, A., Takemoto, M., Kawakami, B., Yamazaki, M., Watanabe, K., Kumagai, A., Itakura, S., Fukuzumi, Y., Fujimori, Y., Komiyama, M., Tashiro, H., Tanigami, A., Fujiwara, T., Ono, T., Yamada, K., Fujii, Y., Ozaki, K., Hiroao, M., Ohmori, Y., Kawabata, A., Hiki, T., Kobatake, N., Inagaki, H., Ikema, Y., Okamoto, S., Okitani, R., Kawakami, T., Noguchi, S., Itoh, T., Shigetani, K., Senba, T., Matsumura, K., Nakajima, Y., Mizuno, T., Morinaga, M., Sasaki, M., Togashi, T., Oyama, M., Hata, H., Watanabe, M., Komatsu, T., Mizushima-Sugano, J., Satoh, T., Shirai, N., Takahashi, Y., Nakagawa, K., Okumura, K., Nagase, T., Nomura, Y., Kikuchi, H., Masuho, Y., Yamashita, R., Nakai, K., Yada, T., Nakamura, Y., Ohara, O., Isogai, T. and Sugano, S. Complete sequencing and characterization of 21,243 full-length human cDNAs
Nat. Genet. 36 (1), 40-45 (2004)
JOURNAL 14702039
PUBMED

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COMMENT
FEATURES
source

BC035562 1540 bp mRNA linear PRI 02-JAN-2004
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BC035562.1 GI:23274141
MGC.
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1 (bases 1 to 1540)
Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G.,
Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D.,
Altschul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.P., Bhat,N.K.,
Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Hsieh,F.,
Diachenko,L., Marusina,K., Farmer,A.A., Rubin,G.M., Hong,L.,
Sapleton,M., Soares,M.B., Bonaldo,M.F., Casavant,T.L.,
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Abramson,R.D., Mullaby,S.J., Bosak,S.A., McEwan,P.J.,
McKernan,K.J., Malek,J.A., Gunaratne,P.H., Richards,S.,
Worley,K.C., Hale,S., Garcia,A.M., Gay,L.J., Hulyk,S.W.,
Vitaloni,D.K., Muzny,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A.,
Fahy,J., Helton,E., Kettman,M., Madan,A., Rodriguez,S.,
Sanchez,A., Whiting,M., Madan,A., Young,A.C., Shevchenko,Y.,
Bouffard,G.G., Blakesley,R.W., Touchman,J.W., Green,E.D.,
Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M.,
Butterfield,Y.S., Krzywinski,M.I., Skalska,U., Smalins,D.E.,
Scherer,A., Schein,J.E., Jones,S.J. and Marra,M.A.
Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
12477932
2 (bases 1 to 1540)
Strausberg,R.
Direct Submission
Submitted (31-JUL-2002) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
USA
NIH-MGC Project URL: <http://mgc.nci.nih.gov>
Contact: MGC help desk
Email: cgabbs@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: National Institutes of Health Intramural
Sequencing Center (NISC),
Gaithersburg, Maryland;
Web site: <http://www.nisc.nih.gov/>
Contact: nisc_mgc@hgrl.nih.gov
Ahter,N., Ayale,K., Beckstrom-Sternberg,S.M., Benjamin,B.,
Blakesley,R.W., Bouffard,G.G., Breen,K., Brinkley,C., Brooks,S.,
Dietrich,N.L., Granite,S., Guan,X., Gupta,J., Haghighi,P.,
Hansen,N., Ho,S.-L., Karlins,E., Kwong,P., Laric,P., Legaspi,R.,
Maduro,Q.L., Masello,C., Maskeri,B., Mastrian,S.D., McCloskey,J.C.,
McDowell,J., Pearson,R., Stantripop,S., Thomas,P.J., Touchman,J.W.,
Tsurgren,C., Vogt,J.D., Walker,M.A., Wetherby,K.D., Wiggins,L.,
Young,A., Zhang,L.-H. and Green,E.D.
Clone distribution: MGC clone distribution information can be found
through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
Series: IRAC Plate: 64 Row: 0 Column: 8
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VERSION																				
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SOURCE																				
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ORGANISM																				
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.																				
1																				
REFERENCE																				
AUTHORS																				
TITLE																				
Venter, C.J., Adams, M.C., Li, P.W. and Myers, E.W.																				
Kits, such as nucleic acid arrays, comprising a majority of																				
human exons or transcripts, for detecting expression and other uses																				
thereof																				
Patent: WO 02068579-A 5493 06-SEP-2002;																				
JOURNAL																				

FEATURES PE Corporation (NY) (US)
Location/Qualifiers
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ORIGIN

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: April 24, 2005, 19:43:00 ; Search time 4597 Seconds
(without alignments)
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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

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- 2: gb_est2:*
- 3: gb_hic:*
- 4: gb_est3:*
- 5: gb_est4:*
- 6: gb_est5:*
- 7: gb_est6:*
- 8: gb_gse1:*
- 9: gb_gse2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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3	958	75.2	1857	3	CR614925
4	894	70.2	1287	3	CR598465
5	849	66.6	849	9	AY402255
6	843.2	66.2	849	9	AY402256
7	832.4	65.3	921	5	EX355841
8	811	63.7	859	5	EX355841
9	749.8	58.9	849	9	AY402257
10	749.2	58.8	824	4	RG619351
11	748.8	58.8	779	1	AI936347
12	747.4	58.7	778	1	AI971258
13	733	57.5	872	5	EX448317
14	719	56.4	785	5	EX384656
15	708.8	55.6	852	5	EX463976
16	699.6	54.9	769	5	EX097203
17	693.6	54.4	714	5	BQ447177
18	686.2	53.9	890	7	CF551876
19	685	53.8	1576	3	CR593197
20	682.4	53.6	693	5	BU662334
21	680.2	53.4	1058	5	EX356371
22	656.6	51.5	848	5	BU614872
23	650.8	51.1	812	1	BU119916
24	645.8	50.7	649	2	BF446537

25	641.4	50.3	647	2	BES03207
26	640.6	50.3	800	4	BI836179
27	631.8	49.6	637	1	AI681134
28	627.4	49.2	647	2	BES02849
29	622	48.8	622	7	CV030563
30	621.8	48.8	715	5	EX459079
31	620.6	48.7	957	5	EX372197
32	620.4	48.7	953	6	CA980024
33	610.8	47.9	842	5	EX459114
34	606.6	47.6	853	4	BG436513
35	594.6	46.7	608	1	AI698102
36	590	46.3	735	4	BI560892
37	587.4	46.1	864	4	BG489183
38	586.2	46.0	716	5	BU260826
39	585.2	45.9	658	4	BG537816
40	582.8	45.7	902	4	BI763325
41	580.2	45.5	734	1	AUI138740
42	575	45.1	1025	5	EX366403
43	571.2	44.8	767	4	BG435333
44	569.6	44.7	976	5	BU191771
45	562.4	44.1	894	2	BF573693

ALIGNMENTS

RESULT 1
LOCUS U70056 1221 bp mRNA linear EST 27-OCT-1999
DEFINITION U70056 Soares infant brain INIB Homo sapiens cDNA clone 25050, mRNA sequence.
ACCESSION U70056
VERSION U70056.1 GI:2731404
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
AUTHORS Volorio, S., Simon, G., Repetto, M., Cucciarini, M., Banfi, S., Borgani, G., Ballabio, A. and Zollo, M.
TITLE Sequencing analysis of forty-eight human image cDNA clones similar to drosophila mutant protein
JOURNAL DNA Seq. 9 (5-6), 307-315 (1998)
MEDLINE 99452388
PubMed 10524757
COMMENT Contact: Zollo, Massimo
Telethon Institute of Genetics and Medicine
Via Olgettina 58, Milan, MI 20132, Italy
Email: zollo@tigem.it.

FEATURES

source
Location/Qualifiers
1..1221
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/map="16q12.1-q13"
/clone="25050"
/sex="female"
/dev_stage="73 days post natal"
/lab_host="DH10B (ampicillin resistant)"
/clone_lib="Soares infant brain INIB"
/note="Organ: whole brain; Vector: Lafmid BA; Site: 1: Not I; Site 2: Hind III; 1st strand cDNA was primed with a Not I - oligo (dT) primer [5', RACTGGAGATTCGCCGCCGAGCAATTTTTTTTTTTT 3']; double-stranded cDNA was ligated to Hind III adaptors (pharmacia), digested with Not I and directionally cloned into the Not I and Hind III sites of the Lafmid BA vector. Library went through one round of normalization. Library constructed by Bento Soares and M.Fatima Bonaldo."

ORIGIN

Query Match 83.4%; Score 1062; DB 7; Length 1221;

		Best Local Similarity	100.0%;	Pred. No. 2.5e-248;	Matches 1062; Conservative	0;	Mismatches	0;	Indels	0;	Gaps	0;
Yy	213	AAATTTTGTATGAACCTTTAAAAGGACTTATGGCATGTAAACATTATTTATAAAGTAAGT	272									
Dd	1	AAATTTTGTATGAACCTTTAAAAGGACTTATGGCATGTAAAACAITATTTATAAAGTAAGT	60									
Yy	273	CATGGTTATAATATTTTTTCCTCGCCCTCCTTAGTGATTTATTTTCAGAAAAAGCCGCACA	332									
Dd	61	CATGGTTATAATATTTTTTCCTCGCCCTCCTTAGTGATTTATTTTCAGAAAAAGCCGCACA	120									
Yy	333	GACTGCTACAGCATTTACCCTACCGGTACCCTCGAAGTGTCACCAATCCCAGAGGGTGCCCTGC	392									
Dd	121	GACTGCTACAGCATTTACCCTACCGGTACCCTCGAAGTGTCACCAATCCCAGAGGGTGCCCTGC	180									
Yy	393	CCTGACTGGCCAACAATGTCATCAAACATGACTGTGGCGAGTCTTTTGTGAGTGTCCAGTCTG	452									
Dd	181	CCTGACTGGCCAACAATGTCATCAAACATGACTGTGGCGAGTCTTTTGTGAGTGTCCAGTCTG	240									
Yy	453	CTTTTGACTATGTGTTACCGGCCATTTCTCAATGTCAGAGTGSCCACTTGTGTTGTAGCAA	512									
Dd	241	CTTTTGACTATGTGTTACCGGCCATTTCTCAATGTCAGAGTGSCCACTTGTGTTGTAGCAA	300									
Yy	513	CTGTCCGCCAACAGCTCACATGTTGTCACATTTGCCGGGGCCCTTTGGGATCCATTCGCAA	572									
Dd	301	CTGTCCGCCAACAGCTCACATGTTGTCACATTTGCCGGGGCCCTTTGGGATCCATTCGCAA	360									
Yy	573	CTTGCGTATGGAGAAAGTGGCTAAATTCAGTACTTTTCCCTGTAATATGCGCTCTTCTGG	632									
Dd	361	CTTGCGTATGGAGAAAGTGGCTAAATTCAGTACTTTTCCCTGTAATATGCGCTCTTCTGG	420									
Yy	633	ATGCGAAATAACTCTGCCACACACAGAAAAAGCAGACCATGAAGAGCTCTGTGAGTTTATG	692									
Dd	421	ATGCGAAATAACTCTGCCACACACAGAAAAAGCAGACCATGAAGAGCTCTGTGAGTTTATG	480									
Yy	693	GCCTTATTCCTGCTGGTGGCCCTGGTCTTCCTGTAATGCGCAAGGCTCTCTGGATGCTGT	752									
Dd	481	GCCTTATTCCTGCTGGTGGCCCTGGTCTTCCTGTAATGCGCAAGGCTCTCTGGATGCTGT	540									
Yy	753	AATGCCCATCTGATGCATCAGCAATGAAGTCATTAACAACCTACAGGGAGAGATATAGT	812									
Dd	541	AATGCCCATCTGATGCATCAGCAATGAAGTCATTAACAACCTACAGGGAGAGATATAGT	600									
Yy	813	TTTTTCTTGCTACAGACATTAATCTTCTCGTGCTGTGTGACTGGTGATGATGCAGTCTCTG	872									
Dd	601	TTTTTCTTGCTACAGACATTAATCTTCTCGTGCTGTGTGACTGGTGATGATGCAGTCTCTG	660									
Yy	873	TTTTTGGCTTTTCATCTTCATGTTAGTCTTTAGAGAAACAGGAAAAATACGATGGTCACCAGCA	932									
Dd	661	TTTTTGGCTTTTCATCTTCATGTTAGTCTTTAGAGAAACAGGAAAAATACGATGGTCACCAGCA	720									
Yy	933	GTTCTTTCGCAATCGTACAGCTGATAGGAAACACCAAGCAAGCTGAAAAATTTTGCTTTACCG	992									
Dd	721	GTTCTTTCGCAATCGTACAGCTGATAGGAAACACCAAGCAAGCTGAAAAATTTTGCTTTACCG	780									
Yy	993	ACTTGAGCTTAAATGFTCAFAGGCGACGATTTGACTTTGGAGAAGCACTCTCGATCTATTCA	1052									
Dd	781	ACTTGAGCTTAAATGFTCAFATGCGACGATTTGACTTTGGAGAAGCACTCTCGATCTATTCA	840									
Yy	1053	TGAGGAATTTGCAACAGCCATTATGAATAGCGACTGTGTAGTCTTTTGACACACCAAGCATTTG	1112									
Dd	841	TGAGGAATTTGCAACAGCCATTATGAATAGCGACTGTGTAGTCTTTTGACACACCAAGCATTTG	900									
Yy	1113	ACAGCTTTTTTGCAAAAAATGGCAATTTAGGCATCAATGTAACTATTTTCCCATGTGTGAAA	1172									
Dd	901	ACAGCTTTTTTGCAAAAAATGGCAATTTAGGCATCAATGTAACTATTTTCCCATGTGTGAAA	960									
Yy	1173	TGGCAATCAACATTTTCTGCGCCAGTGTTTAAAACTTCAGTTTTCACAGAAAAATAAGGCAC	1232									
Dd	961	TGGCAATCAACATTTTCTGCGCCAGTGTTTAAAACTTCAGTTTTCACAGAAAAATAAGGCAC	1020									
Yy	1233	CCATCTGTCTGCCAACACCTAAAACTTTCTCGTAGGTGGAAAGC	1274									

Db 1021 CCAATCTCTGCCAACCTAAACATCTTCGGTAGTGGAGC 1062

RESULT 2
CR607323
LOCUS
DEFINITION
full-length cDNA clone CS0DC023YH14 of Neuroblastoma Cot
25-normalized of Homo sapiens (human).
CR607323
ACCESSION
CR607323.1 GI:50488130
VERSION
HNC; CNSLT_CDNA.
KEYWORDS
Homo sapiens (human)
SOURCE
Homo sapiens
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 1360)
Li, W.B., Gruber, C., Jesse, J. and Polayes, D.
Full-length cDNA libraries and normalization
Unpublished
JOURNAL
Contact : Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
REMARK
Paraday Avenue
2 (bases 1 to 1360)
Genoscope.
Direct Submission
TITLE
Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
JOURNAL
- Web : www.genoscope.cns.fr)
COMMENT
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five primer
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen.
FEATURES
Location/Qualifiers
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/organism="Homo sapiens"
/mol_type="mRNA"
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/clone="CS0DC023YH14"
/tissue_type="Neuroblastoma Cot 25-normalized"
/plasmid="pCMVSPORT_6"
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Query Match 75.2%; Score 958; DB 3; Length 1360;
Best Local Similarity 100.0%; Pred. No. 6.5e-223;
Matches 958; Conservative 0; Mismatches 0; Indels 0; Gaps 0
QY 317 CAGAAATGAGCGTGCAGACTGCTACAGATTACCTACCGGTACCTCGAAGTGTCCACCAT 376
DB 1 CAGAAATGAGCGTGCAGACTGCTACAGATTACCTACCGGTACCTCGAAGTGTCCACCAT 60
QY 377 CCCAGAGGGTGCTGCCCTGACTGGCCACAACATGTCATCCAAATGACTGTGGCGAGTCTTT 436
DB 61 CCCAGAGGGTGCTGCCCTGACTGGCCACAACATGTCATCCAAATGACTGTGGCGAGTCTTT 120
QY 437 TTGAGTGTCCAGTGTGCTTTTGACTATGTGTACCGCCCATTTCTTCAATGTCAAGTGGCC 496
DB 121 TTGAGTGTCCAGTGTGCTTTTGACTATGTGTACCGCCCATTTCTTCAATGTCAAGTGGCC 180
QY 497 ATCTTGTTTGTAGCAACTGTCCGCCAAAGCTCACATGTTGTCCAACTGCCGGGGCCCTT 556
DB 181 ATCTTGTTTGTAGCAACTGTCCGCCAAAGCTCACATGTTGTCCAACTGCCGGGGCCCTT 240
QY 557 TGGGATCCATTCCCAACTTGGCTATGGGAAAGTGGCTAATTCAAGTACTTTTCCCTGTGA 616
DB 241 TGGGATCCATTCCCAACTTGGCTATGGGAAAGTGGCTAATTCAAGTACTTTTCCCTGTGA 300
QY 617 AATATGCGTCTTCTGATGTGAAATTAATCTGCCACACACAGAAAAGCAGACCATGAAG 676
DB 301 AATATGCGTCTTCTGATGTGAAATTAATCTGCCACACACAGAAAAGCAGACCATGAAG 360
QY 677 AGCTCTGTGAGTTTAGCGCTTATTTCTGTGCGGCCCTGGTCTTCTCTGTAATGGCAAG 736

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Db 361 AGCTCTGTGAGTTTAGGCTTATTCTCTGTCGCGCTGCTCTCTGTAATGGCAAG 420
QY 737 GCTCTCTGAGTGTGTAATGCCCATCTGATGATCAGACATAAGTCAATTAACCCCTAC 796
Db 421 GCTCTCTGAGTGTGTAATGCCCATCTGATGATCAGACATAAGTCAATTAACCCCTAC 480
QY 797 AGGAGAGGATATAGTTTCTTCTGCTACACACATTAATCTTCTGCTGCTGCTGCTGG 856
Db 481 AGGAGAGGATATAGTTTCTTCTGCTACACACATTAATCTTCTGCTGCTGCTGCTGG 540
QY 857 TGAATGATGACAGTCTCTGTTTGGCTTTTCACTTTCATGTTAGTCTTAGAGAAACAGGAAAT 916
Db 541 TGAATGATGACAGTCTCTGTTTGGCTTTTCACTTTCATGTTAGTCTTAGAGAAACAGGAAAT 600
QY 917 ACGATGGTCAACGACAGTCTTCTGCAATCTGTAAGTATGAGAAACAGCAAGCTG 976
Db 601 ACGATGGTCAACGACAGTCTTCTGCAATCTGTAAGTATGAGAAACAGCAAGCTG 660
QY 977 AAAATTTTGGCTTACCGACTTGAAGTAAATGGTATAGGCGACCATTTGACTTTGGGAGCGA 1036
Db 661 AAAATTTTGGCTTACCGACTTGAAGTAAATGGTATAGGCGACCATTTGACTTTGGGAGCGA 720
QY 1037 CTCTCTGATCTATTCAATGAAGAAATGCAACAGCCATTTATGAATAGCGACTGTCTAGTCT 1096
Db 721 CTCTCTGATCTATTCAATGAAGAAATGCAACAGCCATTTATGAATAGCGACTGTCTAGTCT 780
QY 1097 TTGACACCGACATGTCACAGCTTTTTCAGAAATAGCAATTTTGGGATCAATGTAACTA 1156
Db 781 TTGACACCGACATGTCACAGCTTTTTCAGAAATAGCAATTTTGGGATCAATGTAACTA 840
QY 1157 TTTCCATGTTTGAATGGCAATCAACATTTTCTGCGCAGTGTTTTAAACTTTCAGTTTC 1216
Db 841 TTTCCATGTTTGAATGGCAATCAACATTTTCTGCGCAGTGTTTTAAACTTTCAGTTTC 900
QY 1217 ACAGAAATAAGGACCCCATCTGCTGCGCAACCTAAACTTTTTCGGTAGGTGGAGG 1274
Db 901 ACAGAAATAAGGACCCCATCTGCTGCGCAACCTAAACTTTTTCGGTAGGTGGAGG 958

RESULT 3
LOCUS CR614925
DEFINITION full-length cDNA clone CS0DK012Y120 of Hela cells HTC 21-JUL-2004
of Homo sapiens (human).
ACCESSION CR614925
VERSION CR614925.1 GI:50495732
KEYWORDS HTC; CNSLT cDNA.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
AUTHORS Li, W.B., Gruber, C., Jesse, J. and Polayes, D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished
REMARK Contact : Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
Faraday Avenue
REFERENCE 2 (bases 1 to 1857)
Genoscope.
AUTHORS Direct Submission
TITLE Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :
JOURNAL BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr)
- Web : www.genoscope.cns.fr)
COMMENT 1st strand cDNA was primed with a NotI-oligo (dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen.
FEATURES
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/organism="Homo sapiens"
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/db_xref="taxon:9606"
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Query Match 75.2%; Score 958; DB 3; Length 1857;
Best Local Similarity 100.0%; Pred. No. 6.8e-223; Indels 0; Gaps 0;
Matches 958; Conservative 0; Mismatches 0;

QY 317 CAGAAATGAGCCGTGAGACTGCTACAGCAATTAATCTACCGGTACCTCGAAGTGTCCACCAT 376
Db 1 CAGAAATGAGCCGTGAGACTGCTACAGCAATTAATCTACCGGTACCTCGAAGTGTCCACCAT 60
QY 377 CCAGAGGGTGGCTGCGCCCTGAGCTGGCAACATGCAATCAATGACTTTGGCGAGTCTTT 436
Db 61 CCAGAGGGTGGCTGCGCCCTGAGCTGGCAACATGCAATCAATGACTTTGGCGAGTCTTT 120
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QY 497 ATCTTCTGTTGTAGCAACTGTGCGCCAAAGCTACATGTTGTGCCAACTTTCGCGGGGCCCTT 556
Db 181 ATCTTCTGTTGTAGCAACTGTGCGCCAAAGCTACATGTTGTGCCAACTTTCGCGGGGCCCTT 240
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QY 677 AGCTCTGTGAGTTTAGGCTTATTCTCTGTCGCGCCCTGCTGCTCTGTAATTTGGAAG 736
Db 361 AGCTCTGTGAGTTTAGGCTTATTCTCTGTCGCGCCCTGCTGCTCTGTAATTTGGAAG 420
QY 737 GCTCTCTGGATGCTGTAATGCCCCCATCTGATGCATCAGCATAAAGTCCATTACACCCCTAC 796
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QY 797 AGGAGAGATATAGTTTCTTCTGCTACAGACATTAATCTTCTGCTGCTGCTGCTGCTGG 856
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QY 977 AAAATTTTCTTACCGACTTGAAGTAAATGGTCTATAGGCGACCATTTGACTTTGGGAGCGA 1036
Db 661 AAAATTTTCTTACCGACTTGAAGTAAATGGTCTATAGGCGACCATTTGACTTTGGGAGCGA 720
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QY 1157 TTTCCATGTTTGAATGGCAATCAACATTTTCTGCGCAGTGTTTTAAACTTTCAGTTTC 1216
Db 841 TTTCCATGTTTGAATGGCAATCAACATTTTCTGCGCAGTGTTTTAAACTTTCAGTTTC 900
QY 1217 ACAGAAATAAGGACCCCATCTGCTGCGCAACCTAAACTTTTTCGGTAGGTGGAGG 1274
Db 901 ACAGAAATAAGGACCCCATCTGCTGCGCAACCTAAACTTTTTCGGTAGGTGGAGG 958
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ORIGIN

Query Match 66.6%; Score 849; DB 9; Length 849;
Best Local Similarity 100.0%; Pred. No. 2.5e-196;
Matches 849; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 322 ATGAGCGCTGACACTGCTACAGCATTTACCTACCGGTACCTCGAAGTGTCCACATCCCGAG 381
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QY 382 AGGGTCCCTGCGCTGACTGGCACAACATGCTCAACAAATGACTTGGCGAGTCTTTTGGAG 441
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QY 442 TGTCCAGTCTGCTTTGACTATGTTTACCGCCCAATCTTTCAATGTCCAGAGTGGCCATCTT 501
DB 121 TGTCCAGTCTGCTTTGACTATGTTTACCGCCCAATCTTTCAATGTCCAGAGTGGCCATCTT 180

QY 502 GTTGTAGCAACTGTCGCCCAAGCTCACATGTTGTCGAATGTCGCCGGGCCCTTTGGGA 561
DB 181 GTTGTAGCAACTGTCGCCCAAGCTCACATGTTGTCGAATGTCGCCGGGCCCTTTGGGA 240

QY 562 TCCATTGCGCAACTGTCGCTATGAGAAAGTGGCTAAATTCAGTACTTTTCCCTGTAATAT 621
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QY 622 GCGTCTTCTGGATGTGAATAAATCTGTCACACACACAGAAAAGCAGACCATGAAGAGCTC 681
DB 301 GCGTCTTCTGGATGTGAATAAATCTGTCACACACACAGAAAAGCAGACCATGAAGAGCTC 360

QY 682 TGTGAGTTTGGCGCTTATTCCTGTCGCTGCGCTGCTTCTGTTAAATGGCAGGCTCT 741
DB 361 TGTGAGTTTGGCGCTTATTCCTGTCGCTGCGCTGCTTCTGTTAAATGGCAGGCTCT 420

QY 742 CTGGATGCTGTAATGCCCATCTGATGCATCAGCATTAAGTCCATTACAAACCTTACAGGGA 801
DB 421 CTGGATGCTGTAATGCCCATCTGATGCATCAGCATTAAGTCCATTACAAACCTTACAGGGA 480

QY 802 GAGGATATAGTTTTCTTGCTACAGACATTAATCTTCTGCTGCTGCTGTTGACTGGGTGATG 861
DB 481 GAGGATATAGTTTTCTTGCTACAGACATTAATCTTCTGCTGCTGCTGTTGACTGGGTGATG 540

QY 862 ATGCGAGTCTGTTTGGCTTTTCACTTATGTTAGTCTTTAGAGAAACAGGAAAAATACGAT 921
DB 541 ATGCGAGTCTGTTTGGCTTTTCACTTATGTTAGTCTTTAGAGAAACAGGAAAAATACGAT 600

QY 922 GGTCAACAGCAGTCTTCCCAATCGTACAGCTGATAGGAACACGCAAGCAAGCTGAATAT 981
DB 601 GGTCAACAGCAGTCTTCCCAATCGTACAGCTGATAGGAACACGCAAGCAAGCTGAATAT 660

QY 982 TTTGCTTACCGACTTGAGCTAAATGGTCAATAGGCGACGATTTGACTTTGGGAAGCGACTCT 1041
DB 661 TTTGCTTACCGACTTGAGCTAAATGGTCAATAGGCGACGATTTGACTTTGGGAAGCGACTCT 720

QY 1042 CGATCTATTCATGAAGGAATTGCAACAGCCATTATGAATAGGCACTGCTAGTCTTTGAC 1101
DB 721 CGATCTATTCATGAAGGAATTGCAACAGCCATTATGAATAGGCACTGCTAGTCTTTGAC 780

QY 1102 ACCAGCATTCACAGCTTTTTCAGAAAATGCAATTTAGGCGATCAATGTAATCTTTCC 1161
DB 781 ACCAGCATTCACAGCTTTTTCAGAAAATGCAATTTAGGCGATCAATGTAATCTTTCC 840

QY 1162 ATGTGTTGA 1170
DB 841 ATGTGTTGA 849

RESULT 6

AY402256
LOCUS Pan troglodytes SIAH1 gene, VIRTUAL TRANSCRIPT, partial sequence,
DEFINITION genomic survey sequence.
ACCESSION AY402256

AY402256.1 GI:39758242

GSS.
Pan troglodytes (chimpanzee)
Pan troglodytes
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.

REFERENCE
AUTHORS
Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A.,
Todd, M.A., Tanenbaum, D.M., Civallo, D.R., Lu, F., Murphy, B.,
Perriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J.,
Adams, M.D. and Cargill, M.

TITLE
Inferring nonneutral evolution from human-chimp-mouse orthologous
gene trios

JOURNAL
Science 302 (5652), 1960-1963 (2003)

PUBMED 14671302

REFERENCE

AUTHORS

Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A.,
Todd, M.A., Tanenbaum, D.M., Civallo, D.R., Lu, F., Murphy, B.,
Perriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J.,
Adams, M.D. and Cargill, M.

TITLE

Direct Submission

JOURNAL
Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
Rockville, MD 20850, USA

COMMENT
This sequence was made by sequencing genomic exons and ordering
them based on alignment.

FEATURES

source

1..849

/organism="Pan troglodytes"

/mol_type="genomic DNA"

/db_xref="taxon:9598"

<1..>849

/gene="SIAH1"

/locus_tag="HCM1163"

ORIGIN

Query Match 66.2%; Score 843.2; DB 9; Length 849;
Best Local Similarity 99.5%; Pred. No. 6.5e-195;
Matches 845; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 322 ATGAGCGCTGACACTGCTACAGCATTTACCTACCGGTACCTCGAAGTGTCCACATCCCGAG 381
DB 1 ATGAGCGCGTACAGCTGCTACAGCATTTACCTACCGGTACCTCGAAGTGTCCACATCCCGAG 60

QY 382 AGGGTCCCTGCGCTGACTGGCACAATGCTCAACAAATGACTTGGCGAGTCTTTTGGAG 441
DB 61 AGGGTCCCTGCGCTGACTGGCACAATGCTCAACAAATGACTTGGCGAGTCTTTTGGAG 120

QY 442 TGTCCAGTCTGCTTTGACTATGTTTACCGCCCAATCTTCAATGTCCAGAGTGGCCATCTT 501
DB 121 TGTCCAGTCTGCTTTGACTATGTTTACCGCCCAATCTTCAATGTCCAGAGTGGCCATCTT 180

QY 502 GTTGTAGCAACTGTCGCCCAAGCTCACATGTTGTCGAATGTCGCCGGGCCCTTTGGGA 561
DB 181 GTTGTAGCAACTGTCGCCCAAGCTCACATGTTGTCGAATGTCGCCGGGCCCTTTGGGA 240

QY 562 TCCATTGCGCAACTGCTGCTATGAGAAAGTGGCTAAATTCAGTACTTTTCCCTGTAATAT 621
DB 241 TCCATTGCGCAACTGCTGCTATGAGAAAGTGGCTAAATTCAGTACTTTTCCCTGTAATAT 300

QY 622 GGGTCTTCTGGATGTGAATAAATCTGTCACACACAGAAAAGCAGACCATGAAGAGCTC 681
DB 301 GGGTCTTCTGGATGTGAATAAATCTGTCACACACAGAAAAGCAGACCATGAAGAGCTC 360

QY 682 TGTGAGTTTAGGCGCTTATTCCTGTCGCTGCGCTGCTTCTGTTAAATGGCAGGCTCT 741
DB 361 TGTGAGTTTAGGCGCTTATTCCTGTCGCTGCGCTGCTTCTGTTAAATGGCAGGCTCT 420

QY 742 CTGGATGCTGTAATGCCCATCTGATGCATCAGCATTAAGTCCATTACAAACCTTACAGGGA 801
DB 421 CTGGATGCTGTAATGCCCATCTGATGCATCAGCATTAAGTCCATTACAAACCTTACAGGGA 480

QY 802 GAGGATATAGTTTTCTTGCTACAGACATTAATCTTCTGCTGCTGCTGTTGACTGGGTGATG 861
DB 481 GAGGATATAGTTTTCTTGCTACAGACATTAATCTTCTGCTGCTGCTGTTGACTGGGTGATG 540


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Db 541 GCAATCGTACGCTGATAGGAACACCAAGCAAGCTGAAATAATTTGCTTACCAGCTTGAG 600
Qy 1000 CTAATAGTGTATAGGCGCAGATTGACTTGGGAAGCGACTCCTCGATCTATTTCATGAAGGA 1059
Db 601 CTAATAGTGTATAGGCGCAGATTGACTTGGGAAGCGACTCCTCGATCTATTTCATGAAGGA 660
Qy 1060 ATTGCAACGCCATT-ATGAATAGCGACTGT-CTAGTCTTTGACACAGCAGATTGCAAGC 1117
Db 661 ATTGCAACGCCATTTCATGAATAGCGACTGTCTAGTCTTTGACACAGCAGATTGCAAGC 720
Qy 1118 TTTTTCGAGAAATGCAATTTAGGCATCAATCTAACTATTTCCAGTTTCCAGAGGA 1177
Db 721 -TTTTCGAGAAATGCAATTTAGGCCTCACTGTAACATATATCCATGTGGTGAATGGC 779
Qy 1178 ATCAACATTTTTCGCCAGTGTTTAAACCTTCAGTTTCCAGAGGA 1223
Db 780 AATCAACATATCTGCCAGTGGTTAAAT-TCAGTTTCCAGAGGA 824

RESULT 11
AI936347
LOCUS
DEFINITION
  wo81b11.x1 NCI CGAP Kid11 Homo sapiens cDNA clone IMAGE:2461725 3'
  similar to TR:043269 O43269 HSI4H1.1; mRNA sequence.
ACCESSION
  AI936347
VERSION
  AI936347.1 GI:5675217
KEYWORDS
  EST.
SOURCE
  Homo sapiens (human)
ORGANISM
  Homo sapiens
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
  1 (bases 1 to 779)
  NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
  Tumor Gene Index
  Unpublished (1997)
JOURNAL
  Contact: Robert Strausberg, Ph.D.
  Email: cgapbs-r@mail.nih.gov
  Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
  Emmert-Buck, M.D., Ph.D.
  cDNA Library Preparation: M. Bento Soares, Ph.D.
  cDNA Library Arrayed by: Greg Lennon, Ph.D.
  DNA Sequencing by: Washington University Genome Sequencing Center
  Clone distribution: NCI-CGAP clone distribution information can be
  found through the I.M.A.G.E. Consortium/LNL at:
  www-bio.llnl.gov/hbrp/image/image.html
  Insert Length: 1411 Std Error: 0.00
  Seq primer: -400P from Gibco
  High quality sequence stop: 444.
  Location/Qualifiers
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      /organism="Homo sapiens"
      /mol_type="mRNA"
      /db_xref="taxon:9606"
      /clone="IMAGE:2461725"
      /lab_host="DH10B"
      /clone_lib="NCI CGAP Kid11"
      /note="Organ: Kidney; Vector: pTT3D-Pac (Pharmacia) with
      a modified polylinker; Site: Not I; Site 2: Eco RI;
      Plasmid DNA from the normalized library NCI CGAP Kid3 was
      prepared, and ss circles were made in vitro. Following HAP
      purification, this DNA was used as tracer in a subtractive
      hybridization reaction. The driver was PCR-amplified cDNAs
      from a pool of 5,000 clones made from the same library
      (cloneIDs 1322376-1323911, 1456007-1456775, and
      1500552-1502855). Subtraction by Bento Soares and M.
      Fatima Bonaldo."
```

ORIGIN

```
Query Match 58.8%; Score 748.8; DB 1; Length 779;
Best Local Similarity 97.4%; Pred. No. 7.4e-172;
Matches 759; Conservative 0; Mismatches 20; Indels 0; Gaps 0;
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Qy 203 TTTGCTCAGTAATAATTTTGTATGAAACTTTTAAAGGACTTATGGCATGTAAACATTATTTA 262
Db 1 TTTGCTCAGTAATAATTTTGTATGAAACTTTTAAAGGACTTATGGCATGTAAACATTATTTA 60
Qy 263 TAAAGTAAAGTCATGGTTATAATTTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 322
Db 61 TAAAGTAAAGTCATGGTTATAATTTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 120
Qy 323 TGAGCCGCTCAGACTGCTACAGCAATTTACCTTACCGGTACCTCGAAGTGTCCACCATCCAGA 382
Db 121 TGAGCCGCTCAGACTGCTACAGCAATTTACCTTACCGGTACCTCGAAGTGTCCACCATCCAGA 180
Qy 383 GGGTGCCTGCCTCAGCTGGCAAACTGCAATCCAACTGCAATGCGGAGTCTTTTGTAGT 442
Db 181 GGGTGCCTGCCTCAGCTGGCAAACTGCAATCCAACTGCAATGCGGAGTCTTTTGTAGT 240
Qy 443 GTCCAGTCTGCTTTGACTATGTTTACCGCCCAATTTCTCAATGTTCAGATGGCCATCTTG 502
Db 241 GTCCAGTCTGCTTTGACTATGTTTACCGCCCAATTTCTCAATGTTCAGATGGCCATCTTG 300
Qy 503 TTTGTAGCAACTGTGCCCCAAAGCTCACATGTTGTCCAACTTGCCTGGGGCCCTTTGGGAT 562
Db 301 TTTGTAGCAACTGTGCCCCAAAGCTCACATGTTGTCCAACTTGCCTGGGGCCCTTTGGGAT 360
Qy 563 CCATTGCGAACTTTGGCTATGGAGAAAGTGGCTAAATTCAGTACTTTTCCCTGTGTAATATG 622
Db 361 CCATTGCGAACTTTGGCTATGGAGAAAGTGGCTAAATTCAGTACTTTTCCCTGTGTAATATG 420
Qy 623 CCTCTCTCGATGTGAAATAACTCTGCCACACACAGAAAAGCAGACCATGAGAGCTCT 682
Db 421 CCTCTCTCGATGTGAAATAACTCTGCCACACACAGAAAAGCAGACCATGAGAGCTCT 480
Qy 683 GTGAGTTTAGGCTTATTCCTGTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 742
Db 481 GTGAGTTTAGGCTTATTCCTGTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 540
Qy 743 TCGATGCTGTAATGCCCCCATCTGATGTCATGATGATGATGATGATGATGATGATGATGATG 802
Db 541 TCGATGCTGTAATGCCCCCATCTGATGTCATGATGATGATGATGATGATGATGATGATGATG 600
Qy 803 AGGATATAGTTTCTTCTGCTACAGACATTAATCTTCTGCTGCTGCTGCTGCTGCTGCTGCTG 862
Db 601 AGGATATAGTTTCTTCTGCTACAGACATTAATCTTCTGCTGCTGCTGCTGCTGCTGCTGCTG 660
Qy 863 TGCAGTCTGTTTTCGCTTTCCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 922
Db 661 TGCAGTCTGTTTTCGCTTTCCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 720
Qy 923 GTCACGAGCAGTTTCTTTCGCAATCGTACAGCTGATAGGAACACGCAAGCAAGCTGAAAT 981
Db 721 GTCACGAGCAGTTTCTTTCGCAATCGTACAGCTGATAGGAACACGCTGCAAGCAAGCTGAAAT 779
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RESULT 12

AI971258

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

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AI971258 778 bp mRNA linear EST 08-MAR-2000
wr27b08.x1 NCI CGAP Pr28 Homo sapiens cDNA clone IMAGE:2488897 3'
similar to TR:043269 O43269 HSI4H1.1; mRNA sequence.
AI971258 1 GI:5768084
EST.
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 778)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
```

Tissue Procurement: Michael J. Brownstein, M.D., Ph.D., Michael R. Emmert-Buck, M.D., Ph.D.
cDNA Library Preparation: M. Bento Soares, Ph.D.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Insert Length: 826 Std Error: 0.00
Seq primer: -400P from Gibco
High quality sequence stop: 455.

FEATURES
source

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   clone_lib="NCI CGAP pr28"
   note="organ: prostate; Vector:
   with a modified polylinker
   normalized library NCI CGA
   circles were made in vitro
   this DNA was used as template
   reaction. The driver was P
   of 5,000 clones made from
   985608-986759, 1101192-110
   Subtraction by Bento Soares

```

ORIGIN

Query Match	58.7%	Score	747.4	DB 1	Length	778			
Best Local Similarity	97.7%	Pred. No.	1.6e-171						
Matches	757	Conservative	0	Mismatches	18	Indels	0	Gaps	0

159	Qy	TTTTATCTTTTAAATATCTTTTAACTCTATTTTCTTCTCTCTTTTGTCTCAGTAAATTT	211
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219	Qy	TGTAATGAACCTTTAAAGGACTTATGGCATGTAAACATATTATTTATAAGTAAGTCATGGT	278
64	Db	TTTATTTATTTTAAAGGACTTATGGCATGTAAACATTTATATAAGTAAGTCATGGT	123
279	Qy	TATAATTAATTTTTCTCTGCCTCTCTATGTATTTATTTTCAGAATAGCCGTCAGACTGC	338
124	Db	TATAATTAATTTTTCTCTGCCTCTCTATGTATTTATTTTCAGAATAGCCGTCAGACTGC	183
339	Qy	TACAGCATTAACCTACCGGTACTCTCGAAGTGTCCACATCCACAGAGGGTCCCTGCCCTGCAC	398
184	Db	TACAGCATTAACCTACCGGTACTCTCGAAGTGTCCACATCCACAGAGGGTCCCTGCCCTGCAC	243
399	Qy	TGGCACAACTGCATCCAAACAATGACTTCGCGAGTCTTTTTTGAAGTCTCCAGTCTGCTTTGA	458
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459	Qy	CTATGTGTTTACCGCCCATCTTTCAATGTCAGAGTGGCCATCTTGTTGTAGCAACTGTGC	518
304	Db	CTATGTGTTTACCGCCCATCTTTCAATGTCAGAGTGGCCATCTTGTTGTAGCAACTGTGC	363
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579	Qy	TATGGAGAAAGTGGCTAACTTCAGTACTTTTTCCCCTGTAATATAGGTCTTCTCGAATGTGA	638
424	Db	TATGGAGAAAGTGGCTAACTTCAGTACTTTTTCCCCTGTAATATAGGTCTTCTCGAATGTGA	483
639	Qy	AATAACTCTGCCACACACAGAAAAAGCAGACCATGAAGAGCTCTGTGAGTTTAGGCCCTTA	698
484	Db	AATAACTCTGCCACACACAGAAAAAGCAGACCATGAAGAGCTCTGTGAGTTTAGGCCCTTA	543
699	Qy	TTCCCTGTCGGTGCCTTGTCCTCTGTAATAATGGCAAGGCTCTCTGGATGCTGTAATGCC	758

544	TTCTCTGTCCTGTCCTGGTCTTCCCTGTAATGGCAAGGCTCTCTCGATGCTGTAATGCC	603
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759	CCATCTGATGCATCAGCATAAAGTCGCAATTAACAACCTTACAGGAGAGATAGTTTTCT	818
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604	CCATCTGATGCATCAGCATAAAGTCCATTAACAACCTTACAGGAGAGNGATATAGTTTTCT	663
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664	TGCTCAGACATTAATCTTCTCGTCTGCTTGACTGGGTGATGATGCAGTCCCTGTTTTGG	723
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879	CTTTTCATCTTCATGTTTAGTCTTACAGAAAACAGGAAAAATACGATGGTCACCAGCAG	933
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724	CTTTTCATCTTCATGTTTAGTCTTACAGAAAACAGGAAAAATACGATGGTCACCAGCAG	778
Db		

RESULT 13
BX448317

EX44831 /	BX448317	872 bp	mRNA	linear	EST 06-MAY-2004
LOCUS	BX448317	Homo sapiens	FETAL LIVER	Homo sapiens cDNA clone	
DEFINITION	CS0DM009YG23	5-PRIME.	mRNA sequence.		

ACCESSION	BX448317
VERSION	BX448317.2
GI	47064237

VERSION	EST.	Homo sapiens (human)
KEYWORDS		
SOURCE		

SOURCE ORGANISM

Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
Catarrhini; Hominoidea; Homo.

REFERENCE

Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
Full-length cDNA libraries and normalization
Unpublished (2001)

COMMENT

Contact: Genoscope

Genoscope - Centre National de Sequencage

2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
Email: sagref@genoscope.cns.fr, Web : www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five primer
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoRV sites of the pCMVSPORT 6 vector. Library
was not normalized. Library was constructed by Life Technologies, a
division of Invitrogen.

This sequence belongs to sequence cluster 8104.r
For more information about this cluster, see
<http://www.genecore.cis.fr/cdna?c=CS0AM009AD120P1&c=8104.r>.

FEATURES

	FEATURES	SOURCE
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3.	100% Pure	100%
4.	100% Pure	100%
5.	100% Pure	100%
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/note="Organ: liver; Vector: pCMVSP6; 1st strand cDNA was primed with a NotI-oligo (dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoRV sites of the pCMVSP6 6 vector. Library was not normalized."

ORIGIN

Query Match	57.5%:	Score 733:	DB 5:	Length 872:
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Query Match	97.3%	Pred. No. 5.4e-168;
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Sequence 74	750				

276

QY 317 CAGAAATGAGCCGTGAGACTGCTACAGCATTACCTACCGGTACCTCGAAGTGTCCACCAI 378

1 CTCTTCCGCGCCTTCCTACAGCAATTACCTACCGGTACTCGAAGTGTCACCAT 60

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377 CCCAGAGGGTGCCTGCCCTGACTGGCACAACCTGCATCCAACTGGCGAGTCT-T 435

37

Dbb 61 CCCAGAGGGTGCCCTGCCCTGACTGGCACAACTGCATCCAACAATGACTTGGCGAGTCTAT 120

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Db 181 CATCTTTGTTGTAGCAACTCTGCGCCCAAGCTCACATGTTGTCAAACTTCCCGGGGCCCT 240
QY 556 TTGGGATCCATTCGCAACTTGGCTATGGAGAAAGTGCTAATTCAGTACTTTTCCCTGT 615
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Db 301 AATATGCGTCTTCTGATGTGAATAAATCTGCCACACACAGAAAAGCAGACCATGAA 360
QY 676 GAGCTCTGTGAGTTTAGGCCCTTATCTCTGTCGCGCCCTGCTTCTTCTTAAATGGCAA 735
Db 361 GAGCTCTGTGAGTTTAGGCCCTTATCTCTGTCGCGCCCTGCTTCTTCTTAAATGGCAA 420
QY 736 GGCTCTCTGATGCTGTAAATGCCCCATCTGATGCATCAGCATAGTCCATTAACAACCTTA 795
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QY 916 TAGATGGTCAACAGCAGTCTTTCGAATCGTACAGTGTATAGAAACAGCAAGCAAGCT 975
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QY 976 GAAATTTTGTCTTACCGACTTGTAGCTTAATGTCATAGGGAGCATTTGGGAAGCG 1035
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Db 721 MYCCTCGTATTCATGAAGAAATTCG-AMAGCCATTATGAATGACGAY 770

BX384656 785 bp mRNA linear EST 26-APR-2004
BX384656 Homo sapiens HELA CELLS COT 25-NORMALIZED Homo sapiens
CDNA clone CS0DK012Y120 5-PRIME, mRNA sequence.
BX384656
BX384656.2 GI:46570911
EST.
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 785)
Li, W.-B., Gruber, C., Jessee, J. and Polayes, D.
Full-length cDNA libraries and normalization
Unpublished (2001)
On May 8, 2003 this sequence version replaced gi:30447286.
Contact: Genoscope
Genoscope - Centre National de Sequencage
2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo (dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen. This sequence belongs to sequence cluster
8104.r
For more information about this cluster, see
```

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http://www.genoscope.cns.fr/cdna?s=CS0DK012BE10QPl&c=8104.r.
Location/Qualifiers
1. 785
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon.9606"
/clone="CS0DK012Y120"
/cell_type="HELA"
/cell_line="HELA"
/notes="1st strand cDNA was primed with a NotI-oligo (dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized."
ORIGIN
Query Match 56.4%; Score 719; DB 5; Length 785;
Best Local Similarity 93.8%; Pred. No. 1.4e-164;
Matches 738; Conservative 26; Mismatches 21; Indels 2; Gaps 2;
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Db 1 CAGAAATGAGCCGTGAGACTGCTTACAGCATTACTTACCGGTACTCTCGAAGTGTCCACCAT 60
QY 377 CCCAGAGGGTGCCTGCCCTGACTGGCAACAACATGCATCCAAATGACTTGGCGAGTCTTT 436
Db 61 CCCAGAGGGTGCCTGCCCTGACTGGCAACAACATGCATCCAAATGACTTGGCGAGTCTTT 120
QY 437 TTGAGTGTCCAGTCTGCTTTGACTATGCTTACCGCCCAATTTCTTCAATGTCAGAGTGGCC 496
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QY 497 ATCTTGTGTTGTAGCAACTCTGCGCCCAAGCTCACATGTTGTCCAACTTGCCTGGGGGCCCTT 556
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QY 557 TGGGATCCATTCGCAACTTGGCTATGGAGAAAGTGCTTAATTCAGTACTTTTCCCTGTGA 616
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QY 617 AATATGCGTCTTCTGATGTGAATAAATCTGCCACACAGAAAAGCAGACCATGAAAG 676
Db 301 AATATGCGTCTTCTGATGTGAATAAATCTGCCACACAGAAAAGCAGACCATGAAAG 360
QY 677 AGCTCTGTGAGTTTAGGCCCTTATCTCTGCTGCGCTGCTTCTCTGTAATGGAAG 736
Db 361 AGCTCTGTGAGTTTAGGCCCTTATCTCTGCTGCGCTGCTTCTCTGTAATGGAAG 420
QY 737 GCTCTCTGATGCTGTAAATGCGCCCACTGATGCATCAGCATTAAGTCCATTACAACCTTAC 796
Db 421 GCTCTCTGATGCTGTAAATGCGCCCACTGATGCATCAGCATTAAGTCCATTACAACCTTAC 480
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QY 1097 TTGACAC 1103
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Search completed: April 24, 2005, 22:53:18

Job time : 4607 secs

Db 779 TTGACAC 785
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 BX463976 Homo sapiens FETAL BRAIN Homo sapiens cDNA clone
 CS0DF021YA01 5-PRIME, mRNA sequence.
 ACCESSION BX463976
 VERSION BX463976.2 GI:47053846
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 852)
 Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
 Full-length cDNA libraries and normalization
 Unpublished (2001)
 On May 22, 2003 this sequence version replaced gi:31023592.
 Contact: Genoscope
 Genoscope - Centre National de Sequencage
 2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
 Email: segref@genoscope.cns.fr, Web : www.genoscope.cns.fr
 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
 end enriched, double-strand cDNA was digested with Not I and cloned
 into the Not I and EcoRV sites of the pCMVSPORT 6 vector. Library
 was not normalized. Library was constructed by Life Technologies, a
 division of Invitrogen.
 This sequence belongs to sequence cluster 8104.r
 For more information about this cluster, see
 http://www.genoscope.cns.fr/cdna?8=CSIAF006ZA01QP1sc=8104.r.
 Location/Qualifiers
 1. 852
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="CS0DF021YA01"
 /tissue_type="FETAL BRAIN"
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 /notes="Organ: Brain; Vector: pCMVSPORT 6; 1st strand cDNA
 was primed with a NotI-oligo(dT) primer. Five prime end
 enriched, double-strand cDNA was digested with Not I and
 cloned into the Not I and EcoRV sites of the pCMVSPORT 6
 vector. Library was not normalized."

FEATURES

source

ORIGIN

Query Match 55.6%; Score 708.8; DB 5; Length 852;
 Best Local Similarity 96.5%; Pred. No. 4.4e-162;
 Matches 738; Conservative 15; Mismatches 9; Indels 3; Gaps 3;
 QY 317 CAGAAATGAGCGCTCAGACTGTCTACAGCTTACTACCGGTACTCGAAGTGTCCACCAT 376
 Db 1 CAGAAATGAGCGCTCAGACTGTCTACAGCTTACTACCGGTACTCGAAGTGTCCACCAT 60
 QY 377 CCCAGAGGGTGCTGCGCTGACCTGGCAGCACTGCATCCCAATGACTTGGCGAGTCTTT 436
 Db 61 CCCAGAGGGTGCTGCGCTGACCTGGCAGCACTGCATCCCAATGACTTGGCGAGTCTTT 120
 QY 437 TTGAGTGTCCAGTCTGCTTTGACTATGTGTTACCGCCCATTTCTCAATGTCAGAGTGGCC 496
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 QY 497 ATCTTGTGTTAGCACTGTGCGCCCAAGCTCAGATGTTGTCCAACTTGCCTGGGGGCCCTT 556
 Db 181 ATCTTGTGTTAGCACTGTGCGCCCAAGCTCAGATGTTGTCCAACTTGCCTGGGGGCCCTT 240
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 Db 241 TGGGATCCATTGCGCACTTGGCTATGGAGAAAGTGGCTAATTCAGTACTTTTCCCTGTGA 300

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2	1042.8	81.9	2440	4	US-09-023-655-588	Sequence 588, App
3	928.4	72.9	1884	4	US-09-544-618-11	Sequence 11, Appl
4	161	12.6	257	4	US-09-016-434-397	Sequence 397, App
5	69.6	5.5	1420	3	US-09-362-506-1	Sequence 1, Appli
6	49	3.8	187169	4	US-09-949-016-12776	Sequence 12776, A
7	49	3.8	191569	4	US-09-949-016-15940	Sequence 15940, A
8	48.2	3.8	1425	3	US-09-325-932A-200	Sequence 200, App
9	48	3.8	7218	1	US-08-232-463-14	Sequence 14, Appl
10	47.6	3.7	5852	1	US-07-867-106-2	Sequence 2, Appli
11	47.4	3.7	612	4	US-09-902-540-1357	Sequence 1357, Ap
12	46.8	3.7	39176	4	US-09-949-016-17603	Sequence 17603, A
13	46.6	3.7	1036	3	US-09-325-932A-39	Sequence 39, Appl
14	46.6	3.7	1039	4	US-09-902-540-1280	Sequence 1280, Ap
15	44.8	3.5	832	4	US-09-621-976-2813	Sequence 2813, Ap
16	43.8	3.4	2861	1	US-08-299-953-1	Sequence 1, Appli
17	43.8	3.4	2861	1	US-08-459-415-1	Sequence 1, Appli
18	43.8	3.4	2861	3	US-09-066-687-1	Sequence 1, Appli
19	43.8	3.4	2861	5	PCR-US95-11231-1	Sequence 1, Appli
20	43.8	3.4	3881	1	US-08-299-953-2	Sequence 2, Appli
21	43.8	3.4	3881	1	US-08-459-415-2	Sequence 2, Appli
22	43.8	3.4	3881	4	US-09-066-687-2	Sequence 2, Appli
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24	43.2	3.4	19124	2	US-08-487-828B-13	Sequence 13, Appl
25	43	3.4	6243	2	US-09-056-075-1	Sequence 1, Appli
26	42.8	3.4	601	4	US-09-949-016-30532	Sequence 30532, A
27	42.8	3.4	601	4	US-09-949-016-30533	Sequence 30533, A

Db 822 GTGGCTAAATTCAGTACTTTTCCCTGTAATATGCGTCTTCTGGATGTAATAATCTCG 881
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Db 882 CCACACACAGAAAGCAGACCAATGAGAGCTCTGTGAGTTAGGCTTATTCCTGTCG 941
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Db 942 TGCCCTGGTCTTCTGTAATGCGAAGGCTCTCTGATGCTGTATGCCCCATCTGATG 1001
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RESULT 3

US-09-544-618-11
; Sequence 11, Application US/09544618
; Patent No. 6503502
; GENERAL INFORMATION:
; APPLICANT: Teleman, Adam
; APPLICANT: Amson, Robert
; APPLICANT: Cohen, Daniel
; TITLE OF INVENTION: NUCLEOTIDE SEQUENCES, PROTEINS, DRUGS AND DIAGNOSTIC
; TITLE OF INVENTION: AGENTS OF USE IN TREATING CANCER
; FILE REFERENCE: 065691-0139
; CURRENT APPLICATION NUMBER: US/09/544,618
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 11
; LENGTH: 1884
; TYPE: DNA
; ORGANISM: TSAP 3
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(846)
US-09-544-618-11

Query Match

72.9%; Score 928.4; DB 4; Length 1884;

Best Local Similarity 99.7%; Pred. No. 4.9e-263;
Matches 951; Conservative 0; Mismatches 1; Indels 2; Gaps 2;
Qy 322 ATGAGCCGTGAGACTGCTACAGCAATTTACCTACCGGTACCTCGAAGTGTCCACCATCCCG 381
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Qy 382 AGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 441
Db 61 AGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 120
Qy 442 TGTCAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 501
Db 121 TGTCAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 180
Qy 502 GTTGTAGCAACTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 561
Db 181 GTTGTAGCAACTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 240
Qy 562 TCATTCGCAACTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 621
Db 241 TCATTCGCAACTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 300
Qy 622 GGTGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 681
Db 301 GGTGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 360
Qy 682 TGTGAGTCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 741
Db 361 TGTGAGTCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 420
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Db 421 CTGGATGCTGTAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 480
Qy 802 GAGGATATAGTCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 861
Db 481 GAGGATATAGTCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 540
Qy 862 ATGCACTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 921
Db 541 ATGCACTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 600
Qy 922 GGTCAACAGCAGTCTTCTGCAATTCGTACAGCTGATAGGAACACGCAAGCAAGCTGAAAT 981
Db 601 GGTCAACAGCAGTCTTCTGCAATTCGTACAGCTGATAGGAACACGCAAGCAAGCTGAAAT 660
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Db 661 TTTGCTTACCGACTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 720
Qy 1042 CGATCTATTTCATGAAGGAATTCGAACAGCATTATGAATAGGAGTCTGTCTGTCTTTGAC 1101
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Qy 1161 CATGTTGTAATGCAATCAACATTTTCTGCGCAGTGTTTAAACCTTCAGTTTCACAG 1220
Db 840 CATGTTGTAATGCAATCAACATTTTCTGCGCAGTGTTTAAACCTTCAGTTTCACAG 899
Qy 1221 AAAATAAGGCACCCATCTGCTGCGCAACCTTAAACCTCTTTTCGTTAGGTAGGAGC 1274
Db 900 AAAATAAGGCACCCATCTGCTGCGCAACCTTAAACCTCTTTTCGTTAGGTAGGAGC 953

RESULT 4

US-09-016-434-397
; Sequence 397, Application US/09016434
; Patent No. 6500938
; GENERAL INFORMATION:

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; APPLICANT: Janice Au-Young
; APPLICANT: Jeffrey J. Seilhamer
; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING
; TITLE OF INVENTION: PATHWAY GENE EXPRESSION
; NUMBER OF SEQUENCES: 1490
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
; STREET: 3174 PORTER DRIVE
; CITY: PALO ALTO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/016,434
; FILING DATE: HEREWITH
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Zeller, Karen J.
; REGISTRATION NUMBER: 37,071
; REFERENCE/DOCKET NUMBER: PA-0002 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 855-0555
; TELEFAX: (650) 845-4166
; INFORMATION FOR SEQ ID NO: 397:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 257 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: BRAITUT03
; CLONE: 2113436
; US-09-016-434-397

Query Match      12.6%; Score 161; DB 4; Length 257;
Best Local Similarity 76.7%; Pred. No. 2.7e-37;
Matches 197; Conservative 0; Mismatches 60; Indels 0; Gaps. 0;

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QY      689  TTAGGCTTATTCCTGTCCGTGCCCTGCTTCCTGTAATGCGAAGGCTCTCTGGATG 748
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QY      749  CTGTAATGCCCATCTGATGCATCAGCATAAAGTCCATTACCAACCTACAGGGAGAGGATA 808
DB      121  CTGTGATGTCCTATCTCATGACGCCACAGAGCAATTACACCCCTCAGGGAGAGAGACA 180

QY      809  TAGTTTTCTTGTACAGACATTAACTTCTCGTGTCTGTGTGATCGGTGATCATGCAGT 868
DB      181  TCGTCTTTCTAGCTACAGACATTAACTTGCCAGGGGCTGTCGACTGGTGTGATGTCAGT 240

QY      869  CCTGTTTGGCTTTCAC 885
DB      241  CATGTTTGGCCATCAC 257

RESULT 5
US-09-362-506-1
; Sequence 1, Application US/09362506
; Patent No. 611167
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12776
; LENGTH: 187169
; TYPE: DNA

; APPLICANT: Mahajan, Pramod B.
; TITLE OF INVENTION: Maize SINA Orthologue-1 and Uses Thereof
; FILE REFERENCE: 0936
; CURRENT APPLICATION NUMBER: US/09/362,506
; CURRENT FILING DATE: 1999-07-27
; EARLIER APPLICATION NUMBER: 60/100,258
; EARLIER FILING DATE: 1998-09-14
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 1420
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (202)...(1140)
; US-09-362-506-1

Query Match      5.5%; Score 69.6; DB 3; Length 1420;
Best Local Similarity 51.4%; Pred. No. 6.7e-10;
Matches 187; Conservative 0; Mismatches 174; Indels 3; Gaps 1;

QY      420  TGACTTGGCGAGTCTTTTGGAGTGCAGTCTGTTTGACTATGTGTACCGCCCATCTCT 479
DB      366  TGGCTTGAATGATTTGCTCGAATGCCAGTGTGTACCAACTCGATGCCGCCCATTACT 425

QY      480  TCAATGTCAGAGTGGCCATCTTTTGTAGCAACTGTGCGCCCAAGCT---CACATGTTG 536
DB      426  CCAGTGGCCCAATGGCCACACAGATCTGCTAGTTGCAAGCACAGGGTAGAGAACCATG 485

QY      537  TCCAACTTGGCGGGCCCTTTGGGATCCATTGCGCACTTGGCTATGGAGAAAGTGGCTAA 596
DB      486  CCCAACTGTGCGCCAGGAACCTGGGAAACATCAGGTGCTAGCTCTCGAGAAAGTGGCAGA 545

QY      597  TTCAGTACTTTTCCCTCTGTAATATGCTCTTCTGATGTGAAATAAATCTCTGCCACACAC 656
DB      546  GCAACTCCAGCTTCGTCGAAGTACAGACACGCGATGCCCGAGATCCACCCATACAA 605

QY      657  AGAAAAAGCAGACCATGAGAGCTCTGTGAGTTTGAAGCTTATTCCTGTCGTGCCCTGG 716
DB      606  GAGCAAACTGAAGCACGAGGAGCTCTGCAGGTTTCAGGCGGTACAGCTGCCGTACGCAGG 665

QY      717  TGTCTCTGTAATGCGAAGGCTCTCTGATGCTGTATGCCCATCTGATGATCATCAGCA 776
DB      666  TTCCGAGTGCCTGATGCGCAGGCGACGTCCTGTTGTTGCCATCTCATCAACGACCA 725

QY      777  TAAG 780
DB      726  TAAG 729

RESULT 6
US-09-949-016-12776/c
; Sequence 12776, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12776
; LENGTH: 187169
; TYPE: DNA
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; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(187169)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-12776

Query Match      3.8%; Score 49; DB 4; Length 187169;
Best Local Similarity 48.4%; Pred. No. 0.015;
Matches 136; Conservative 0; Mismatches 145; Indels 0; Gaps 0;

QY 10 TTGTTATGGTCATTTCTATTTAGCAATTTATTTAGTATTTCTATGCTATCCAGAGCG 69
Db 883 TTATATATTTTATATATTTTATATATTTTATATATTTTATATATTTTATATATTTATAT 824

QY 70 ATTAAGGGAGTTCCACATGTTTCCGAAACATTTTGAAAGAGAGCTTATCCAGTGACA 129
Db 823 ATTTTATATTTTATATATTTTATATATTTTATATATTTTATATATTTTATATATTTTATATA 764

QY 130 GATCCTAATAAGTGACATTCAGTGTAAATTTTATTTTATTTTATATCTTTTAAATCCTA 189
Db 763 TATTATATATTTTATATTTTATATATATTTTATATATTTTATATATTTTATATATTTATA 704

QY 190 TTTTCTCTCTCTTTGCTCAGTAAATTTTGATGAACTTTTAAAGGACTTATGCGATG 249
Db 703 TATTATATATTTTATATGATTTATATATTTTATATATTTTATATATTTTATATATTTATA 644

QY 250 TAAACATTTTATTAAGTCAAGTCAATTTTATGTAATTTTATGTAATTTATTTT 290
Db 643 TATATTTTATATATTTTATATATTTTATATATTTTATATATTTTATATATTTTATATAT 603

RESULT 7
US-09-949-016-15940/c
; Sequence 15940, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15940
; LENGTH: 191569
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(191569)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-15940

Query Match      3.8%; Score 49; DB 4; Length 191569;
Best Local Similarity 48.4%; Pred. No. 0.015;
Matches 136; Conservative 0; Mismatches 145; Indels 0; Gaps 0;

QY 10 TTGTTATGGTCATTTCTATTTAGCAATTTTATTTAGTATTTCTATGCTATCCAGAGCG 69
Db 883 TTATATATTTTATATATTTTATATATTTTATATATTTTATATATTTTATATATTTATAT 824

QY 70 ATTAAGGGAGTTCCACATGTTTCCGAAACATTTTGAAAGAGAGCTTATCCAGTGACA 129
Db 823 ATTTTATATTTTATATATTTTATATATTTTATATATTTTATATATTTTATATATTTTATATA 764
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QY 130 GATCCTAATAAAGTGACATTCAGTGTAAATTTTATTTTATTTTATATCTTTTAAATCCTA 189
Db 763 TATTATATATTTTATATATTTTATATATTTTATATATTTTATATATTTTATATATTTATA 704

QY 190 TTTTCTCTCTCTTTGCTCAGTAAATTTTGATGAACTTTTAAAGGACTTATGCGATG 249
Db 703 TATTATATATTTTATGATTTATATATTTTATATATTTTATATATTTTATATATTTATA 644

QY 250 TAAACATTTTATTAAGTCAAGTCAATTTTATGTAATTTTATGTAATTTATTTT 290
Db 643 TATATTTTATATATTTTATATATTTTATATATTTTATATATTTTATATATTTTATATAT 603

RESULT 8
US-09-325-932A-200
; Sequence 200, Application US/09325932A
; Patent No. 6451604
; GENERAL INFORMATION:
; APPLICANT: Flinn, Barry
; APPLICANT: Lasham, Annette
; TITLE OF INVENTION: Compositions affecting programmed cell
; death and their use in the modification of forestry plant develop
; FILE REFERENCE: 1022
; CURRENT APPLICATION NUMBER: US/09/325,932A
; CURRENT FILING DATE: 1999-06-04
; NUMBER OF SEQ ID NOS: 206
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 200
; LENGTH: 1425
; TYPE: DNA
; ORGANISM: Pinus radiata
US-09-325-932A-200

Query Match      3.8%; Score 48.2; DB 3; Length 1425;
Best Local Similarity 43.4%; Pred. No. 0.0014;
Matches 273; Conservative 0; Mismatches 353; Indels 3; Gaps 1;

QY 528 CACATGTTGTCCAACCTTCGCGGGGCCCTTTGGGATCCATTCCGCACTTCGCTATGAGAA 587
Db 341 CAATGGTGTCGCTCTGCAGATGCAACCTTGGAATTTTAGTGCTTAGCTCTCTGAAAC 400

QY 588 AGTGGCTAATTCAGTACTTTTCCCTGTAAATATGGCTTCTGGATGTGAATAACTCT 647
Db 401 GGAGACATCATCTCAAGAACTTTACTTGCATGTATCAAGCTATGTTGTGAGGATATGA 460

QY 648 GCCACACACAGAAAAAGCAGACCATGAAGAGCTCTGTGAGTTTAGGCTTTAGGCTTATTCCTGTCC 707
Db 461 TCTTTACTACAGTGAATTAAGACATGAAGCTCACTGCAATTTTAGGCCATACACATGTC 520

QY 708 GTGCCCTGTGTCTCTCTGTAATGGCAAGGCTCTCTGGATGCTGTAAATCCCCCATCTGAT 767
Db 521 CTATGCTGGCTCCGAATGCAAGCTAGTTGGAGATATTCCTTTTGGTGGCTCATTTAAG 580

QY 768 GCATCAGCATAGTCCATTCACAACTTACAGGAGGAGGATATAGTTTTCCTGCTACAGA 827
Db 581 AGATGATCACAAAGTTTATATGATATAGTTTGCACCTTTGATCATCGATATGTAAGTC 640

QY 828 CATTAAATCTTCTGTGTG---CTGTTGACGTGGGTGATGATGTCAGTCTCTGTTGGCTTTCA 884
Db 641 AAATCCACTCGAGGTTGAGATGCTATTTGGATGCCAAGCTGAATCAATGTTTGGGGA 700

QY 885 CTTCAATGTTAGTCTTTAGAGAAAACAGAAAAATACGATGGTCCAGCAGCTTCTTCGCAAT 944
Db 701 ATCTTTTGCTACATTTTGAAGCGTTTCTATTAGACATGGCCCTGTATATATATAGCTTT 760

QY 945 CCGACAGCTGATAGAACACAGCAAGCTGAAATTTTGGCTTACCGACTTGAGCTAA 1004
Db 761 TCTGATTTTTCATGGGAGATGATATGAAGCTAAAACTTTAGCTATTTGCTCGAGACTGG 820

QY 1005 TGGTCATAGGCGACCATTCACCTTGGGAGGAGCTCTCGATCTATTCATGAAGGATTCG 1064
Db 821 AGGCAATGTCGGAACAACTGATTTGGCATGGGGTCTCTCGAAGCATCAGAGATTTGCACAG 880
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QY 1065 AACACCCATTATGAATAGGACTGTCTAGTCTTTGACACGAGCATTGACAGCTTTTTCG 1124
Db 881 GAAAGTTCATGACAGTAGTGACGAGCTAATATTACAAAGAGATGGGCACTCTTTTCTC 940
QY 1125 AGAAATGCGAATTTAGGCATCAATGTAA 1153
Db 941 AGGTGGTGACATAAATGAATGAATCTTA 969

RESULT 9
US-08-232-463-14
; Sequence 14, Application US/08232463
; Patent No. 5670367
; GENERAL INFORMATION:
; APPLICANT: DORNER, F.
; APPLICANT: SCHEIFLINGER, F.
; APPLICANT: FALKNER, F. G.
; TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
; NUMBER OF SEQUENCES: 52
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 1800 Diagonal Road, Suite 500
; CITY: Alexandria
; STATE: VA
; COUNTRY: USA
; ZIP: 22313-0299
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/232,463
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/935,313
; FILING DATE:
; APPLICATION NUMBER: EP 91 114 300.6
; FILING DATE: 26-AUG-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: BENT, Stephen A.
; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 30472/114 IMMU
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703)836-9300
; TELEFAX: (703)683-4109
; TELEX: 899149
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7218 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; CLONE: pTZgpt-Fls
; US-08-232-463-14

Query Match 3.8%; Score 48; DB 1; Length 7218;
Best Local Similarity 6.9%; Pred. No. 0.0041;
Matches 30; Conservative 218; Mismatches 188; Indels 0; Gaps 0;

QY 109 AGAGAGCTTATCCAGTGTACAGATCTCTAATAAGTGACACATTCAGTGTAAATTTT 168
Db 1021 ACAGATAATATCCAGCTTGGCTGCAGGTCGAGGAGCTTGGATVYVYVYVYVYVY 1080
QY 169 TTAATATCTTTTAACTCTAATTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 228
Db 1081 VY 1140
QY 229 TTTAAAGGACCTTATGGCATCTAAACATTAATTATAAGTAAGTCATGGTTAATTA 288
Db 1141 VY 1200

QY 289 TTCTCTCTGCTCTCTATGTAATTTATTTTACAAATGAGCGTCCAGACTGCTACAGCATTA 348
Db 1201 YY 1260
QY 349 CCTACCGGTACTCGAAGTGTCCACCATCCAGAGGTGCTGCTCCCTGACTGGCACAACT 408
Db 1261 YY 1320
QY 409 GCATCCAACTGACTTGGCGAGTCTTTTGGAGTGTCCAGTCTGCTTGACTATGCTTA 468
Db 1321 YY 1380
QY 469 CCGCCCAATCTTCAATGTCAGAGTGGCCATCTTTGTTAGTAGCACTGTCGCCAAAGTCT 528
Db 1381 YY 1440
QY 529 ACATGTTGTCCAACTT 544
Db 1441 AATCTTCTATCTCTT 1456

RESULT 10
US-07-867-106-2
; Sequence 2, Application US/07867106
; Patent No. 5389526
; GENERAL INFORMATION:
; APPLICANT: Slade, Martin B
; APPLICANT: Chang, Andy C M
; APPLICANT: Williams, Keith L
; TITLE OF INVENTION: Improved Plasmid Vectors for Cellular
; TITLE OF INVENTION: Slime Moulds of the Genus Dictyostelium
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 5389526ris
; STREET: One Liberty Place 46th Floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: USA
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/867,106
; FILING DATE: 19920625
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: AU BJ 7187
; APPLICATION NUMBER: PCT/AU90/00530
; FILING DATE: 02-NOV-1989
; ATTORNEY/AGENT INFORMATION:
; NAME: Feeney, Joanne Longo
; REGISTRATION NUMBER: 35,134
; REFERENCE/DOCKET NUMBER: RICE-0002
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-568-3100
; TELEFAX: 215-568-3439
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5852 base pairs
; TYPE: NUCLEIC ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; ANTI-SENSE: NO
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 2378..5038
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 2378..5038

Matches 272; Conservative 0; Mismatches 354; Indels 3; Gaps 1;
 QY 528 CACATGTTGTCCAACTTCGCGGGCCCTTTGGGATCCATTGCGAACTTGGCTATGGAGAA 587
 Db 345 CAACTGGTGTGCTGCTCGAGATGCAACCTTGGAAATTTTAGGTGCTTAGCTCCTGAAAC 404
 QY 588 AGTGCTTAATTCAGTACTTTTCCCTGTAATAATGCGTCTCTGATGTAAGAAATCACTCT 647
 Db 405 GGAGACATCATCTCAAGAACTTACTTGCATGATCAAGAGTAAGTTGTGAGGATATGTA 464
 QY 648 GCCACACACAGAAAAAGCAGACCATGAGAGCTCTGTGAGTTTAGGCTTTATCTCTGCC 707
 Db 465 TCTTACTACAGTGAATTAAGACATGAGCTCAGTGCAATTTTAGGCCATACAACTGCTC 524
 QY 708 GTGCCCTGTGTCTCTGTAATGGAAGGCTCTCTGGAATGCTGAATGCCCACTCTGAT 767
 Db 525 CTATGTGCTCGAATGCAAGCTAGTTGGAGATATTCCTTTTGGTGGCTCATTTAAG 584
 QY 768 GCATCAGATAGTCAATTAACAACCTACAGGAGAGGATATAGTTTCTTCTGTACAGA 827
 Db 585 AGATGATCAAGAAAGTTTATGATATAGTTTGCACCTTTGATCATCGATATGAAGTC 644
 QY 828 CATTAATCTTCTCGTGTG---CTGTGACTGGGTGATGATGAGTCTCTGTTGGCTTTCA 884
 Db 645 AATCCACTCGAGTTGAGATGCTATTTGGATGCCAAGCTGAATCAATGTTTGGGCA 704
 QY 885 CTTTCATGTTAGTCTTAGAGAAACAGAAAAATACGATGTCCAGCAGTCTTCTCGCAAT 944
 Db 705 ATTCTTTTGTCTACATTTTGAAGCGTTTCTATTAGACATGGCCCTGTATATATAGCTTT 764
 QY 945 CGTACAGCTGATAGGAACACGCAAGCTGAATTTTGTACCGACTTTCAGCTAAA 1004
 Db 765 TCTGATTTTCATGGAGATGATATGAGCTAAACTTTAGCTATTGCTCGAGACTGG 824
 QY 1005 TGCTCATAGCGCAGATTGACTTTGGGAAGCACTCTCTGATCTATTCATGAAGAAATTC 1064
 Db 825 AGCAATGTCGAACTGATTTGGCATGGGTTCTCGAAGCATCAGAGATTGTACACAG 884
 QY 1065 AACAGCATTAATGAATAGGAGCTGTCTAGTCTTTGACACCAAGCATTCGACAGTTTTCG 1124
 Db 885 GAAAGTTTCATGACAGTAGTACGAGCTAAATTATACAAAGAGATGTGGCACTCTTTTCTC 944
 QY 1125 AGAAATGCAATTTTAGGCATCAATGTAA 1153
 Db 945 AGTGTGACATAAATGAATGATCTTA 973

RESULT 14
 US-09-540-1280/c
 ; Sequence 1280, Application US/09902540
 ; Patent No. 6833447
 ; GENERAL INFORMATION:
 ; APPLICANT: Goldman, Barry S.
 ; APPLICANT: Hinkle, Gregory J.
 ; APPLICANT: Slater, Steven C.
 ; APPLICANT: Wiegand, Roger C.
 ; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
 ; FILE REFERENCE: 38-10(15849)B
 ; CURRENT APPLICATION NUMBER: US/09/902,540
 ; PRIOR FILING DATE: 2001-07-10
 ; PRIOR APPLICATION NUMBER: 60/217,883
 ; PRIOR FILING DATE: 2000-07-10
 ; NUMBER OF SEQ ID NOS: 16825
 ; SEQ ID NO 1280
 ; LENGTH: 1039
 ; TYPE: DNA
 ; ORGANISM: Myxococcus xanthus
 ; FEATURE:
 ; NAME/KEY: unsure
 ; LOCATION: (1)-(1039)
 ; OTHER INFORMATION: unsure at all n locations
 US-09-902-540-1280

Query Match 3.7%; Score 46.6; DB 4; Length 1039;
 Best Local Similarity 49.4%; Pred. No. 0.0034;
 Matches 154; Conservative 0; Mismatches 150; Indels 8; Gaps 1;
 QY 5 TTTAGTGTGTTATGGTCCATTTCTTATTTTAGCATTTTATTTCTATGCTAGTCTATCCAA 64
 Db 799 TTTATATTTTATATTTTGTGTTTATAGGATTTTGTATATTTGGGTGTTGATT 740
 QY 65 AGACGATTAAAGGAGTTCCACATGTTTCCGAAACATTTGAAAGAGAGCTTATCCAGT 124
 Db 739 AGAGCCTTGTAATTTCTTTTATTTTATTTTATGTTTATAGGGAGATTTTATTTT 680
 QY 125 GTACAGATCCTAATPAAGTGCACATCAGTGAATTTTATTTTATATCTTTTAA 184
 Db 679 TTA-----AGAAAAAACACTTTTGTGTTTATAGTTTATTTATTTATAT 628
 QY 185 TCCTATTTTCTCTCTTTTGTCTCAGTAATTTTGTATGAACCTTTTAAAGGACTTATG 244
 Db 627 TTTATGCGGNGTTTTTTTTTTTGTGTTTAAATTAATGATTTTATTTTATTTTATTTT 568
 QY 245 GCATGTAACATTTTATAAAGTAAGTCATGTTTATAATTTTATTTTCTCTGCTCCTT 304
 Db 567 TCTTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTT 508
 QY 305 ATGTAATTTATTT 316
 Db 507 GTTTTCATTTT 496

RESULT 15
 US-09-621-976-2813
 ; Sequence 2813, Application US/09621976
 ; Patent No. 6639063
 ; GENERAL INFORMATION:
 ; APPLICANT: Dumas Milne Edwards, J.B.
 ; APPLICANT: Jobert, S.
 ; APPLICANT: Giordano, J.Y.
 ; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
 ; FILE REFERENCE: GENSET.054PR2
 ; CURRENT APPLICATION NUMBER: US/09/621,976
 ; CURRENT FILING DATE: 2000-07-21
 ; NUMBER OF SEQ ID NOS: 19335
 ; SOFTWARE: Patent.pm
 ; SEQ ID NO 2813
 ; LENGTH: 832
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: 235..399
 US-09-621-976-2813

Query Match 3.5%; Score 44.8; DB 4; Length 832;
 Best Local Similarity 9.0%; Pred. No. 0.01;
 Matches 31; Conservative 169; Mismatches 146; Indels 0; Gaps 0;
 QY 38 ATTATATTCTATGATGCTATCCAGTGTACAGATCCTTAATAAGTGCACATTTCAGTGA 97
 Db 3 WYWKYTTWYAKWTWKWSYMYWKYMYWKYMYWKYMYWKYMYWKYMYWKYMYWKYMYWKY 62
 QY 98 ACATTTTGAAGAGAGCTTATCCAGTGTACAGATCCTTAATAAGTGCACATTTCAGTGA 157
 Db 63 AMWGYTKKAMCETKTKKKKKYMMWYMGWRRSYMAWMTWTGTYAYRSMYMYWYR 122
 QY 158 ATTTATTTTATATCTTTTATCTTTTATCTTTTCTCTCTCTCTCTCTCTCTCTCTCT 217
 Db 123 CWKKKAYYKTTTCYSSKGTWKWKWKAWTWWWKTYWAAATRYMMWMMCTKRWASW 182
 QY 218 TTGTATGAACCTTAAAGAGCTTATGGCATGTAAACATTTATTTATAAAGTAACTCATGG 277
 Db 183 YCWWGKARKWSTWRKRSYASARSACCCYSCSWGMSWKYMYWRRWRRWRRWRRWRRWRR 242
 QY 278 TTATAATTATTTTCTCTGCT 337

Search completed: April 24, 2005, 22:57:24
Job time : 248 secs

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Index	Sequence 1, Appl1	Sequence 22959, A	Sequence 25457, A	Sequence 28822, A	Sequence 8070, Ap	Sequence 269, App	Sequence 588, App	Sequence 1117, Ap	Sequence 1117, Ap	Sequence 426, App	Sequence 424, App
1	1274	100.0	1274	18	US-10-679-246-1						
2	1274	100.0	2924	18	US-10-357-930-22959						
3	1274	100.0	2924	18	US-10-357-930-25457						
4	1274	100.0	2924	18	US-10-357-930-28822						
5	1274	100.0	6107	10	US-09-768-891-8679						
6	1272.4	99.9	2829	17	US-10-104-260A-280						
7	1042.8	84.3	2440	17	US-10-641-643-588						
8	429	33.7	975	17	US-10-172-118-1117						
9	429	33.7	975	17	US-10-342-887-1117						
10	429	33.7	3502	15	US-10-177-293-426						
11	427.4	33.5	2540	15	US-10-177-293-424						

Qy 61 CCAAGACGATTAAGGGAGTCCACATGTTTCCGGAACATTTGAAAAGAGAGCTTATC 120

Db 720 TATGGCATGTAACATATTTATAAAGTAAGTCATGGTTATAATATATTTTCTCTCGCCT 779
Qy 301 CCTATATGATTTATTTTCAGAAATAGCCGTACAGCTGCTACAGCAATTAACCTACCGGTACC 360
Db 780 CCTATATGATTTATTTTCAGAAATAGCCGTACAGCTGCTACAGCAATTAACCTACCGGTACC 839
Qy 361 TCGAAGTGTCCACCATCCAGAGGGTGCCTGCCTGACTGGGCAACAAGTGCATCCACAAT 420
Db 840 TCGAAGTGTCCACCATCCAGAGGGTGCCTGCCTGACTGGGCAACAAGTGCATCCACAAT 899
Qy 421 GACTTGGCGAGTCTTTTTCAGTGTCCAGTCTGCTTTGACTATGTGTGTACCGCCATCTT 480
Db 900 GACTTGGCGAGTCTTTTTCAGTGTCCAGTCTGCTTTGACTATGTGTGTACCGCCATCTT 959
Qy 481 CAATGTCCAGTGGCCATCTTTTGTAGCAACTGTGCGCCAAAGTGCATGTTGTCCA 540
Db 960 CAATGTCCAGTGGCCATCTTTTGTAGCAACTGTGCGCCAAAGTGCATGTTGTCCA 1019
Qy 541 ACTTGGCGGGGCCCTTTGGGATCCATTGGCACTTGGCTATGGAGAAAGTGGCTAATTC 600
Db 1020 ACTTGGCGGGGCCCTTTGGGATCCATTGGCACTTGGCTATGGAGAAAGTGGCTAATTC 1079
Qy 601 GTACTTTTCCCTGTAAATATGCTCTCTGGATGTGAATAACTCTGCCACACAGAA 660
Db 1080 GTACTTTTCCCTGTAAATATGCTCTCTGGATGTGAATAACTCTGCCACACAGAA 1139
Qy 661 AAAGCAGACATGAAGAGCTCTGTAGTGTAGGCTTATTCCTGCTCGGCTGGTGTCT 720
Db 1140 AAAGCAGACATGAAGAGCTCTGTAGTGTAGGCTTATTCCTGCTCGGCTGGTGTCT 1199
Qy 721 TCTGTAAATGGCAAGCTCTCTGGATGTGTAAATGCCCATCTGATGCATCAGCATAAG 780
Db 1200 TCTGTAAATGGCAAGCTCTCTGGATGTGTAAATGCCCATCTGATGCATCAGCATAAG 1259
Qy 781 TCCATTACACCTACAGGAGAGGATATAGTTTCTTCTGCTACACACATTAATCTTCT 840
Db 1260 TCCATTACACCTACAGGAGAGGATATAGTTTCTTCTGCTACACACATTAATCTTCT 1319
Qy 841 GGTGCTGTGACTGGGTGATGATGAGTCTGCTGTTTGGCTTTCACCTCATGTTAGTCTTA 900
Db 1320 GGTGCTGTGACTGGGTGATGATGAGTCTGCTGTTTGGCTTTCACCTCATGTTAGTCTTA 1379
Qy 901 GAGAAACAGGAAATACGATGGTCAACGAGTCTTCCGCAATCGTACAGCTGATAGA 960
Db 1380 GAGAAACAGGAAATACGATGGTCAACGAGTCTTCCGCAATCGTACAGCTGATAGA 1439
Qy 961 ACACGCAAGCAAGCTGAAAATTTTGTACCGACTTGGAGTAAATGGTCAATGGCAGCA 1020
Db 1440 ACACGCAAGCAAGCTGAAAATTTTGTACCGACTTGGAGTAAATGGTCAATGGCAGCA 1499
Qy 1021 TTGACTTGGGAAGCGACTCTCTGATCTATTTCATGAAGGAATTCGAACAGCCATTATGAAT 1080
Db 1500 TTGACTTGGGAAGCGACTCTCTGATCTATTTCATGAAGGAATTCGAACAGCCATTATGAAT 1559
Qy 1081 AGCGACTGTCTAGTCTTTGACACACGATGTGCAAGCTTTTTCAGAAAAATGGCAATTTA 1140
Db 1560 AGCGACTGTCTAGTCTTTGACACACGATGTGCAAGCTTTTTCAGAAAAATGGCAATTTA 1619
Qy 1141 GGCATCAATGTAATCTATTTCATGTTGAAATGGCAATCAACAATTTTTCGCCAGTGT 1200
Db 1620 GGCATCAATGTAATCTATTTCATGTTGAAATGGCAATCAACAATTTTTCGCCAGTGT 1679
Qy 1201 TTAATACTTCAGTTTCACAGAAAAATAGGCACCCATCTGTCTGCCAACCTTAAACTCTTT 1260
Db 1680 TTAATACTTCAGTTTCACAGAAAAATAGGCACCCATCTGTCTGCCAACCTTAAACTCTTT 1739
Qy 1261 CGGTAGGTGGAGC 1274
Db 1740 CGGTAGGTGGAGC 1753

; Sequence 25457, Application US/10357930
; Publication No. US20040259086A1
; GENERAL INFORMATION:
; APPLICANT: Schlegel, Robert
; APPLICANT: Endege, Wilson
; APPLICANT: Monahan, John
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
; TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY OF
; TITLE OF INVENTION: HUMAN PROSTATE CANCER
; FILE REFERENCE: MRI-007BCN
; CURRENT APPLICATION NUMBER: US/10/357,930
; PRIOR FILING DATE: 2003-02-04
; PRIOR APPLICATION NUMBER: 09/785,276
; PRIOR FILING DATE: 2003-02-16
; PRIOR APPLICATION NUMBER: 60/183,319
; PRIOR FILING DATE: 2000-02-17
; PRIOR APPLICATION NUMBER: 60/189,862
; PRIOR FILING DATE: 2000-03-16
; PRIOR APPLICATION NUMBER: 60/207,454
; PRIOR FILING DATE: 2000-05-25
; PRIOR APPLICATION NUMBER: 60/211,314
; PRIOR FILING DATE: 2000-06-09
; PRIOR APPLICATION NUMBER: 60/219,007
; PRIOR FILING DATE: 2000-07-18
; PRIOR APPLICATION NUMBER: 60/255,281
; PRIOR FILING DATE: 2000-12-13
; NUMBER OF SEQ ID NOS: 62232
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 25457
; LENGTH: 2924
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 1, 57, 2923, 2924
; OTHER INFORMATION: n = A,T,C or G
; US-10-357-930-25457

Query Match 100.0%; Score 1274; DB 18; Length 2924;
Best Local Similarity 100.0%; Pred No. 3,1e-301;
Matches 1274; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 TTTCTTTAGTGTGTTATGTTCCATTTTCTATTTTAGCATTTTATTTCTATGATGATGCTAT 60
Db 480 TTTCTTTAGTGTGTTATGTTCCATTTTCTATTTTAGCATTTTATTTCTATGATGATGCTAT 539
Qy 61 CCAAGACCATTAAGGGAGTTCCACATGTTTTCCGGAACATTTTGAAGAGAGCTTATC 120
Db 540 CCAAGACCATTAAGGGAGTTCCACATGTTTTCCGGAACATTTTGAAGAGAGCTTATC 599
Qy 121 CAGTGTACAGATCCCTAAATAAGTGACATTCAGTGTAAATTTTATTTTATTTTAAATATCTTTT 180
Db 600 CAGTGTACAGATCCCTAAATAAGTGACATTCAGTGTAAATTTTATTTTATTTTAAATATCTTTT 659
Qy 181 TTAATCCTATTTTCTCTCTCTTTTGTCTCAGTAAATTTTGTATGAAACTTTTAAAGGACT 240
Db 660 TTAATCCTATTTTCTCTCTCTTTTGTCTCAGTAAATTTTGTATGAAACTTTTAAAGGACT 719
Qy 241 TATGGCATGTAACATTAATTAAGTAAGTCATGGTTATAATTAATTTTCTCTCGCCT 300
Db 720 TATGGCATGTAACATTAATTAAGTAAGTCATGGTTATAATTAATTTTCTCTCGCCT 779
Qy 301 CCTTATGATTTTATTTTCAGAAATAGCCGTACAGCTGCTACAGCAATTAACCTACCGGTACC 360
Db 780 CCTTATGATTTTATTTTCAGAAATAGCCGTACAGCTGCTACAGCAATTAACCTACCGGTACC 839
Qy 361 TCGAAGTGTCCACCATCCAGAGGGTGCCTGCCTGACTGGCAACAAGTGCATCCACAAT 420
Db 840 TCGAAGTGTCCACCATCCAGAGGGTGCCTGCCTGACTGGCAACAAGTGCATCCACAAT 899
Qy 421 GACTTGGCGAGTCTTTTTCAGTGTCCAGTCTGCTTTGACTATGTGTGTACCGCCATCTT 480
Db 900 GACTTGGCGAGTCTTTTTCAGTGTCCAGTCTGCTTTGACTATGTGTGTACCGCCATCTT 959

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QY 481 CAATGTCAGAGTGGCCATCTGTTGTAGCAACTGTGCGCCAAAGCTCACATGTTGTCCA 540
Db |||||||
QY 960 CAATGTCAGAGTGGCCATCTGTTGTAGCAACTGTGCGCCAAAGCTCACATGTTGTCCA 1019
Db |||||||
QY 541 ACTTCCGGGGCCCTTGGATCCATTCGCACTTGGCTATGGAGAAAGTGGCTAAATCA 600
Db |||||||
QY 1020 ACTTCCGGGGCCCTTGGATCCATTCGCACTTGGCTATGGAGAAAGTGGCTAAATCA 1079
Db |||||||
QY 601 GTACTTTTCCCTGTAAATATACGCTCTCTCGATGTGAATAACTCTGCCACACAGAA 660
Db |||||||
QY 1080 GTACTTTTCCCTGTAAATATACGCTCTCTCGATGTGAATAACTCTGCCACACAGAA 1139
Db |||||||
QY 661 AAAGCAGACCATGAGAGCTCTGAGATTAGGCTTATCTGCTGCGTGGCCCTGGTCT 720
Db |||||||
QY 1140 AAAGCAGACCATGAGAGCTCTGAGATTAGGCTTATCTGCTGCGTGGCCCTGGTCT 1199
Db |||||||
QY 721 TCCTGTAAATGGCAAGCTCTCTGGATGCTGAATGCCCATCTGATGCATCAGCATAAG 780
Db |||||||
QY 1200 TCCTGTAAATGGCAAGCTCTCTGGATGCTGAATGCCCATCTGATGCATCAGCATAAG 1259
Db |||||||
QY 781 TCATTACAAACCTCAGGGAGAGGATATAGTTTCTTGCTTACAGACATTAATCTTCT 840
Db |||||||
QY 1260 TCATTACAAACCTCAGGGAGAGGATATAGTTTCTTGCTTACAGACATTAATCTTCT 1319
Db |||||||
QY 841 GGTGCTGTTGACTGGGTGATGATGAGTCTCTGTTTGGCTTTCACCTCATGTTAGTCTTA 900
Db |||||||
QY 1320 GGTGCTGTTGACTGGGTGATGATGAGTCTCTGTTTGGCTTTCACCTCATGTTAGTCTTA 1379
Db |||||||
QY 901 GAGAAACAGGAAATACAGTGTGACAGCAGTCTTCCGCAATCGTACAGCTGATAGGA 960
Db |||||||
QY 1380 GAGAAACAGGAAATACAGTGTGACAGCAGTCTTCCGCAATCGTACAGCTGATAGGA 1439
Db |||||||
QY 961 ACACGCAAGCAAGCTGAAATTTTGTCTTACCGACTTGAGCTAAATGGTCATAGGGACGA 1020
Db |||||||
QY 1440 ACACGCAAGCAAGCTGAAATTTTGTCTTACCGACTTGAGCTAAATGGTCATAGGGACGA 1499
Db |||||||
QY 1021 TTGACTTGGGAAGGACTCTCGATCTATTCATGAAGGAATGCAACAGCCATTAATGAAT 1080
Db |||||||
QY 1500 TTGACTTGGGAAGGACTCTCGATCTATTCATGAAGGAATGCAACAGCCATTAATGAAT 1559
Db |||||||
QY 1081 AGCAGCTGTCTAGTCTTTGACACAGCAATGACAGCTTTTTCAGAGAAATGCAATTTA 1140
Db |||||||
QY 1560 AGCAGCTGTCTAGTCTTTGACACAGCAATGACAGCTTTTTCAGAGAAATGCAATTTA 1619
Db |||||||
QY 1141 GGCATCAATGTAATTTCCATGTTGAAATGGCAATCAACATTTTCGCCAGTGT 1200
Db |||||||
QY 1620 GGCATCAATGTAATTTCCATGTTGAAATGGCAATCAACATTTTCGCCAGTGT 1679
Db |||||||
QY 1201 TTAACCTTCAGTTTACAGAAATAGGCACCCATCTGTCTGCCAACCTTAAACTCTTT 1260
Db |||||||
QY 1680 TTAACCTTCAGTTTACAGAAATAGGCACCCATCTGTCTGCCAACCTTAAACTCTTT 1739
Db |||||||
QY 1261 CGGTAGGTGGAAGC 1274
Db |||||||
QY 1740 CGGTAGGTGGAAGC 1753
Db |||||||
```

```
RESULT 4
US-10-357-930-28822
; Sequence 28822, Application US/10357930
; Publication No. US20040259086A1
; GENERAL INFORMATION:
; APPLICANT: Schlögel, Robert
; APPLICANT: Endege, Wilson
; APPLICANT: Monahan, John
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
; IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY OF
; TITLE OF INVENTION: HUMAN PROSTATE CANCER
; FILE REFERENCE: MRI-007BCN
; CURRENT APPLICATION NUMBER: US/10/357,930
; CURRENT FILING DATE: 2003-02-04
; PRIOR APPLICATION NUMBER: 09/785,276
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; PRIOR FILING DATE: 2003-02-16
; PRIOR APPLICATION NUMBER: 60/183,319
; PRIOR FILING DATE: 2000-02-17
; PRIOR APPLICATION NUMBER: 60/189,862
; PRIOR FILING DATE: 2000-03-16
; PRIOR APPLICATION NUMBER: 60/207,454
; PRIOR FILING DATE: 2000-05-25
; PRIOR APPLICATION NUMBER: 60/211,314
; PRIOR FILING DATE: 2000-06-09
; PRIOR APPLICATION NUMBER: 60/219,007
; PRIOR FILING DATE: 2000-07-18
; PRIOR APPLICATION NUMBER: 60/255,281
; PRIOR FILING DATE: 2000-12-13
; NUMBER OF SEQ ID NOS: 62232
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 28822
; LENGTH: 2924
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 1..57..2923..2924
; OTHER INFORMATION: n = A,T,C or G
US-10-357-930-28822

Query Match 100.0%; Score 1274; DB 18; Length 2924;
Best Local Similarity 100.0%; Pred. No. 3.le-301;
Matches 1274; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTTCTTTAGTTGTTATGTCCTATTTCTATTTTAGCAATTTATTTATTTCTATGTTAGTCTAT 60
Db |||||||
QY 480 TTTCTTTAGTTGTTATGTCCTATTTCTATTTTAGCAATTTATTTATTTCTATGTTAGTCTAT 539
Db |||||||
QY 61 CCAAGACAGATTAAAGGAGTTCCACATCTTTTCCGGAACATTTTGAAGAGAGCTTATC 120
Db |||||||
QY 540 CCAAGACAGATTAAAGGAGTTCCACATCTTTTCCGGAACATTTTGAAGAGAGCTTATC 599
Db |||||||
QY 121 CAGTGTACAGATCTCTAATAAAGTGACATTCAGTGTAAATTTTATTTTATTTTATTTT 180
Db |||||||
QY 600 CAGTGTACAGATCTCTAATAAAGTGACATTCAGTGTAAATTTTATTTTATTTTATTTT 659
Db |||||||
QY 181 TTAATCTTATTTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 240
Db |||||||
QY 660 TTAATCTTATTTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 719
Db |||||||
QY 241 TATGCAATGTAACATTAATTTATAAAGTAAGTCAATGTTTATTAATTTATTTTCTCTCTCT 300
Db |||||||
QY 720 TATGCAATGTAACATTAATTTATAAAGTAAGTCAATGTTTATTAATTTATTTTCTCTCTCT 779
Db |||||||
QY 301 CTTATGTAATTTATTTTCAAAATGAGCGTCAAGTGTACAGCATTTACCTACCGGTACC 360
Db |||||||
QY 780 CTTATGTAATTTATTTTCAAAATGAGCGTCAAGTGTACAGCATTTACCTACCGGTACC 839
Db |||||||
QY 361 TCGAAGTGTCCACCATCCAGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 420
Db |||||||
QY 840 TCGAAGTGTCCACCATCCAGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 899
Db |||||||
QY 421 GACTTGGCGAGTCTTTTTCAGTGTCCAGTGTCCAGTGTCCAGTGTCCAGTGTCCAGTGTCTT 480
Db |||||||
QY 900 GACTTGGCGAGTCTTTTTCAGTGTCCAGTGTCCAGTGTCCAGTGTCCAGTGTCCAGTGTCTT 959
Db |||||||
QY 481 CAATGTACAGTGGCCATCTTCTGTTGTAGCAACTGTGCGCCAAAGCTCACATGTTGTCCA 540
Db |||||||
QY 960 CAATGTACAGTGGCCATCTTCTGTTGTAGCAACTGTGCGCCAAAGCTCACATGTTGTCCA 1019
Db |||||||
QY 541 ACTTCCGGGGCCCTTGGATCCATTTGGATCCATTTGGCTATGGAGAAAGTGGCTAAATCA 600
Db |||||||
QY 1020 ACTTCCGGGGCCCTTGGATCCATTTGGATCCATTTGGCTATGGAGAAAGTGGCTAAATCA 1079
Db |||||||
QY 601 GTACTTTTCCCTGTAAATATAGGCTCTTCTGATGTGAATAACTCTGCCACACAGAA 660
Db |||||||
QY 1080 GTACTTTTCCCTGTAAATATAGGCTCTTCTGATGTGAATAACTCTGCCACACAGAA 1139
Db |||||||
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Db 4304 GCATCAATGTAACATATTTCCATGTTGAAATGCAATCAAACTTTTCGGCCAGTGT 4363
Qy 1201 TTAATACTTCACTTTTACAGAAAATAAGCAACCAATCTGTCTGCAACCTAAACTCTTT 1260
Db 4364 TTAATACTTCACTTTTACAGAAAATAAGCAACCAATCTGTCTGCAACCTAAACTCTTT 4423
Qy 1261 CGTAGGTGGAAGC 1274
Db 4424 CGTAGGTGGAAGC 4437

RESULT 6
US-10-108-260A-269
; Sequence 269, Application US/10108260A
; Publication No. US20040005560A1
; GENERAL INFORMATION:
; APPLICANT: HELIX RESEARCH INSTITUTE
; TITLE OF INVENTION: No. US20040005560A1e1 full length cDNA
; FILE REFERENCE: H1-A0106
; CURRENT APPLICATION NUMBER: US/10/108,260A
; CURRENT FILING DATE: 2002-03-27
; NUMBER OF SEQ ID NOS: 548
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 269
; LENGTH: 2829
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-10-108-260A-269

Query Match 99.9%; Score 1272.4; DB 17; Length 2829;
Best Local Similarity 99.9%; Pred. No. 7.4e-301;
Matches 1273; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 TTTCTTTAGTTGTTATGGTCCATTTTCTATTTTAGCAATTTATTTCTATGTCAT 60
Db 1134 TTTCTTTAGTTGTTATGGTCCATTTTCTATTTTAGCAATTTATTTCTATGTCAT 1193

Qy 61 CCAAGACGATTAAAGGAGTTCCACATGTTTCCGGAACATTTTGAAAAGAGAGCTTATC 120
Db 1194 CCAAGACGATTAAAGGAGTTCCACATGTTTCCGGAACATTTTGAAAAGAGAGCTTATC 1253

Qy 121 CAGGTACAGATCCTAATAAAGTGCAATTCAGTGAATTTTATTTTATATATCTTTT 180
Db 1254 CAGGTACAGATCCTAATAAAGTGCAATTCAGTGAATTTTATTTTATATATCTTTT 1313

Qy 181 TTAATCCTATTTTCTCTCTTTTCTGTCAGTAAATTTTGTATGAACTTTTAAAGGACT 240
Db 1314 TTAATCCTATTTTCTCTCTTTTCTGTCAGTAAATTTTGTATGAACTTTTAAAGGACT 1373

Qy 241 TATGGCATGTAACATTTATTTATAAAGTAAGTCATGTTATTAATTTTCTCTGCT 300
Db 1374 TATGGCATGTAACATTTATTTATAAAGTAAGTCATGTTATTAATTTTCTCTGCT 1433

Qy 301 CTTATGTTATTTTACAGAAAAGAGCCGTGACATGCTACAGATTTACCTACCGTACC 360
Db 1434 CTTATGTTATTTTACAGAAAAGAGCCGTGACATGCTACAGATTTACCTACCGTACC 1493

Qy 361 TCGAAGTGTCCACCATCCAGAGGTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 420
Db 1494 TCGAAGTGTCCACCATCCAGAGGTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1553

Qy 421 GACTTGGCGAGTCTTTTGTAGTGTCCAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 480
Db 1554 GACTTGGCGAGTCTTTTGTAGTGTCCAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1613

Qy 481 CAATGTACAGTGTGCTCTTTTGTAGCAACTGTGCTGCTGCTGCTGCTGCTGCTGCTGCT 540
Db 1614 CAATGTACAGTGTGCTCTTTTGTAGCAACTGTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1673

Qy 541 ACTTGGCGGGCCCTTTTGGGATCCATTCGCAACTTGGCTATGGGAAAGTGGCTAAATCA 600
Db 1674 ACTTGGCGGGCCCTTTTGGGATCCATTCGCAACTTGGCTATGGGAAAGTGGCTAAATCA 1733

Qy 601 GTACTTTTCCCTGTAAATATGCGTCTTCTGGATGTGAATAAATAACTCTGCGCACACAGAA 660
Db 1734 GTACTTTTCCCTGTAAATATGCGTCTTCTGGATGTGAATAAATAACTCTGCGCACACAGAA 1793

Qy 661 AAAGCAGACCATGAGAGCTCTGTGAGTTTAGGCTTATTTCCCTGCGTGGCTGGTGTCT 720
Db 1794 AAAGCAGACCATGAGAGCTCTGTGAGTTTAGGCTTATTTCCCTGCGTGGCTGGTGTCT 1853

Qy 721 TCCTGTAATGGCAAGGCTCTCTGATGCTGTAAATGCCCATCTGTATCGATCAAGTAAG 780
Db 1854 TCCTGTAATGGCAAGGCTCTCTGATGCTGTAAATGCCCATCTGTATCGATCAAGTAAG 1913

Qy 781 TCCATTACAAACCTTACAGGGAGAGATATAGTTTCTTGTCTACAGACATTAATTTCTCT 840
Db 1914 TCCATTACAAACCTTACAGGGAGAGATATAGTTTCTTGTCTACAGACATTAATTTCTCT 1973

Qy 841 GGTGCTGTGACTGGGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 900
Db 1974 GGTGCTGTGACTGGGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2033

Qy 901 GAGAAACAGGAAAAATACGATGGTCAACAGATGTCACAGAGTTCCTGCAATCGTACAGCTATAGGA 960
Db 2034 GAGAAACAGGAAAAATACGATGGTCAACAGATGTCACAGAGTTCCTGCAATCGTACAGCTATAGGA 2093

Qy 961 ACAGCAAGAGAGCTGAAAAATTTTGTCTTACCGATTCGAGCTAAATGTTGATGCGACGA 1020
Db 2094 ACAGCAAGAGAGCTGAAAAATTTTGTCTTACCGATTCGAGCTAAATGTTGATGCGACGA 2153

Qy 1021 TTGACTTGGGAAGGAGCTCTCGATCTATTATGAAGGAATTTGCAACAGCCATATATGAAT 1080
Db 2154 TTGACTTGGGAAGGAGCTCTCGATCTATTATGAAGGAATTTGCAACAGCCATATATGAAT 2213

Qy 1081 AGCGACTCTCTAGTCTTTTGACACAGCATTTGACAGCTTTTTCGAGAAAAATGGCAATTTA 1140
Db 2214 AGCGACTCTCTAGTCTTTTGACACAGCATTTTTCGAGAAAAATGGCAATTTA 2273

Qy 1141 GCATCAATGTAACATTTTCCATGTTGAAATGCAATCAAACTTTTCTGCGCAGTGT 1200
Db 2274 GCATCAATGTAACATTTTCCATGTTGAAATGCAATCAAACTTTTCTGCGCAGTGT 2333

Qy 1201 TTAATACTTCACTTTTACAGAAAATAAGGCAACCAATCTGTCTGCGCAACTAAACTCTTT 1260
Db 2334 TTAATACTTCACTTTTACAGAAAATAAGGCAACCAATCTGTCTGCGCAACTAAACTCTTT 2393

Qy 1261 CGTAGGTGGAAGC 1274
Db 2394 CGTAGGTGGAAGC 2407

RESULT 7
US-10-641-643-588
; Sequence 588, Application US/10641643
; Publication No. US20040077003A1
; GENERAL INFORMATION:
; APPLICANT: Cocks, Benjamin G.
; Susan G. Stuart
; Jeffrey J. Seilhamer
; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL
; GENE EXPRESSION
; NUMBER OF SEQUENCES: 1508
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
; STREET: 3174 PORTER DRIVE
; CITY: PALO ALTO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
; CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/641,643
FILING DATE: 14-Aug-2003
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: <Unknown>
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Zeller, Karen J.
REGISTRATION NUMBER: 37,071
REFERENCE/DOCKET NUMBER: PA-0001 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 855-0555
TELEFAX: (650) 845-4166
INFORMATION FOR SEQ ID NO: 588:
SEQUENCE CHARACTERISTICS:
LENGTH: 2440 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: SPLNFET01
CLONE: 29244
SEQUENCE DESCRIPTION: SEQ ID NO: 588 :
US-10-641-643-588

Query Match 81.9%; Score 1042.8; DB 17; Length 2440;
Best Local Similarity 99.8%; Pred. No. 1.2e-244;
Matches 1044; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

229 TTTAAAGGACTTATGGCATGTAAACATTTATTAAGTAAGTCACTGGTTAATATT 288
Db
462 TTTGAAGGACTTATGGCATGTAAACATTTATTAAGTAAGTCACTGGTTAATATT 521
Qy
289 TTTCTCTGCTCCTTATGTATTTATTTACAGAAATGAGCGGTGAGACTGCTACAGCATTA 348
Db
522 TTTCTCTGCTCCTTATGTATTTATTTACAGAAATGAGCGGTGAGACTGCTACAGCATTA 581
Qy
349 CTTACCGGTACTCGAAGTGTCCACATCCAGAGGGTGCCTGCCCTGACTGGCACACT 408
Db
582 CTTACCGGTACTCGAAGTGTCCACATCCAGAGGGTGCCTGCCCTGACTGGCACACT 641
Qy
409 GCATCCACAAATGACTTGGCGAGTCTTTTGTAGTGCAGTCTGCTTGGACTATGTGTTA 468
Db
642 GCATCCACAAATGACTTGGCGAGTCTTTTGTAGTGCAGTCTGCTTGGACTATGTGTTA 701
Qy
469 CGGCCCATCTTCAATGTGAGAGTGGCCATCTTTGTAGCAACTGTCCGCCAAAGCTC 528
Db
702 CGGCCCATCTTCAATGTGAGAGTGGCCATCTTTGTAGCAACTGTCCGCCAAAGCTC 761
Qy
529 ACATGTGTCCAACTTGC CGGGGCCCTTTGGGATCCATTCGCAACTTGGCTATGGAGAA 588
Db
762 ACATGTGTCCAACTTGC CGGGGCCCTTTGGGATCCATTCGCAACTTGGCTATGGAGAA 821
Qy
589 GTGGCTAATTCAGTACTTTTCCCTGTAATATAGTCTTCTGGATGGAATAACTCTG 648
Db
822 GTGGCTAATTCAGTACTTTTCCCTGTAATATAGTCTTCTGGATGGAATAACTCTG 881
Qy
649 CCACACACAGAAAGAGCAGACCATGAAGAGCTGTGTAGTGTAGGCTTTATTCCTGTCG 708
Db
882 CCACACACAGAAAGAGCAGACCATGAAGAGCTGTGTAGTGTAGGCTTTATTCCTGTCG 941
Qy
709 TGCCCTGTGTCTTCTGTAATAGGCAAGGCTCTCTGGATGCTGTAAATGCCCATCTGATG 768
Db
942 TGCCCTGTGTCTTCTGTAATAGGCAAGGCTCTCTGGATGCTGTAAATGCCCATCTGATG 1001
Qy
769 CATCAGCATAAGTCCATTAACACCCCTACAGGAGAGGATATAGTTTTTCTTCTGCTACAG 828
Db
1002 CATCAGCATAAGTCCATTAACACCCCTACAGGAGAGGATATAGTTTTTCTTCTGCTACAG 1061
Qy
829 ATTAATCTTCCTGGTGTCTGCTGAGTGGGTGATGATGACGTCTGTTTGGCTTTCACATTC 888
Db
1062 ATTAATCTTCCTGGTGTCTGCTGAGTGGGTGATGATGACGTCTGTTTGGCTTTCACATTC 1121

RESULT 8

US-10-172-118-1117
; Sequence 1117, Application US/10172118
; Publication No. US20030224374A1
; GENERAL INFORMATION:
; APPLICANT: Dai, Hongyue
; APPLICANT: He, Hongyue
; APPLICANT: Linsley, Peter
; APPLICANT: Mao, Mao
; APPLICANT: Roberts, Chris
; APPLICANT: Van 't Veer, Laura
; APPLICANT: Van de Vijver, Marc
; APPLICANT: Bernarde, Rene
; TITLE OF INVENTION: Diagnosis and Prognosis of Breast Cancer Patients
; FILE REFERENCE: 9301-175-999
; CURRENT APPLICATION NUMBER: US/10/172,118
; PRIOR FILING DATE: 2002-06-14
; PRIOR APPLICATION NUMBER: 60/380,770
; NUMBER OF SEQ ID NOS: 2699
; SEQ ID NO 1117
; LENGTH: 975
; TYPE: DNA
; ORGANISM: Homo sapiens
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: NM 005067
; DATABASE ENTRY DATE: 2001-06-18
US-10-172-118-1117

Query Match 33.7%; Score 429; DB 17; Length 975;
Best Local Similarity 73.8%; Pred. No. 1.7e-94;
Matches 559; Conservative 0; Mismatches 195; Indels 3; Gaps 1;

Qy 416 ACAATGACTTGGCGAGTCTTTTGTAGTGTCCAGTCTGCTTTGACTATGTATACGCCCA 475
Db 212 ACCAGAGCTGACTCGTCTTCGAGTGTCCGCTGCTTTGACTATGTCTTGCCTCCTA 271
Qy 476 TTTCTCAATGTGAGAGTGGCCATCTTGTGTGAGCAACTGTCCGCCAAAGCTCACAATGT 535
Db 272 TTTCTCAGTCCAGCGCGGCACTTGTGTGTAACTGAGTGTGAGTGTGAGTGTGAGTGT 331
Qy 536 GTCCCAACTTCCCGGGGCCCTTTGGGATC---CATTCGCAACTTGGCTATGGAGAAAGTGG 592
Db 332 GCCCGAGTGCAGGGGGCGCCCTGACGCCCAAGCATCAGGAACCTGGCTATGGAGAAAGTGG 391

593 CTAATTCAGTACTTTTCCCTGTAAATATGCGTCTTCTGGATGTGAATAAATACTCTGCCAC 652
 392 CTTGGGAGTCTCTTTTCCCTGTAAATATGCGCACCACCGGCTGTTCCTGACCCCTGCCAC 451
 653 ACACAGAAAGACACACCATGAAGCTCTGTGAGTTTATAGGCTTTATTCCTGTCCGTGCC 712
 452 ATACGGAGAAACCAAGACATGAAGACATATGTAATACCGTCCCTACTCTCTGCCCATGTC 511
 713 CTGCTGCTTCTCTGTAATAGGCAAGGCTCTCTGGATGCTGTAATGCCCATCTGATGCATC 772
 512 CTGCTGCTTCTCTGTAATAGGCAAGGCTCTCTGGATGCTGTAATGCCCATCTGATGCAC 571
 773 AGCAATAGTCCATTAACACCCCTACAGGAGAGGATATAGTTTCTCTCTACAGACATTA 832
 572 CCCAAGAGCAATTAACACCCCTACAGGAGAGGATATAGTTTCTCTCTACAGACATTA 631
 833 ATCTTCTCTGCTGCTGTGACTGGGTGATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 892
 632 ACTTGCAGGGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 691
 893 TAGTCTTTAGAGAAACAGGAAATAACGATGCTCACAGCAGTTCTTGGCAATCGTACAGC 952
 692 TGGTCTGAGAGAAACAGGAAATAACGATGCTCACAGCAGTTCTTGGCAATCGTACAGC 751
 953 TGATAGGAACAGCAAGCAAGCTGAAATTTTCTTACCGACTTACGCTGAGCTAAATGCTCAT 1012
 752 TCATTTGGCAACCGCAAGCAAGCTGAAATTTTCTTACCGACTTACGCTGAGCTAAATGCTCAT 811
 1013 GCGCAGGATTTGCTTGGGAGGAGCTCTCTGATCTATTTATGAAAGAAATTTGCAACAGCCA 1072
 812 GCGGAGATTTGCTTGGGAGGAGCTCTCTGATCTATTTATGAAAGAAATTTGCAACAGCCA 871
 1073 TTATGAATAGCAGCTGTCTGATCTTTTGAACACGAGCTTTTGGCAATCGTACAGC 1132
 872 TCATGAACAGCAGCTGTCTGATCTTTTGAACACGAGCTTTTGGCAATCGTACAGC 931
 1133 GCAATTTAGGCAATCAATGTAATTTTCCATGTTG 1169
 932 GGAACCTTGAATCAATGTAATTTTCCATGTTG 968

RESULT 9
 US-10-342-887-1117
 ; Sequence 1117, Application US/10342887
 ; Publication No. US20040058340A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Dai, Hongyue
 ; APPLICANT: He, Yudong
 ; APPLICANT: Linsley, Peter S.
 ; APPLICANT: Mao, Mao
 ; APPLICANT: Roberts, Christopher J.
 ; APPLICANT: Van 't Veer, Laura Johanna
 ; APPLICANT: Van de Vijver, Marc J.
 ; APPLICANT: Bernards, Rene
 ; TITLE OF INVENTION: Diagnosis and Prognosis of Breast Cancer Patients
 ; FILE REFERENCE: 9301-188-999
 ; CURRENT APPLICATION NUMBER: US/10/342,887
 ; CURRENT FILING DATE: 2003-01-15
 ; PRIOR APPLICATION NUMBER: 60/298,918
 ; PRIOR FILING DATE: 2001-06-18
 ; PRIOR APPLICATION NUMBER: 60/380,710
 ; PRIOR FILING DATE: 2002-05-14
 ; PRIOR APPLICATION NUMBER: 10/172,118
 ; PRIOR FILING DATE: 2002-06-14
 ; NUMBER OF SEQ ID NOS: 2699
 ; SEQ ID NO 1117
 ; LENGTH: 975
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 US-10-342-887-1117

Query Match 33.7%; Score 429; DB 17; Length 975;

Best Local Similarity 73.8%; Pred. No. 1.7e-94;
 Matches 559; Conservative 0; Mismatches 195; Indels 3; Gaps 1;
 416 ACATGACTTGGGAGTCTTTTGGAGTGTCCAGTCTGCTTTGACTATGTGTACCGGCCA 475
 212 ACCAGAGCTGACCTCGCTCTTGGAGTGTCCGGTCTGCTTTGACTATGTCTCTCTCTA 271
 476 TTCTTCAATGTCAGAGTGGCCATCTTGTGTAGCAATCTGCGCCCAAGCTCACATGTT 535
 272 TTCTGAGTGGCCAGCCCGGCACTGTGTGTAAACCAATGCCGCCAGAAAGTTGAGCTGCT 331
 536 GTCCAACTTGGCGGGCCCTTTGGGATC---CATTCGCAACTTGGCTATGGAGAAAGTGG 592
 332 GCCCGAGCTGCGAGGGGGCCCTGACGCGCCAGCATCAGGAACTTGGCTATGGAGAAAGTGG 391
 593 CTAATTCAGTACTTTTCCCTGTAAATATGCGTCTTCTGGATGTGAATAAATACTCTGCCAC 652
 392 CCTCGGAGTCTCTTTCCTCTGTAAGTATGCCACACGGGCTGTTCCTGACCTGCCAC 451
 653 ACACAGAAAGACAGACCATGAAGAGCTCTGTGAGTTTATAGGCTTTATCTCTGCTGCC 712
 452 ATACGGAGAAACAGAAACATGAAGACATATGTGAATACCGTCCCTACTCTCTGCCATGTC 511
 713 CTGCTGCTTCTGTAATGCAAGGCTCTCTGGATGCTGTAATGCCCATCTGATGCATC 772
 512 CTGCTGCTTCTGCAAGTGGCAGGGGCTCCCTGGAAGCTGTGATGCTCCATCTCTGACG 571
 773 AGCATAAGTCCATTAACACCCCTACAGGAGAGGATATAGTTTCTTCTGCTACAGACATTA 832
 572 CCCAAGAGCATTTACACCCCTTACGGGAGAGACATGCTCTTCTAGCTACAGACATTA 631
 833 ATCTTCTGCTGCTTTCATCTGGGTGATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 892
 632 ACTTGCAGGGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 691
 893 TAGTCTTGAAGAAACAGGAAATAACGATGCTCACAGCAGTTCTTGGCAATCGTACAGC 952
 692 TGGTCTGAGAGAAACAGGAAATAACGATGCTCACAGCAGTTCTTGGCAATCGTACAGC 751
 953 TGATAGGAACAGCAAGCAAGCTGAAATTTTCTTACCGACTTACGCTGAGCTAAATGCTCAT 1012
 752 TCATTTGGCAACCGCAAGCAAGCTGAAATTTTCTTACCGACTTACGCTGAGCTAAATGCTCAT 811
 1013 GCGCAGGATTTGCTTGGGAGGAGCTCTCTGATCTATTTATGAAAGAAATTTGCAACAGCCA 1072
 812 GCGGAGATTTGCTTGGGAGGAGCTCTCTGATCTATTTATGAAAGAAATTTGCAACAGCCA 871
 1073 TTATGAATAGCAGCTGTCTGATCTTTTGAACACGAGCTTTTGGCAATCGTACAGC 1132
 872 TCATGAACAGCAGCTGTCTGATCTTTTGAACACGAGCTTTTGGCAATCGTACAGC 931
 1133 GCAATTTAGGCAATCAATGTAATTTTCCATGTTG 1169
 932 GGAACCTTGAATCAATGTAATTTTCCATGTTG 968

RESULT 10
 US-10-177-293-426
 ; Sequence 426, Application US/10177293
 ; Publication No. US20030124128A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Lillie, James
 ; APPLICANT: Glatt, Karen
 ; APPLICANT: Zhao, Xumei
 ; APPLICANT: Gannavarpu, Manjula
 ; APPLICANT: Kamatkar, Shubhangi
 ; APPLICANT: Mertens, Maureen
 ; APPLICANT: Myer, Vic
 ; APPLICANT: Wang, Youzhen
 ; APPLICANT: Xu, Yongyao
 ; APPLICANT: Hoersch, Sebastian
 ; APPLICANT: Monahan, John
 ; APPLICANT: Meyers, Rachel E.

; APPLICANT: Bast Jr., Robert C.
; APPLICANT: Hortobagyi, Gabriel N.
; APPLICANT: Puzstai, Lajos
; APPLICANT: Meric, Funda
; APPLICANT: Sahin, Aysegul
; APPLICANT: Mills, Gordon B.
; TITLE OF INVENTION: COMPOSITIONS, KITS, AND METHODS FOR IDENTIFICATION, ASSESSMENT,
; TITLE OF INVENTION: PREVENTION, AND THERAPY OF BREAST CANCER
; FILE REFERENCE: MRI-038
; CURRENT APPLICATION NUMBER: US/10/177,293
; CURRENT FILING DATE: 2002-06-21
; PRIOR APPLICATION NUMBER: US 60/299,887
; PRIOR FILING DATE: 2001-06-21
; PRIOR APPLICATION NUMBER: US 60/301,572
; PRIOR FILING DATE: 2001-06-27
; PRIOR APPLICATION NUMBER: US 60/306,501
; PRIOR FILING DATE: 2001-07-18
; PRIOR APPLICATION NUMBER: US 60/325,002
; PRIOR FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: US 60/362,585
; PRIOR FILING DATE: 2002-03-05
; PRIOR APPLICATION NUMBER: US 60/xxx,xxx
; PRIOR FILING DATE: 2002-05-14
; NUMBER OF SEQ ID NOS: 506
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 426
; LENGTH: 2502
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-177-293-426

Query Match 33.7%; Score 429; DB 15; Length 2502;
Best Local Similarity 73.8%; Pred. No. 2.7e-94;
Matches 559; Conservative 0; Mismatches 195; Indels 3; Gaps 1;

QY 416 ACAATGACTGGCGAGCTCTTTTGGTGTCCAGTCTGCTTGGACTATGTGTTACCGCCCA 475
DB ACCAGAGCTGACCTCGCTCTTCGAGTGTCCGCTGCTTTGACTATGTGCTTCCCTCCTTA 797
QY 476 TTCTTCAATGTCCAGAGTGGCCATCTTTTGTAGCAACTGTGCCCCAAAGCTCACATGTT 535
DB TTCTGAGTGCACGGCGCGGACCTGTGTGTAAACCAATGCCGCCAGAGTTGAGCTGCT 857
QY 536 GTCCAACTTCCGGGGCCCTTTGGGATC---CATTCGCAACTTGGCTATGGAGAAAGTGG 592
DB GCCCGAGTGCAGGGGCGCCCTGACGCCAGCATCAGGAACCTGGCTATGGAGAGTGG 917
QY 593 CTAAATTCAGTACTTTTCCCTCTGAATATGCGTCTTCTGATGTGAAATTAATCTGCCAC 652
DB CTCTGCGCATCTCTTTCCCTCTGAATATGCGCATGCCACCGGGCTGTCCCTGACCCCTGACC 977
QY 653 ACACAGAAAAAGCAGACCATGAAGAGCTCTGTGAGTTTAGGCTTATCTGTCCGTGCC 712
DB ATACGGAGAAACAGAAACATGAGACATATGTAATACCGTCCCTACTCTGCCCATGTC 1037
QY 713 CTGGTCTTCTGTAATGGCAAGGCTCTCTGAGTGTCTGTAATGCCCCATCTGATCATC 772
DB CTGGTCTTCTGCAAGTGGCAGGGTCCCTGGAAGCTGTGATGTCCTCATCTCATGCAAG 1097
QY 773 AGCATTAAGTCCATTACAAACCTACAGGAGAGATATAGTTTCTTGTACAGACATTA 832
DB CCCACAAGAGCATTAACACCCCTTCAGGGAGAGACATGCTCTTCTTAGCTACAGACATTA 1157
QY 833 ATCTTCTCGTGTGTGTGACTGGGTGATGATGAGTCCCTGTTTGTGGCTTTTCACTTCATGT 892
DB ACTTGCAGGGGCTGTGACTGGGTGATGATGAGTCACTGTTTGGCCATCACTTCATGCT 1217
QY 893 TAGTCTTACAGAAACAGGAAAAATACGATGGTCCACAGAGATTTCTTGGCAATCGTACAGC 952
DB TGGTGTGTGAGAAAAAAGAGAGAGTACGAAGGCCACCCAGCAGTTTTTTTGGCATGCTCTGC 1277
QY 953 TGATAGGAACAGCAAGCAAGCTGAAATTTTGTCTTACCGACTTGTAGCTTAATGTGTCATA 1012

DB 1278 TCATTGGCACCCCAAGCCGAGAACTTTCCCTACAGACTGGAGTTGAATGGGAACC 1337
QY 1013 GGCGACGATTGACTTGGGAAGCGACTCTCTGATCTATTATGAAGGAATTCACACAGCCA 1072
DB GGCGGAGATTGACTTGGGAGGCCACGCCCGTTTCGATTATGACGGTGTGCTGCGGCCCA 1397
QY 1073 TTATGAATAGCGACTGTCTAGTCTTTTGACACACGACATTCGACAGCTTTTTCGAGAAATG 1132
DB TCATGAACAGCGACTGCTCTTGTTCGACACAGCCATAGCACATCTTTTTCGACGATAATG 1457
QY 1133 GCAATTTAGCATCAATGTAACCTATTTCATGATGTTG 1169
DB GGAACCTTGAATCAATGTTACTATTTCATGTTG 1494

RESULT 11
US-10-177-293-424
; Sequence 424, Application US/10177293
; Publication No. US20030124128A1
; GENERAL INFORMATION:
; APPLICANT: Lillie, James
; APPLICANT: Glatt, Karen
; APPLICANT: Zhao, Xumei
; APPLICANT: Gannavarpu, Manjula
; APPLICANT: Kamatkar, Shubhangi
; APPLICANT: Mertens, Maureen
; APPLICANT: Myer, Vic
; APPLICANT: Wang, Youzhen
; APPLICANT: Xu, Yongyao
; APPLICANT: Hoersch, Sebastian
; APPLICANT: Monahan, John
; APPLICANT: Meyers, Rachel E.
; APPLICANT: Bast Jr., Robert C.
; APPLICANT: Hortobagyi, Gabriel N.
; APPLICANT: Puzstai, Lajos
; APPLICANT: Meric, Funda
; APPLICANT: Sahin, Aysegul
; APPLICANT: Mills, Gordon B.
; TITLE OF INVENTION: COMPOSITIONS, KITS, AND METHODS FOR IDENTIFICATION, ASSESSMENT,
; TITLE OF INVENTION: PREVENTION, AND THERAPY OF BREAST CANCER
; FILE REFERENCE: MRI-038
; CURRENT APPLICATION NUMBER: US/10/177,293
; CURRENT FILING DATE: 2002-06-21
; PRIOR APPLICATION NUMBER: US 60/299,887
; PRIOR FILING DATE: 2001-06-21
; PRIOR APPLICATION NUMBER: US 60/301,572
; PRIOR FILING DATE: 2001-06-27
; PRIOR APPLICATION NUMBER: US 60/306,501
; PRIOR FILING DATE: 2001-07-18
; PRIOR APPLICATION NUMBER: US 60/325,002
; PRIOR FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: US 60/362,585
; PRIOR FILING DATE: 2002-03-05
; PRIOR APPLICATION NUMBER: US 60/xxx,xxx
; PRIOR FILING DATE: 2002-05-14
; NUMBER OF SEQ ID NOS: 506
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 424
; LENGTH: 2240
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-177-293-424

Query Match 33.5%; Score 427.4; DB 15; Length 2240;
Best Local Similarity 73.7%; Pred. No. 6.2e-94;
Matches 558; Conservative 0; Mismatches 196; Indels 3; Gaps 1;

QY 416 ACAATGACTGGCGAGTCTTTTGGTGTCCAGTCTGCTTTGACTATGTGTTACCGCCCA 475
DB ACCAGAGCTGACCTCGCTCTTCGAGTGTCCGCTCTGCTTTGACTATGTCTCTGCTCCTTA 797
QY 476 TTCTTCAATGTCCAGAGTGGCCATCTTGTGTAGCAACTGTGCCCCAAAGCTCACATGTT 535

Query Match	33.5%	Score 427.4	DB 18	Length 2240
Best Local Similarity	73.7%	Pred. No. 6.2e-94		
Matches 558	Conservative	0	Mismatches 196	Indels 3
Gaps	1			
416	ACAATGACTTGGCGAGTCTTTTGTAGTGTCCAGTCTGCTTTGAGCTATGTGTACGCCCA	475		
738	ACCAAGCTGACCTCGCTCTTCGAGTGTCCGGTCTGCTTTGACTATGTCTGCTGCCCTCCTA	797		
476	TTCTTCAATGTCCAGTGTGCCATCTTTTGTAGCAACTGTCTGCCCAAGCTCACATGTT	535		
798	TTCTGCAGTGTCCAGGCGCGGCACTGTGTGTAAACAATGCCGCCAGAAAGTTGACTGCT	857		
536	GTCCAACTTGTCCGGGGCCCTTTGGGATC---CAITTCGCAACTTGGCTATGGAGAAAGTGG	592		
858	GCCCGAGCTGCAGGGGCGCCCTGACGCCCAGCATCAGGAACCTGGCTATGGAGAAAGTGG	917		
593	CTAAATTCAGTACTTTTCCCTGTAAATATGCTTCTTGAGTGTGAAATAAATCTTGCCAC	652		
918	CCTCGGAGTCTTTCCTGTGAAGTATGCCACACGCGCTGTTCCTTCAGCCCTGCACC	977		
653	ACACAGAAAAGCAGACCATGAAGACTCTGTGAGTTTAGGCGCTTAATCCTGTCCGTGCC	712		
978	ATACGGAGAAACAGAAACATGAAGACATATGTGAATACCGGCCCTACTCCTGCCCATGTC	1037		
713	CTGGTGCTTCTGTAAATGGCAAGGCTCTCTGGATGCTTAATGCCCATCTGATGCATC	772		
1038	CTGGTGCTTCTGCAAGTGGCAGGGTCCCTGGAAGCTGTGATGTCCCATCTCATGCAGC	1097		
773	AGCAATAGTCCATTAACAACCTACAGGGAGAGATATAGTTTTTCTGTGTACAGACATTA	832		
1098	CCCAAGAGCAATTAACCCCTTCAGAAAGACATCGTCTTCTTAGCTACAGACATTA	1157		
833	ATCTTCTGTGCTGTGTACTGGGTGATGATGACGTCTGTGTGTGTGTGTCTTCACTCATGT	892		
1158	ACTTGCAGGGGCTGTGCACTGGGTGATGATGACGTCAATGTTTTGGCCATCACTTCATGC	1217		
893	TAGTCTTTAGAGAAACAGGAAAAATACGATGGTCCACAGCAGTGTCTTGGCAATCGTACAGC	952		
1218	TGTTGCTGGAGAAACAAGAGAAGTACGAAGGCCACAGCAGTTTTTTTGGCATCGTCTGC	1277		
953	TGATAGAAACACGACAGACGTGAAATTTTCTTACCGACTTGAGCTAAATGGTCAATA	1012		
1278	TCATTTGGCAACCCGACAGCAAGCCGAGAACTTTTGCTTACAGCTGGAGTTGAAATGGNAAC	1337		
1013	GGCGACGATTTGACTTGGGAAGCGACTCTCGATCTATTCATGAAGGAATTTGCAACAGCCA	1072		
1338	GGCGGAGATTGACCTGGGAGGCCACGCCCGCTCGATTCATGACGGTGTGGCTGCGCGCCA	1397		
1073	TTATCAATAGGACTGTCTAGTCTTTTGACACACGACATTTGACAGCTTTTTTGCAGAAAAATG	1132		
1398	TCATGAACAGCGACTGCGCTTGTTTTGACACAGCCATGACACATCTTTTTCGACATAATG	1457		
1133	GCAATTTAGGCATCAATGTAACTATTTCCATGTGTG	1169		
1458	GGAACCTTGAATCAATGTACTATTTCTACATGTTG	1494		

RESULT 13
US-10-755-889-123
; Sequence 123, Application US/10/755889
; Publication No. US20040171823A1
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES ASSOCIATED WITH THE NF-KB
; TITLE OF INVENTION: PATHWAY
; FILE REFERENCE: D0284 NP
; CURRENT APPLICATION NUMBER: US/10/755,889
; CURRENT FILING DATE: 2004-01-13
; PRIOR APPLICATION NUMBER: U.S. 60/440,068
; PRIOR FILING DATE: 2003-01-14
; PRIOR APPLICATION NUMBER: U.S. 60/469,757

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: April 24, 2005, 19:49:27 ; Search time 5406 Seconds
(without alignments)
9620.525 Million cell updates/sec

Title: US-10-679-246-1

Perfect score: 1274

Sequence: 1 ttcttttggtgtttatggt.....ctctttcgtagtggaagc 1274

Scoring table: IDENTITY_NUC

Gapex 10.0 , Gapext 1.0

Searched: 45554873 seqs, 20411521753 residues

Total number of hits satisfying chosen parameters: 91109746

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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128: /cgn2_6/ptodata/1/pna/US6058_COMB.seq:
129: /cgn2_6/ptodata/1/pna/US6059_COMB.seq:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	1274	100.0	1274	20	US-09-330-517-1	Sequence 1, Appli
2	1274	100.0	1274	58	US-10-679-246-1	Sequence 1, Appli
3	1274	100.0	1435	21	US-09-359-922-5961	Sequence 5961, Ap
4	1274	100.0	1435	21	US-09-359-922-5961	Sequence 5961, Ap
5	1274	100.0	1435	39	US-09-919-002-5961	Sequence 5961, Ap
6	1274	100.0	1735	29	US-09-644-867-5326	Sequence 5326, Ap
7	1274	100.0	1735	29	US-09-652-918-7745	Sequence 7745, Ap
8	1274	100.0	2270	49	US-10-170-235-39760	Sequence 39760, A
9	1274	100.0	2599	102	US-60-324-185-25086	Sequence 25086, A
10	1274	100.0	2921	29	US-09-644-867-7203	Sequence 7203, Ap
11	1274	100.0	2921	31	US-09-698-013-6733	Sequence 6733, Ap
12	1274	100.0	2921	33	US-09-726-811-5469	Sequence 5469, Ap
13	1274	100.0	2924	34	US-09-785-276A-22959	Sequence 22959, A
14	1274	100.0	2924	34	US-09-785-276A-25457	Sequence 25457, A
15	1274	100.0	2924	34	US-09-785-276A-28822	Sequence 28822, A
16	1274	100.0	2924	53	US-10-357-930-22959	Sequence 22959, A
17	1274	100.0	2924	53	US-10-357-930-25457	Sequence 25457, A
18	1274	100.0	2924	53	US-10-357-930-28822	Sequence 28822, A
19	1274	100.0	6107	1	PCT-US01-01329-2898	Sequence 2898, Ap
20	1274	100.0	6107	1	PCT-US01-01339-8070	Sequence 8070, Ap
21	1274	100.0	6107	34	US-09-764-891-8070	Sequence 8070, Ap
22	1274	100.0	6107	47	US-10-080-090-2898	Sequence 2898, Ap
23	1274	100.0	6107	50	US-10-205-303-2898	Sequence 2898, Ap
24	1272.8	99.9	2270	114	US-60-443-566-1446	Sequence 1446, Ap
25	1272.8	99.9	2270	114	US-60-449-629-24	Sequence 24, Appli
26	1272.8	99.9	2270	115	US-60-455-444-558	Sequence 558, App
27	1272.8	99.9	2270	116	US-60-465-241-558	Sequence 558, App
28	1272.8	99.9	27755	65	US-10-918-754-16927	Sequence 16927, A
29	1272.8	99.9	27755	119	US-60-495-114-16827	Sequence 16827, A
30	1272.8	99.9	37093	65	US-10-918-754-16929	Sequence 16929, A
31	1272.8	99.9	37093	119	US-60-495-114-16929	Sequence 16929, A
32	1272.8	99.9	37093	120	US-60-505-218-7506	Sequence 7506, Ap
33	1272.8	99.9	38141	114	US-60-449-629-854	Sequence 854, App
34	1272.8	99.9	42955	116	US-60-465-241-51333	Sequence 51333, A
35	1272.8	99.9	140599	65	US-10-918-754-16526	Sequence 16526, A
36	1272.8	99.9	140599	119	US-60-495-114-16526	Sequence 16526, A
37	1272.4	99.9	2829	48	US-10-108-260A-258	Sequence 269, App
38	1254.4	98.5	2347	97	US-60-278-258-17389	Sequence 17389, A
39	1090.8	85.6	2030	120	US-60-505-218-276	Sequence 276, App
40	1061.4	83.3	3477	86	US-60-172-360-20587	Sequence 20587, A
41	1042.8	81.9	2440	58	US-10-641-643-588	Sequence 588, App
42	958	75.2	1298	33	US-09-724-676-6973	Sequence 6973, Ap
43	958	75.2	1298	33	US-09-724-676A-6973	Sequence 6973, Ap
44	958	75.2	1649	33	US-09-724-676-6970	Sequence 6970, Ap
45	958	75.2	1649	33	US-09-724-676A-6970	Sequence 6970, Ap

ALIGNMENTS

RESULT 1		US-09-330-517-1		US-09-330-517-1	
		; Sequence 1, Application US/09330517			
		; GENERAL INFORMATION:			
		; APPLICANT: Reed, John S.			
		; TITLE OF INVENTION: Nucleic Acid Encoding Proteins Involved in Protein			
		; TITLE OF INVENTION: Degradation, Products and Methods Related Thereto			
		; FILE REFERENCE: P-LJ 3530			
		; CURRENT APPLICATION NUMBER: US/09/330,517			
		; CURRENT FILING DATE: 1999-06-11			
		; NUMBER OF SEQ ID NOS: 14			
		; SOFTWARE: PatentIn Ver. 2.0			
		; SEQ ID NO 1			
		; LENGTH: 1274			
		; TYPE: DNA			
		; ORGANISM: Homo sapiens			
		; FEATURE:			
		; NAME/KEY: CDS			
		; LOCATION: (274)..(1170)			
		US-09-330-517-1			
		Query Match		100.0%; Score 1274; DB 20; Length 1274;	
		Best Local Similarity		100.0%; Pred. No. 8.9e-235;	
		Matches 1274; Conservative		0; Mismatches 0; Indels 0; Gaps 0;	
QY	1	TTCTTTAGTTGTTTATGGTCCATTTCTATTAGCAATTTATTATTCTATGTAGTCTAT	60		
DB	1	TTCTTTAGTTGTTTATGGTCCATTTCTATTAGCAATTTATTATTCTATGTAGTCTAT	60		
QY	61	CCAAAGCAGATTAGGGAGTTCCCATGTTTCCGGAACATTTTGAAGAGAGCTTATC	120		
DB	61	CCAAAGCAGATTAGGGAGTTCCCATGTTTCCGGAACATTTTGAAGAGAGCTTATC	120		
QY	121	CAGTGTACAGATCCCTAATAAAGTCAGATTCAGTGTAAATTTTATTTTATATCTTTT	180		
DB	121	CAGTGTACAGATCCCTAATAAAGTCAGATTCAGTGTAAATTTTATTTTATATCTTTT	180		
QY	181	TTAATCCTATTTTCT	240		
DB	181	TTAATCCTATTTTCT	240		
QY	241	TATGCATGTAAACATTTATTTAATAAGTAAAGTCATGGTTATATTTTCTCTCTGCT	300		
DB	241	TATGCATGTAAACATTTATTTAATAAGTAAAGTCATGGTTATATTTTCTCTCTGCT	300		
QY	301	CCTTATGTATTTATTTTCAAGAAAGCGCTCAGATCTCAGATCTACGATTTACCGGTACC	360		
DB	301	CCTTATGTATTTATTTTCAAGAAAGCGCTCAGATCTCAGATCTACGATTTACCGGTACC	360		
QY	361	TCGAAGTGTCCACCATCCAGAGGGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	420		
DB	361	TCGAAGTGTCCACCATCCAGAGGGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	420		
QY	421	GACTTGGCGAGTCTTTTTCAGTGTCTCAGTGTCTGCTTGTGCTTGTGCTTGTGCTTGT	480		
DB	421	GACTTGGCGAGTCTTTTTCAGTGTCTCAGTGTCTGCTTGTGCTTGTGCTTGTGCTTGT	480		
QY	481	CAATGTACAGTGGCCATCTTGTGTTAGCAACTGTGCTGCTGCTGCTGCTGCTGCTGCT	540		
DB	481	CAATGTACAGTGGCCATCTTGTGTTAGCAACTGTGCTGCTGCTGCTGCTGCTGCTGCT	540		
QY	541	ACTTGGCGGGGGCTTTGGATCCATTCGCACTTGGCTATGGAGAAAGTGGCTAATTC	600		
DB	541	ACTTGGCGGGGGCTTTGGATCCATTCGCACTTGGCTATGGAGAAAGTGGCTAATTC	600		
QY	601	GTACTTTTCCCTGTAAATATGCGTCTTGGATGAAATTAATCTGCGCACACAGAA	660		
DB	601	GTACTTTTCCCTGTAAATATGCGTCTTGGATGAAATTAATCTGCGCACACAGAA	660		
QY	661	AAAGCAGACCATGAAGAGCTCTGTGAGTTTATGAGCTTTATCTGCTGCTGCTGCTGCT	720		
DB	661	AAAGCAGACCATGAAGAGCTCTGTGAGTTTATGAGCTTTATCTGCTGCTGCTGCTGCT	720		

QY 721 TCCTGTAATGGCAAGGCTCTCTGGATGCTGTAATGCCCATCTGATGCATCAGCATAG 780
DB 721 TCCTGTAATGGCAAGGCTCTCTGGATGCTGTAATGCCCATCTGATGCATCAGCATAG 780
QY 781 TCATTACAACCTACAGGAGAGGATAGATTTTCTTGTCTACAGACATTAATCTTCCT 840
DB 781 TCATTACAACCTACAGGAGAGGATAGATTTTCTTGTCTACAGACATTAATCTTCCT 840
QY 841 GGTGCTGTTGACGTGGGTGATGATGAGTCTCTGTTTGGCTTTCATCTTCAATGTTAGTCTTA 900
DB 841 GGTGCTGTTGACGTGGGTGATGATGAGTCTCTGTTTGGCTTTCATCTTCAATGTTAGTCTTA 900
QY 901 GAGAACAGGAAATACAGATGCTCACCAGCAGTCTTCCGCAATCGTACAGCTGATAGCA 960
DB 901 GAGAACAGGAAATACAGATGCTCACCAGCAGTCTTCCGCAATCGTACAGCTGATAGCA 960
QY 961 ACACGCAAGCAAGCTGAAATTTTGTCTTACCGACTTGAGCTAAATGGTATAGGCGACGA 1020
DB 961 ACACGCAAGCAAGCTGAAATTTTGTCTTACCGACTTGAGCTAAATGGTATAGGCGACGA 1020
QY 1021 TTGACTTGGGAAGCGACTCTCTCGATCTATTCATGAAAGGAATGCAACAGCCATTAATGAAT 1080
DB 1021 TTGACTTGGGAAGCGACTCTCTCGATCTATTCATGAAAGGAATGCAACAGCCATTAATGAAT 1080
QY 1081 AGCGACTGTCTAGTCTTTGACACACAGCATGACAGCTTTTGCAGAAAATGCAATTTA 1140
DB 1081 AGCGACTGTCTAGTCTTTGACACACAGCATGACAGCTTTTGCAGAAAATGCAATTTA 1140
QY 1141 GGCATCAATGTAATCTATTTCCATGTTGAAATGGCAATCAAAACATTTTCTGCGCCAGTGT 1200
DB 1141 GGCATCAATGTAATCTATTTCCATGTTGAAATGGCAATCAAAACATTTTCTGCGCCAGTGT 1200
QY 1201 TTAAACTTCAGTTTCCAGAAAATAGGCAACCATCTGTCTGCCAACCTTAAACTCTTTT 1260
DB 1201 TTAAACTTCAGTTTCCAGAAAATAGGCAACCATCTGTCTGCCAACCTTAAACTCTTTT 1260
QY 1261 CGGTAGTGGAGC 1274
DB 1261 CGGTAGTGGAGC 1274

RESULT 2
US-10-679-246-1
; Sequence 1, Application US/10679246
; GENERAL INFORMATION:
; APPLICANT: Matsuzawa, Shu-ichi
; TITLE OF INVENTION: Nucleic Acid Encoding Proteins Involved
; FILE REFERENCE: 66821-235
; CURRENT FILING DATE: 2003-10-02
; PRIOR APPLICATION NUMBER: US/09/591,694
; PRIOR FILING DATE: 2000-06-09
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 1274
; TYPE: DNA
; ORGANISM: Homo sapien
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (274) ... (1167)

US-10-679-246-1
Query Match 100.0%; Score 1274; DB 58; Length 1274;
Best Local Similarity 100.0%; Pred. No. 8.9e-235;
Matches 1274; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTTCTTTAGTTGTTATGTCCTATTTTCTATTTTATGCAATTTATTTCTATGTTAGTCTAT 60
DB 1 TTTCTTTAGTTGTTATGTCCTATTTTCTATTTTATGCAATTTATTTCTATGTTAGTCTAT 60

QY 61 CCAGACAGATTAAGGGAGTCCACATGTTTTCGGAAACATTTTGAAGAGAGAGCTTATC 120
DB 61 CCAGACAGATTAAGGGAGTCCACATGTTTTCGGAAACATTTTGAAGAGAGAGCTTATC 120
QY 121 CAGGTGACAGATCTTAATAAAGTGACATTCAGTGTAAATTTTATTTTAAATATCTTTT 180
DB 121 CAGGTGACAGATCTTAATAAAGTGACATTCAGTGTAAATTTTATTTTAAATATCTTTT 180
QY 181 TTAATCCTATTTTCT 240
DB 181 TTAATCCTATTTTCT 240
QY 241 TATGGCATGTAACATTTATTAAGTAAGTATGTTTATTAATTTTCTCTCTCTCTCTCT 300
DB 241 TATGGCATGTAACATTTATTAAGTAAGTATGTTTATTAATTTTCTCTCTCTCTCTCT 300
QY 301 CTTTATGTTATTTATTTTTCAGAAATGAGCCGTGAGCTGCTACAGCATTTACCTACCGGTACC 360
DB 301 CTTTATGTTATTTATTTTTCAGAAATGAGCCGTGAGCTGCTACAGCATTTACCTACCGGTACC 360
QY 361 TCGAAGTGTCCACCATCCAGAGGGTGCCTGCCCTGACTGGCAAACTGCATCCAAAT 420
DB 361 TCGAAGTGTCCACCATCCAGAGGGTGCCTGCCCTGACTGGCAAACTGCATCCAAAT 420
QY 421 GACTTGGCGAGTCTTTTTCAGTGTCCAGTCTGCTTTGACTATGTTTACCGCCATCTT 480
DB 421 GACTTGGCGAGTCTTTTTCAGTGTCCAGTCTGCTTTGACTATGTTTACCGCCATCTT 480
QY 481 CAATGTGACAGTGGCCATCTGTTTGTAGCAACTGCGCCCAAGCTCAGCTGTGTTCCA 540
DB 481 CAATGTGACAGTGGCCATCTGTTTGTAGCAACTGCGCCCAAGCTCAGCTGTGTTCCA 540
QY 541 ACTTGC CGGGGGCTTTTGGGATCCATTCGCAACTTGGCTATGGAGAAAGTGGCTAATTTCA 600
DB 541 ACTTGC CGGGGGCTTTTGGGATCCATTCGCAACTTGGCTATGGAGAAAGTGGCTAATTTCA 600
QY 601 GTACTTTTCCCTGTAAATATGCGTCTTCTGGATGCTGTAATGCCCATCTGATGCATCAGCATAG 660
DB 601 GTACTTTTCCCTGTAAATATGCGTCTTCTGGATGCTGTAATGCCCATCTGATGCATCAGCATAG 660
QY 661 AAAGCAGACCATGAAGAGCTCTCTGATGCTGTAATGCCCATCTGATGCATCAGCATAG 720
DB 661 AAAGCAGACCATGAAGAGCTCTCTGATGCTGTAATGCCCATCTGATGCATCAGCATAG 720
QY 721 TCCTGTAATGGCAAGGCTCTCTGATGCTGTAATGCCCATCTGATGCATCAGCATAG 780
DB 721 TCCTGTAATGGCAAGGCTCTCTGATGCTGTAATGCCCATCTGATGCATCAGCATAG 780
QY 781 TCATTACAACCTACAGGAGAGGATAGATTTTCTTGTCTACAGACATTAATCTTCCT 840
DB 781 TCATTACAACCTACAGGAGAGGATAGATTTTCTTGTCTACAGACATTAATCTTCCT 840
QY 841 GGTGCTGTTGACGTGGGTGATGATGAGTCTCTGTTTGGCTTTTCACTTCAATGTTAGTCTTA 900
DB 841 GGTGCTGTTGACGTGGGTGATGATGAGTCTCTGTTTGGCTTTTCACTTCAATGTTAGTCTTA 900
QY 901 GAGAACAGGAAATACAGATGCTCACCAGCAGTCTTCCGCAATCGTACAGCTGATAGCA 960
DB 901 GAGAACAGGAAATACAGATGCTCACCAGCAGTCTTCCGCAATCGTACAGCTGATAGCA 960
QY 961 ACACGCAAGCAAGCTGAAATTTTGTCTTACCGACTTGAGCTAAATGGTATAGGCGACGA 1020
DB 961 ACACGCAAGCAAGCTGAAATTTTGTCTTACCGACTTGAGCTAAATGGTATAGGCGACGA 1020
QY 1021 TTGACTTGGGAAGCGACTCTCTCGATCTATTCATGAAAGGAATGCAACAGCCATTAATGAAT 1080
DB 1021 TTGACTTGGGAAGCGACTCTCTCGATCTATTCATGAAAGGAATGCAACAGCCATTAATGAAT 1080
QY 1081 AGCGACTGTCTAGTCTTTGACACACAGCATGACAGCTTTTGCAGAAAATGCAATTTA 1140
DB 1081 AGCGACTGTCTAGTCTTTGACACACAGCATGACAGCTTTTGCAGAAAATGCAATTTA 1140
QY 1141 GGCATCAATGTAATCTATTTCCATGTTGAAATGGCAATCAAAACATTTTCTGCGCCAGTGT 1200

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Db 1141 GGCATCAATGTAATTTCCATGTTGAATGGCAATCAACATTTTCGCCAGTGT 1200
QY 1201 TTAACACTTCAGTTTCACAGAAATAAGGCAACCATCTGTCTGGCAACTTAACTCTTTT 1260
Db 1201 TTAACACTTCAGTTTCACAGAAATAAGGCAACCATCTGTCTGGCAACTTAACTCTTTT 1260
QY 1261 CGGTAGTGGAGC 1274
Db 1261 CGGTAGTGGAGC 1274

RESULT 3
US-09-359-922-5961
; Sequence 5961, Application US/09359922
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
; TITLE OF INVENTION: NOVEL CONTIGS OBTAINED FROM VARIOUS CDNA
; FILE REFERENCE: 20411-752CON1
; CURRENT APPLICATION NUMBER: US/09/359,922
; CURRENT FILING DATE: 1999-07-22
; EARLIER APPLICATION NUMBER: US 09/205,155
; EARLIER FILING DATE: 1998-12-03
; NUMBER OF SEQ ID NOS: 13203
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 5961
; LENGTH: 1435
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-359-922-5961

Query Match 100.0%; Score 1274; DB 21; Length 1435;
Best Local Similarity 100.0%; Pred. No. 9.1e-235;
Matches 1274; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTTCTTTAGTTGTTATGTTCCATTTTCTATTTTAGCATTTTATTTCTATGAGTCTAT 60
Db 3 TTTCTTTAGTTGTTATGTTCCATTTTCTATTTTAGCATTTTATTTCTATGAGTCTAT 62
QY 61 CCAAGACGATTAAGGAGTTCCACATGTTTCCGGAACATTTGAAAGAGAGCTTATC 120
Db 63 CCAAGACGATTAAGGAGTTCCACATGTTTCCGGAACATTTGAAAGAGAGCTTATC 122
QY 121 CAGGTACAGATCCTAATAAGTGCACTTCAGTGTAATTTTATTTTATATATCTTTT 180
Db 123 CAGGTACAGATCCTAATAAGTGCACTTCAGTGTAATTTTATTTTATATCTTTT 182
QY 181 TTAATCCTATTTTCTTCCTCTTTTCTCAGTAAATTTTGTATGAAACTTTAAAGGACT 240
Db 183 TTAATCCTATTTTCTTCCTCTTTTCTCAGTAAATTTTGTATGAAACTTTAAAGGACT 242
QY 241 TATGGCATGTAACATTTATTAAGTAGTCACTGTTATATTTTCTCCTGCCT 300
Db 243 TATGGCATGTAACATTTATTAAGTAGTCACTGTTATATTTTCTCCTGCCT 302
QY 301 CCTATGATTTATTTTCAAGAAATGAGCGCTCAGACTGTACAGCAATTAACCTACCGTACC 360
Db 303 CCTATGATTTATTTTCAAGAAATGAGCGCTCAGACTGTACAGCAATTAACCTACCGTACC 362
QY 361 TCGAAGTGTCCACATCCAGAGGGTCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 420
Db 363 TCGAAGTGTCCACATCCAGAGGGTCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 422
QY 421 GACTGCGAGTCTTTTGTAGTCCAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 480
Db 423 GACTGCGAGTCTTTTGTAGTCCAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 482
QY 481 CAATGTACAGATGGCCATCTTTTGTAGCAACTGTGCGCAAGCTTCACATGTGTCCA 540
Db 483 CAATGTACAGATGGCCATCTTTTGTAGCAACTGTGCGCAAGCTTCACATGTGTCCA 542
QY 541 ACTTGGCGGGCCCTTTGGGATCCATTCGCAACTTGGCTATGGAGAAAGTGCTAATCA 600
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Db 543 ACTTGGCGGGCCCTTTGGGATCCATTCGCAACTTGGCTATGGAGAAAGTGCTAATTTCA 602
QY 601 GTACTTTTCCCTCTGTAATATGCGTCTTCTGGATGTGAAATAAATCTGCCACACACAGAA 660
Db 603 GTACTTTTCCCTCTGTAATATGCGTCTTCTGGATGTGAAATAAATCTGCCACACACAGAA 662
QY 661 AAAGCAGACCATGAAGAGCTCTGTGAGTTTATAGGCTTTATTTCTGTCCTGCGCTGGTGT 720
Db 663 AAAGCAGACCATGAAGAGCTCTGTGAGTTTATAGGCTTTATTTCTGTCCTGCGCTGGTGT 722
QY 721 TCCTGTAATGGCAAGGCTCTCTGAGATGCTGTATAGCCCATCTGATGATCATCAGCATTAAG 780
Db 723 TCCTGTAATGGCAAGGCTCTCTGAGATGCTGTATAGCCCATCTGATGATCATCAGCATTAAG 782
QY 781 TCCATTACAACCTTACAGGAGAGATATAGTTTCTTGTCTACAGACATTAATCTTCT 840
Db 783 TCCATTACAACCTTACAGGAGAGATATAGTTTCTTGTCTACAGACATTAATCTTCT 842
QY 841 GGTGCTGTTGATGGGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 900
Db 843 GGTGCTGTTGATGGGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 902
QY 901 GAGAAACAGGAAATATAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 960
Db 903 GAGAAACAGGAAATATAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 962
QY 961 ACACGCAAGCAAGCTGAAATTTTCTTACCGACTTGAGCTAAATGCTATAGGCGACGA 1020
Db 963 ACACGCAAGCAAGCTGAAATTTTCTTACCGACTTGAGCTAAATGCTATAGGCGACGA 1022
QY 1021 TTGACTTGGGAGCGACTCTCGATCTATTCATGAAGGAATTTGCAAGAAATGCGCAATTTA 1140
Db 1023 TTGACTTGGGAGCGACTCTCGATCTATTCATGAAGGAATTTGCAAGAAATGCGCAATTTA 1142
QY 1081 AGCGACTGCTAGTCTTTGACACACAGCATTTGACAGCTTTTGTGCAAGAAATGCGCAATTTA 1200
Db 1083 AGCGACTGCTAGTCTTTGACACACAGCATTTGACAGCTTTTGTGCAAGAAATGCGCAATTTA 1202
QY 1141 GGCATCAATGTAATTTTCCATGTTTGAATGGCAATCAACATTTTCTGCCAGTGT 1200
Db 1143 GGCATCAATGTAATTTTCCATGTTTGAATGGCAATCAACATTTTCTGCCAGTGT 1202
QY 1201 TTAACACTTCAGTTTCACAGAAATAAGGCAACCATCTGTCTGGCAACTTAACTCTTTT 1260
Db 1203 TTAACACTTCAGTTTCACAGAAATAAGGCAACCATCTGTCTGGCAACTTAACTCTTTT 1262
QY 1261 CGGTAGTGGAGC 1274
Db 1263 CGGTAGTGGAGC 1276
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RESULT 4
US-09-359-922-5961
; Sequence 5961, Application US/09359922A
; GENERAL INFORMATION:
; APPLICANT: Leshkowitz, Dena
; APPLICANT: Liu, Jin
; TITLE OF INVENTION: NOVEL CONTIGS OBTAINED FROM VARIOUS CDNA
; TITLE OF INVENTION: LIBRARIES
; FILE REFERENCE: 20411-752CON1
; CURRENT APPLICATION NUMBER: US/09/359,922A
; CURRENT FILING DATE: 1999-07-22
; EARLIER APPLICATION NUMBER: US 09/205,155
; EARLIER FILING DATE: 1998-12-03
; EARLIER APPLICATION NUMBER: US 09/034,341
; EARLIER FILING DATE: 1998-02-13
; NUMBER OF SEQ ID NOS: 13203
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 5961
; LENGTH: 1435
; TYPE: DNA
; ORGANISM: Homo sapiens
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US-09-359-922-5961

Query Match 100.0%; Score 1274; DB 21; Length 1435;
Best Local Similarity 100.0%; Pred. No. 9,1e-235;
Matches 1274; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 TTTCTTTAGTTGTTATGTCCTATTTCTTATTTTATGCAATTTATTTCTATGTCAT 60
DB 3 TTTCTTTAGTTGTTATGTCCTATTTCTTATTTTATGCAATTTATTTCTATGTCAT 62
QY 61 CCAAGACGATTAAAGGAGTTCACATGTTTCCGGAACATTTTGAAGAGAGAGCTTATC 120
DB 63 CCAAGACGATTAAAGGAGTTCACATGTTTCCGGAACATTTTGAAGAGAGAGCTTATC 122
QY 121 CAGTGACAGATCTTAATAAGTGCAATTCAGTGTAATTTTATTTTAAATATCTTTT 180
DB 123 CAGTGACAGATCTTAATAAGTGCAATTCAGTGTAATTTTATTTTAAATATCTTTT 182
QY 181 TTAATCCTATTTTCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 240
DB 183 TTAATCCTATTTTCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 242
QY 241 TATGCAATGTAACATTTATTAAGTAAGTTCATGTTTATTTTCTCTCTCTCTCTCT 300
DB 243 TATGCAATGTAACATTTATTAAGTAAGTTCATGTTTATTTTCTCTCTCTCTCTCT 302
QY 301 CTTATGTTATTTTATTTTCAAGATGAGCGTCTGACATGCTACAGCAATACCTACCGGTACC 360
DB 303 CTTATGTTATTTTATTTTCAAGATGAGCGTCTGACATGCTACAGCAATACCTACCGGTACC 362
QY 361 TCGAAGTGTCACCATCCAGAGGGTCCCTGCTGACCTGACCTGGCACTGCTGCAAT 420
DB 363 TCGAAGTGTCACCATCCAGAGGGTCCCTGCTGACCTGACCTGGCACTGCTGCAAT 422
QY 421 GACTTGGCGAGTCTTTTTCAGTGTCAGTCTGCTTTCAGTATGTTTACCGCCATCTT 480
DB 423 GACTTGGCGAGTCTTTTTCAGTGTCAGTCTGCTTTCAGTATGTTTACCGCCATCTT 482
QY 481 CAATGTCAGAGTGGCAATCTTTGTTTGTAGCAATCTGCGCCCAAGCTCATGTTTCCA 540
DB 483 CAATGTCAGAGTGGCAATCTTTGTTTGTAGCAATCTGCGCCCAAGCTCATGTTTCCA 542
QY 541 ACTTGGCGGGGCTTTGGATTCATTCGCACTTGGCTATGGAGAAAGTGGCTAATTTCA 600
DB 543 ACTTGGCGGGGCTTTGGATTCATTCGCACTTGGCTATGGAGAAAGTGGCTAATTTCA 602
QY 601 GTACTTTTCCCTGTAAATATGCTCTCTGAGTGTGAATAACTCTGCGCCACACACAGAA 660
DB 603 GTACTTTTCCCTGTAAATATGCTCTCTGAGTGTGAATAACTCTGCGCCACACACAGAA 662
QY 661 AAAGCAGACCATGAAGAGCTCTGTGAGTTTGGCCCTTATTCCTGTCGCTGCTGCTGCT 720
DB 663 AAAGCAGACCATGAAGAGCTCTGTGAGTTTGGCCCTTATTCCTGTCGCTGCTGCTGCT 722
QY 721 TCCTGTAAATGGAGGCTCTCTGAGTGTGTAATGCCCTCATGATGATGATGATGATGAT 780
DB 723 TCCTGTAAATGGAGGCTCTCTGAGTGTGTAATGCCCTCATGATGATGATGATGATGAT 782
QY 781 TCCTGTAAATGGAGGCTCTCTGAGTGTGTAATGCCCTCATGATGATGATGATGATGAT 840
DB 783 TCCTGTAAATGGAGGCTCTCTGAGTGTGTAATGCCCTCATGATGATGATGATGATGAT 842
QY 841 GGTGCTGTTGACTGGGTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 900
DB 843 GGTGCTGTTGACTGGGTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 902
QY 901 GAGAAACAGGAAATATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 960
DB 903 GAGAAACAGGAAATATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 962
QY 961 ACACCGACGACCTGAAATTTTGGCTTACCGCTTACCGCTTACCGCTTACCGCTTACCG 1020
DB 963 ACACCGACGACCTGAAATTTTGGCTTACCGCTTACCGCTTACCGCTTACCGCTTACCG 1022
```

RESULT 5

US-09-919-002-5961

; Sequence 5961, Application US/09919002

; GENERAL INFORMATION:

; APPLICANT: Leshkowitz, Dena

; APPLICANT: Liu, Jin

; TITLE OF INVENTION: NOVEL CONTIGS OBTAINED FROM VARIOUS CDNA

; TITLE OF INVENTION: LIBRARIES

; FILE REFERENCE: 20411-752CON1

; CURRENT APPLICATION NUMBER: US/09/919,002

; PRIOR FILING DATE: 2001-07-30

; PRIOR FILING DATE: FILING DATE: 1999-07-22

; PRIOR FILING DATE: FILING DATE: 1998-02-13

; NUMBER OF SEQ ID NOS: 13203

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 5961

; LENGTH: 1435

; TYPE: DNA

; ORGANISM: Homo sapiens

US-09-919-002-5961

Query Match 100.0%; Score 1274; DB 39; Length 1435;

Best Local Similarity 100.0%; Pred. No. 9,1e-235;

Matches 1274; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 TTTCTTTAGTTGTTATGTCCTATTTCTTATTTTATGCAATTTATTTCTATGTCAT 60
DB 3 TTTCTTTAGTTGTTATGTCCTATTTCTTATTTTATGCAATTTATTTCTATGTCAT 62
QY 61 CCAAGACGATTAAAGGAGTTCACATGTTTCCGGAACATTTTGAAGAGAGAGCTTATC 120
DB 63 CCAAGACGATTAAAGGAGTTCACATGTTTCCGGAACATTTTGAAGAGAGAGCTTATC 122
QY 121 CAGTGACAGATCTTAATAAGTGCAATTCAGTGTAATTTTATTTTAAATATCTTTT 180
DB 123 CAGTGACAGATCTTAATAAGTGCAATTCAGTGTAATTTTATTTTAAATATCTTTT 182
QY 181 TTAATCCTATTTTCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 240
DB 183 TTAATCCTATTTTCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 242
QY 241 TATGCAATGTAACATTTATTAAGTAAGTTCATGTTTATTTTCTCTCTCTCTCTCT 300
DB 243 TATGCAATGTAACATTTATTAAGTAAGTTCATGTTTATTTTCTCTCTCTCTCTCT 302
QY 301 CTTATGTTATTTTATTTTCAAGATGAGCGTCTGACATGCTACAGCAATACCTACCGGTACC 360
DB 303 CTTATGTTATTTTATTTTCAAGATGAGCGTCTGACATGCTACAGCAATACCTACCGGTACC 362
```

QY	361	TCGAAGTGTCCACCATCCAGAGGGTGCCTGCCCTGACTGSCACAACATGCATCCAAAT	420
Db	363	TCGAAGTGTCCACCATCCAGAGGGTGCCTGCCCTGACTGSCACAACATGCATCCAAAT	422
QY	421	GACTTGGGGAGTCTTTTGGAGTCCAGTCTGCTTTGACTATGTGTACCGCCCATCTTT	480
Db	423	GACTTGGGGAGTCTTTTGGAGTCCAGTCTGCTTTGACTATGTGTACCGCCCATCTTT	482
QY	481	CAATGTCCAGAGTGGCCATCTTTTGTAGCAACTCTGCGCCCAAGCTCACATGTGTCCA	540
Db	483	CAATGTCCAGAGTGGCCATCTTTTGTAGCAACTCTGCGCCCAAGCTCACATGTGTCCA	542
QY	541	ACTTGGCGGGCCCTTTGGGATCCATTCGCAACTTGGCTATGGAGAAAGTGCATATTC	600
Db	543	ACTTGGCGGGCCCTTTGGGATCCATTCGCAACTTGGCTATGGAGAAAGTGCATATTC	602
QY	601	GTACTTTTCCCTGTAAATATATGCTCTCTGGATGTGAATAAATCTCTGCCACACAGAA	660
Db	603	GTACTTTTCCCTGTAAATATATGCTCTCTGGATGTGAATAAATCTCTGCCACACAGAA	662
QY	661	AAAGCAGACCATGAAGAGCTCTGTAGATTTAGGCTTATTCCTGTCCGTGCCCTGTGCT	720
Db	663	AAAGCAGACCATGAAGAGCTCTGTAGATTTAGGCTTATTCCTGTCCGTGCCCTGTGCT	722
QY	721	TCCTGTAAATGGCAAGCTCTCTGGATGTGAATAAATCTCTGCCACATCAGCATTAAG	780
Db	723	TCCTGTAAATGGCAAGCTCTCTGGATGTGAATAAATCTCTGCCACATCAGCATTAAG	782
QY	781	TCCATTACAAACCTCAGCGGAGAGATATAGTTTTTCTGTGTACAGACATTAATCTTCT	840
Db	783	TCCATTACAAACCTCAGCGGAGAGATATAGTTTTTCTGTGTACAGACATTAATCTTCT	842
QY	841	GGTGTGTGACTGGGTGATGATGCTGCTGTTTGGCTTTTCTGCTTCACTTCACTTGTGCTTA	900
Db	843	GGTGTGTGACTGGGTGATGATGCTGCTGTTTGGCTTTTCTGCTTCACTTCACTTGTGCTTA	902
QY	901	GAGAAACAGAAATACAGATGTCCACAGAGTCTTCTGCAATCGTACAGCTGTATGGA	960
Db	903	GAGAAACAGAAATACAGATGTCCACAGAGTCTTCTGCAATCGTACAGCTGTATGGA	962
QY	961	ACACGCAAGCAAGCTGAAATTTTGTCTACCGACTTGAAGTAAATGCATAGGCGACCA	1020
Db	963	ACACGCAAGCAAGCTGAAATTTTGTCTACCGACTTGAAGTAAATGCATAGGCGACCA	1022
QY	1021	TTGACTTGGAGGAGTCTCTGCTATTCATGAAAGGAAATTCACAGCACTTATGAAT	1080
Db	1023	TTGACTTGGAGGAGTCTCTGCTATTCATGAAAGGAAATTCACAGCACTTATGAAT	1082
QY	1081	AGGACTGTCTAGTCTTTTGACACAGCATTTGCACAGCTTTTTCAGAAAATGGCAATTTA	1140
Db	1083	AGGACTGTCTAGTCTTTTGACACAGCATTTGCACAGCTTTTTCAGAAAATGGCAATTTA	1142
QY	1141	GGCATCAATGTAATTTTCCATGTGTGAATGGCAATCAACATTTTCTGCGCCAGTGT	1200
Db	1143	GGCATCAATGTAATTTTCCATGTGTGAATGGCAATCAACATTTTCTGCGCCAGTGT	1202
QY	1201	TTAAACTTTCAGTTTTCAGAAAATAAGGCAACCATCTGTCTGCCACCTTAAATCTTTT	1260
Db	1203	TTAAACTTTCAGTTTTCAGAAAATAAGGCAACCATCTGTCTGCCACCTTAAATCTTTT	1262
QY	1261	CGGTAGGTGGAAGC 1274	
Db	1263	CGGTAGGTGGAAGC 1276	

RESULT 6

US-09-644-867-5326

Sequence 5326, Application US/09644867

GENERAL INFORMATION:

APPLICANT: Holtzman, Douglas A.

APPLICANT: Donovan, Michael J.

APPLICANT: Leiby, Kevin R.

APPLICANT: Culpepper, Janice A.

QY	304	TTTCTTTAGTTGTTTATGCTCCATTTTCTATTTTAGCATTTTATTATTCTATGTAGTCTAT	360
Db	304	TTTCTTTAGTTGTTTATGCTCCATTTTCTATTTTAGCATTTTATTATTCTATGTAGTCTAT	363
QY	61	CCAAAGCAGTAAAGGAGATTCACATGTTTTCGGGAACATTTTGAAGAAGAGCTTATC	120
Db	364	CCAAAGCAGTAAAGGAGATTCACATGTTTTCGGGAACATTTTGAAGAAGAGCTTATC	423
QY	121	CAGTGTACAGATCCCTAATAAAGTGACATTCAGTGTAAATTTTATTATTATTAAATCTTTT	180
Db	424	CAGTGTACAGATCCCTAATAAAGTGACATTCAGTGTAAATTTTATTATTATTAAATCTTTT	483
QY	181	TTAATCTTATTTTCT	240
Db	484	TTAATCTTATTTTCT	543
QY	241	TATGCATGTAAACATTTTATAAAGTAAAGTCAATGTTTAAATTTTCTCTCTCTCTCTCT	300
Db	544	TATGCATGTAAACATTTTATAAAGTAAAGTCAATGTTTAAATTTTCTCTCTCTCTCTCT	603
QY	301	CTTATGTATTTTATTTTCAAGATGAGCGTCACTGCTACAGCATTTACCTACCGGTACC	360
Db	604	CTTATGTATTTTATTTTCAAGATGAGCGTCACTGCTACAGCATTTACCTACCGGTACC	663
QY	361	TCGAAGTGTCCACCATCCAGAGGGTGCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	420
Db	664	TCGAAGTGTCCACCATCCAGAGGGTGCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	723
QY	421	GACTTGGGAGTCTTTTGGAGTCCAGTCTGCTTTGACTATGTGTACCGCCCATCTTT	480
Db	724	GACTTGGGAGTCTTTTGGAGTCCAGTCTGCTTTGACTATGTGTACCGCCCATCTTT	783
QY	481	CAATGTCCAGTGGCCATCTTCTTTGTAGCAACTGTGCGCCCAAGCTCACATGTTGTCCA	540
Db	784	CAATGTCCAGTGGCCATCTTCTTTGTAGCAACTGTGCGCCCAAGCTCACATGTTGTCCA	843
QY	541	ACTTGGCGGGGCCCTTTGGGATCCATTTGGGATCCATTTGGGATCCATTTGGGATCCATTT	600
Db	844	ACTTGGCGGGGCCCTTTGGGATCCATTTGGGATCCATTTGGGATCCATTTGGGATCCATTT	903
QY	601	GTACTTTTCCCTGTAAATATGCGTCTTCTGGATGTGAATAAATCTCTGCCACACAGAA	660
Db	904	GTACTTTTCCCTGTAAATATGCGTCTTCTGGATGTGAATAAATCTCTGCCACACAGAA	963
QY	661	AAAGCAGACCATGAAGAGCTCTGTGAGTTTGGCCCTTATTTCTGTCCGTGCCCTGTGCT	720
Db	964	AAAGCAGACCATGAAGAGCTCTGTGAGTTTGGCCCTTATTTCTGTCCGTGCCCTGTGCT	1023
QY	721	TCCTGTAAATGGCAAGGCTCTCTGGATGTGAATAAATCTCTGCCACATCAGCATTAAG	780

Query Match 100.0%; Score 1274; DB 29; Length 1735;
Best Local Similarity 100.0%; Pred. No. 9.4e-235;
Matches 1274; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 TTTCTTTAGTTGTTTATGCTCCATTTTCTATTTTAGCATTTTATTATTCTATGTAGTCTAT 60
304 TTTCTTTAGTTGTTTATGCTCCATTTTCTATTTTAGCATTTTATTATTCTATGTAGTCTAT 363

61 CCAAAGCAGTAAAGGAGATTCACATGTTTTCGGGAACATTTTGAAGAAGAGCTTATC 120
364 CCAAAGCAGTAAAGGAGATTCACATGTTTTCGGGAACATTTTGAAGAAGAGCTTATC 423

121 CAGTGTACAGATCCCTAATAAAGTGACATTCAGTGTAAATTTTATTATTATTAAATCTTTT 180
424 CAGTGTACAGATCCCTAATAAAGTGACATTCAGTGTAAATTTTATTATTATTAAATCTTTT 483

181 TTAATCTTATTTTCT 240
484 TTAATCTTATTTTCT 543

241 TATGCATGTAAACATTTTATAAAGTAAAGTCAATGTTTAAATTTTCTCTCTCTCTCTCT 300
544 TATGCATGTAAACATTTTATAAAGTAAAGTCAATGTTTAAATTTTCTCTCTCTCTCTCT 603

301 CTTATGTATTTTATTTTCAAGATGAGCGTCACTGCTACAGCATTTACCTACCGGTACC 360
604 CTTATGTATTTTATTTTCAAGATGAGCGTCACTGCTACAGCATTTACCTACCGGTACC 663

361 TCGAAGTGTCCACCATCCAGAGGGTGCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 420
664 TCGAAGTGTCCACCATCCAGAGGGTGCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 723

421 GACTTGGGAGTCTTTTGGAGTCCAGTCTGCTTTGACTATGTGTACCGCCCATCTTT 480
724 GACTTGGGAGTCTTTTGGAGTCCAGTCTGCTTTGACTATGTGTACCGCCCATCTTT 783

481 CAATGTCCAGTGGCCATCTTCTTTGTAGCAACTGTGCGCCCAAGCTCACATGTTGTCCA 540
784 CAATGTCCAGTGGCCATCTTCTTTGTAGCAACTGTGCGCCCAAGCTCACATGTTGTCCA 843

541 ACTTGGCGGGGCCCTTTGGGATCCATTTGGGATCCATTTGGGATCCATTTGGGATCCATTT 600
844 ACTTGGCGGGGCCCTTTGGGATCCATTTGGGATCCATTTGGGATCCATTTGGGATCCATTT 903

601 GTACTTTTCCCTGTAAATATGCGTCTTCTGGATGTGAATAAATCTCTGCCACACAGAA 660
904 GTACTTTTCCCTGTAAATATGCGTCTTCTGGATGTGAATAAATCTCTGCCACACAGAA 963

661 AAAGCAGACCATGAAGAGCTCTGTGAGTTTGGCCCTTATTTCTGTCCGTGCCCTGTGCT 720
964 AAAGCAGACCATGAAGAGCTCTGTGAGTTTGGCCCTTATTTCTGTCCGTGCCCTGTGCT 1023

721 TCCTGTAAATGGCAAGGCTCTCTGGATGTGAATAAATCTCTGCCACATCAGCATTAAG 780

TITLE OF INVENTION: NOVEL NUCLEIC ACID MOLECULES AND USES
TITLE OF INVENTION: THEREFOR
FILE REFERENCE: 1600.1173-001
CURRENT APPLICATION NUMBER: US/09/644,867
CURRENT FILING DATE: 2000-08-28
PRIOR APPLICATION NUMBER: 60/151,061
PRIOR FILING DATE: 1999-08-27
NUMBER OF SEQ ID NOS: 8090
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 5326
LENGTH: 1735
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc feature
LOCATION: (1)-(1735)
OTHER INFORMATION: n = A, T, C or G
US-09-644-867-5326

Db 1024 TCCTGTAATGGCAAGGCTCTCTGGATGCTGTAATGCCCCATCTGATGATCAGCATAAG 1083
QY 781 TCATTACACCCCTACAGGAGAGGATATAGTTTTTCTTGCTACAGACATTAATCTTCCT 840
Db 1084 TCATTACACCCCTACAGGAGAGGATATAGTTTTTCTTGCTACAGACATTAATCTTCCT 1143
QY 841 GGTGCTGTTGACCTGGCTGATGATGAGTCTCTGTTTTTGGCTTTCACATTCATGTTAGTCTTA 900
Db 1144 GGTGCTGTTGACCTGGCTGATGATGAGTCTCTGTTTTTGGCTTTCACATTCATGTTAGTCTTA 1203
QY 901 GAGAAACAGGAAATATACGATGCTCACCAGCAGTCTCTTGCCAACTCGTACAGCTGATAGGA 960
Db 1204 GAGAAACAGGAAATATACGATGCTCACCAGCAGTCTCTTGCCAACTCGTACAGCTGATAGGA 1263
QY 961 ACACGCAAGAGCTGAAATATTTTGTCTTACCCGACTTGAGCTAAATGGTCAATGAGCGACGA 1020
Db 1264 ACACGCAAGAGCTGAAATATTTTGTCTTACCCGACTTGAGCTAAATGGTCAATGAGCGACGA 1323
QY 1021 TTGACTTGGGAAGCGACTCTCGATCTATTTCATGAAGGAATGCAACAGCCATTATGAAT 1080
Db 1324 TTGACTTGGGAAGCGACTCTCGATCTATTTCATGAAGGAATGCAACAGCCATTATGAAT 1383
QY 1081 AGCGACTGTCTAGTCTTGACACACGATTTGACACAGCTTTTTCAGAAAAATGGCAATTTA 1140
Db 1384 AGCGACTGTCTAGTCTTGACACACGATTTGACACAGCTTTTTCAGAAAAATGGCAATTTA 1443
QY 1141 GGCATCAATGTAATTTTCCATGTTGAAATGGCAATCAAACTTTTCTGGCCAGTGT 1200
Db 1444 GGCATCAATGTAATTTTCCATGTTGAAATGGCAATCAAACTTTTCTGGCCAGTGT 1503
QY 1201 TTAAACTTCAGTTTTCACAGAAATGAAGCACCCTCTGCTGCCAACTTAAACTCTTT 1260
Db 1504 TTAAACTTCAGTTTTCACAGAAATGAAGCACCCTCTGCTGCCAACTTAAACTCTTT 1563
QY 1261 CGGTAGTGGAGC 1274
Db 1564 CGGTAGTGGAGC 1577

RESULT 7 918-7745

US-09-652-918-7745
; Sequence 7745, Application US/09652918
; GENERAL INFORMATION:
; APPLICANT: Galvin, Katherine
; APPLICANT: Holtzman, Douglas A.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID MOLECULES AND USBS
; TITLE OF INVENTION: THEREFOR
; FILE REFERENCE: 1600.1187-001
; CURRENT APPLICATION NUMBER: US/09/652,918
; CURRENT FILING DATE: 2000-08-30
; PRIOR APPLICATION NUMBER: 60/151,130
; PRIOR FILING DATE: 1999-08-30
; NUMBER OF SEQ ID NOS: 8985
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7745
; LENGTH: 1735
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(1735)
; OTHER INFORMATION: n = A,T,C or G
US-09-652-918-7745

Query Match 100.0%; Score 1274; DB 29; Length 1735;
Best Local Similarity 100.0%; Pred. No. 9,4e-235;
Matches 1274; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TTTCTTTAGTTGTTATGGTCCATTTTCTATTATTTAGCATTTATTTCTATGTTAGTCTAT 60
Db 304 TTTCTTTAGTTGTTATGGTCCATTTTCTATTATTTAGCATTTATTTCTATGTTAGTCTAT 363
QY 61 CCAAGACGATTAAGGAGTTCACATGTTTTCGGAACATTTTGAAGAGAGAGCTTATC 120

Db 364 CCAAGACGATTAAGGAGTTCACATGTTTTCGGAACATTTTGAAGAGAGAGCTTATC 423
QY 121 CAGTGTACAGATCTTAATAAAGTGACATTCAGTGTAAATTTTATTTTATATATCTTTT 180
Db 424 CAGTGTACAGATCTTAATAAAGTGACATTCAGTGTAAATTTTATTTTATATCTTTT 483
QY 181 TTAATCTTATTTTCT 240
Db 484 TTAATCTTATTTTCT 543
QY 241 TATGCGATGTAAACATTAATTTATAAGTAAGTCATCGTTTATATTAATTTTCTCTG 300
Db 544 TATGCGATGTAAACATTAATTTATAAGTAAGTCATCGTTTATATTAATTTTCTCTG 603
QY 301 CCTTATGATTTTATTTTTCAGAAATGAGCCGTACAGCTGTCTACAGCATTACCTAC 360
Db 604 CCTTATGATTTTATTTTTCAGAAATGAGCCGTACAGCTGTCTACAGCATTACCTAC 663
QY 361 TCGAAGTGTCCACATCCAGAGGGTCCCTGCGCTGACCTGGCACAACCTGATCCAAAT 420
Db 664 TCGAAGTGTCCACATCCAGAGGGTCCCTGCGCTGACCTGGCACAACCTGATCCAAAT 723
QY 421 GACTTGGCGAGTCTTTTTCAGTGTCCAGTCTGCTTTGAGCTATGTTTACCGCCATCT 480
Db 724 GACTTGGCGAGTCTTTTTCAGTGTCCAGTCTGCTTTGAGCTATGTTTACCGCCATCT 783
QY 481 CAATGTACAGTGGCCATCTTGTGTTAGCAACTGTGCGCCAAAGCTCACATGTTGTCCA 540
Db 784 CAATGTACAGTGGCCATCTTGTGTTAGCAACTGTGCGCCAAAGCTCACATGTTGTCCA 843
QY 541 ACTTGGCGGGGCTTTTGGGATCCATTCGCAACTGTTGGCTATGGAGAAAGTGGCTAAT 600
Db 844 ACTTGGCGGGGCTTTTGGGATCCATTCGCAACTGTTGGCTATGGAGAAAGTGGCTAAT 903
QY 601 GTACTTTCCCTCTGTAATATATGCTCTCTGATGTGAATTAACCTGCGCACACAGAA 660
Db 904 GTACTTTCCCTCTGTAATATATGCTCTCTGATGTGAATTAACCTGCGCACACAGAA 963
QY 661 AAAGCAGACCATGAAGAGCTCTGTGATGTTAGGCCCTTATTCCTGTCGTCCTGCTGT 720
Db 964 AAAGCAGACCATGAAGAGCTCTGTGATGTTAGGCCCTTATTCCTGTCGTCCTGCTGT 1023
QY 721 TCCTGTAATGCAAGGCTCTCTGATGCTGTAATGCCCATCTGATGATCAGCATAAG 780
Db 1024 TCCTGTAATGCAAGGCTCTCTGATGCTGTAATGCCCATCTGATGATCAGCATAAG 1083
QY 781 TCCATTACACCCCTACAGGAGAGGATATAGTTTTTCTTGCTACAGACATTAATCTTCT 840
Db 1084 TCCATTACACCCCTACAGGAGAGGATATAGTTTTTCTTGCTACAGACATTAATCTTCT 1143
QY 841 GGTGCTGTTGACTGGGTGATGATGATGCTCTGTTTGGCTTTTCACTTCATGTTAGTCTTA 900
Db 1144 GGTGCTGTTGACTGGGTGATGATGATGCTCTGTTTGGCTTTTCACTTCATGTTAGTCTTA 1203
QY 901 GAGAAACAGGAAATATACGATGCTCACCAGCAGTCTTTCGCAATCGTACAGCTGATAGGA 960
Db 1204 GAGAAACAGGAAATATACGATGCTCACCAGCAGTCTTTCGCAATCGTACAGCTGATAGGA 1263
QY 961 ACACGCAAGAGCTGAAATATTTTCTTACCCGACTTGAGCTAAATGGTCAATGAGCGACGA 1020
Db 1264 ACACGCAAGAGCTGAAATATTTTCTTACCCGACTTGAGCTAAATGGTCAATGAGCGACGA 1323
QY 1021 TTGACTTGGGAAGCGACTCTCTGATCTATTTCATGAAGGAATTTGCAACAGCCATTATGAAT 1080
Db 1324 TTGACTTGGGAAGCGACTCTCTGATCTATTTCATGAAGGAATTTGCAACAGCCATTATGAAT 1383
QY 1081 AGCGACTGTCTAGTCTTGACACACGATTTGACAGCTTTTTCAGAAAAATGGCAATTTA 1140
Db 1384 AGCGACTGTCTAGTCTTGACACACGATTTGACAGCTTTTTCAGAAAAATGGCAATTTA 1443
QY 1141 GGCATCAATGTAATTTTCCATGTTGAAATGGCAATCAAACTTTTCTGGCCAGTGT 1200

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Db 1444 GCATCAATGTAACATATTTCCATGTTGAAATGGCAATCAAAACATTTTCTGGCCAGTGT 1503
Qy 1201 TTAACAACTTCAGTTTCACAGAAAATAAGGACCCATCTGTCTGCGCAACCTTAAACTCTTTT 1260
Db 1504 TTAACAACTTCAGTTTCACAGAAAATAAGGACCCATCTGTCTGCGCAACCTTAAACTCTTTT 1563
Qy 1261 CGGTAGGTGGAAGC 1274
Db 1564 CGGTAGGTGGAAGC 1577

RESULT 8
US-10-170-235-39760
; Sequence 39760, Application US/10170235
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig
; TITLE OF INVENTION: KITS, SUCH AS NUCLEIC ACID ARRAYS, COMPRISING A MAJORITY OF HUMAN
; TITLE OF INVENTION: TRANSCRIPTS, FOR DETECTING EXPRESSION AND OTHER USES THEREOF
; FILE REFERENCE: CL001380
; CURRENT APPLICATION NUMBER: US/10/170,235
; CURRENT FILING DATE: 2003-03-17
; NUMBER OF SEQ ID NOS: 42514
; SEQ ID NO 39760
; LENGTH: 2270
; TYPE: DNA
; ORGANISM: HUMAN
US-10-170-235-39760

Query Match 100.0%; Score 1274; DB 49; Length 2270;
Best Local Similarity 100.0%; Pred. No. 9.8e-235;
Matches 1274; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTTCTTTAGTTGTTATGTTGTCATTTTCTATTTTACATTTATTTCTATGTTCTAT 60
Db 3 TTTCTTTAGTTGTTATGTTGTCATTTTCTATTTTACATTTATTTCTATGTTCTAT 62
Qy 61 CCAAGACCATTAAGGAGTTCACATGTTTCCGGAAACATTTTGAAGAGAGAGCTTATC 120
Db 63 CCAAGACCATTAAGGAGTTCACATGTTTCCGGAAACATTTTGAAGAGAGAGCTTATC 122
Qy 121 CAGTGTACAGATCCTAATAAGTGCAATTCAGTGTAAATTTATTTTATTAATCTTTT 180
Db 123 CAGTGTACAGATCCTAATAAGTGCAATTCAGTGTAAATTTATTTTATTAATCTTTT 182
Qy 181 TTAATCCTATTTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 240
Db 183 TTAATCCTATTTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 242
Qy 241 TATGGCATGTAAACATTAATTTATAAGTAAGTCATGTTTATTAATTTTCTCTGCTT 300
Db 243 TATGGCATGTAAACATTAATTTATAAGTAAGTCATGTTTATTAATTTTCTCTGCTT 302
Qy 301 CTTATGTATTTATTTTACAGAAATGAGCGTGCAGCTGCATCAGCATTTACCTACCGTACC 360
Db 303 CTTATGTATTTATTTTACAGAAATGAGCGTGCAGCTGCATCAGCATTTACCTACCGTACC 362
Qy 361 TCGAAGTGTCCACATCCAGAGGGTCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 420
Db 363 TCGAAGTGTCCACATCCAGAGGGTCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 422
Qy 421 GACTTGGCGAGTCTTTTGTAGTGTCCAGTCTGTTTGTAGTGTATGTTTACCGCCATCTTT 480
Db 423 GACTTGGCGAGTCTTTTGTAGTGTCCAGTCTGTTTGTAGTGTATGTTTACCGCCATCTTT 482
Qy 481 CAATGTACAGTGGCCATCTTTTGTAGTGTCCAGTCTGTTTGTAGTGTATGTTTACCGTCCA 540
Db 483 CAATGTACAGTGGCCATCTTTTGTAGTGTCCAGTCTGTTTGTAGTGTATGTTTACCGTCCA 542
Qy 541 ACTTGGCGGGCCCTTTGGGATCCATTCGCAACTTGGCTATGGAGAAAGTGGTAATTC 600
Db 543 ACTTGGCGGGCCCTTTGGGATCCATTCGCAACTTGGCTATGGAGAAAGTGGTAATTC 602
Qy 601 GTACTTTTCCCTGTAAATATGCGTCTTCTGGATGTGAAATACTCTGCCACACACAGAA 660
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Db 603 GTACTTTTCCCTGTAAATATGCGTCTTCTGGATGTGAAATAAATCTGTGCCACACAGAA 662
Qy 661 AAAGCAGACCATTAAGAGCTCTGTGAGTTTGAAGGCTTATTCCTGTCGTCGCTGGTGTCT 720
Db 663 AAAGCAGACCATTAAGAGCTCTGTGAGTTTGAAGGCTTATTCCTGTCGTCGCTGGTGTCT 722
Qy 721 TCCTGTAATGGCAAGGCTCTCTGATGCTGTAATGCCCCCATCTGTGATGATGATGATGAT 780
Db 723 TCCTGTAATGGCAAGGCTCTCTGATGCTGTAATGCCCCCATCTGTGATGATGATGATGAT 782
Qy 781 TCCATTACAACCCCTACAGGAGAGATATATGTTTCTTGTCTACAGACATTAATCTTCTCT 840
Db 783 TCCATTACAACCCCTACAGGAGAGATATATGTTTCTTGTCTACAGACATTAATCTTCTCT 842
Qy 841 GGTGCTGTGAGTGGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 900
Db 843 GGTGCTGTGAGTGGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 902
Qy 901 GAGAAACAGGAAAAATACGATGGTCCAGCAGATTTCTTGGCAATCGTACAGCTGATAGGA 960
Db 903 GAGAAACAGGAAAAATACGATGGTCCAGCAGATTTCTTGGCAATCGTACAGCTGATAGGA 962
Qy 961 ACACGCAAGCAAGCTGAAAAATTTTGTCTTACCGACTTGAAGTAAATGGTCAATAGGCG 1020
Db 963 ACACGCAAGCAAGCTGAAAAATTTTGTCTTACCGACTTGAAGTAAATGGTCAATAGGCG 1022
Qy 1021 TTGACTTCGGGAAGGAGCTCCTCGATCTATTCATGAAGAAATTCGCAACAGCCATATGAT 1080
Db 1023 TTGACTTCGGGAAGGAGCTCCTCGATCTATTCATGAAGAAATTCGCAACAGCCATATGAT 1082
Qy 1081 AGCGACTCTCTAGTCTTTGACACCAAGCAATGACAGCTTTTTCGAGAAAAATGGCAATTT 1140
Db 1083 AGCGACTCTCTAGTCTTTGACACCAAGCAATGACAGCTTTTTCGAGAAAAATGGCAATTT 1142
Qy 1141 GCATCAATGTAACATTTTCCATGTTTGAATGCAATCAAAACATTTTCTGGCCAGTGT 1200
Db 1143 GCATCAATGTAACATTTTCCATGTTTGAATGCAATCAAAACATTTTCTGGCCAGTGT 1202
Qy 1201 TTAACAACTTCAGTTTCACAGAAAATAAGGACCCATCTGTCTGCGCAACCTTAAACTCTTT 1260
Db 1203 TTAACAACTTCAGTTTCACAGAAAATAAGGACCCATCTGTCTGCGCAACCTTAAACTCTTT 1262
Qy 1261 CGGTAGGTGGAAGC 1274
Db 1263 CGGTAGGTGGAAGC 1276
```

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RESULT 9
US-60-324-185-25086
; Sequence 25086, Application US/60324185
; GENERAL INFORMATION:
; APPLICANT: Morris, Macdonald
; APPLICANT: Lal, Preeti
; APPLICANT: Diep, Binh
; TITLE OF INVENTION: METHOD FOR THE IDENTIFICATION OF SEQUENCE POLYMORPHISMS USING
; TITLE OF INVENTION: POLYNUCLEOTIDE SEQUENCE DATABASES, AND SINGLE NUCLEOTIDE
; FILE REFERENCE: GX-0019-1 P
; CURRENT APPLICATION NUMBER: US/60/324,185
; CURRENT FILING DATE: 2001-09-21
; NUMBER OF SEQ ID NOS: 35862
; SOFTWARE: PERL Program
; SEQ ID NO 25086
; LENGTH: 2599
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No: 348851.1
; NAME/KEY: unsure
; LOCATION: 2470
; OTHER INFORMATION: a, t, c, g, or other
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US-60-324-185-25086

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Query Match      100.0%; Score 1274; DB 102; Length 2599;
Best Local Similarity 100.0%; Pred. No. 1e-234;
Matches 1274; Conservative 0; Mismatches 0; Indels 0;
```

1	QY	TTTTCTTTAGTTGTTTATAGTGTCACATTTTCTATTTTGTAGCATTTATTTCTATGTAGTCTAT	60
198	DB	TTTTCTTTAGTTGTTTATAGTGTCACATTTTCTATTTTGTAGCATTTATTTCTATGTAGTCTAT	257
61	QY	CCAAAGACGATTAAGGGAGTTTCCACATGTTTTCCGGAAACATTTTGGAAAAGAGAGCTTATC	120
258	DB	CCAAAGACGATTAAGGGAGTTTCCACATGTTTTCCGGAAACATTTTGGAAAAGAGAGCTTATC	317
121	QY	CAGTGTACAGATCCTAATAAAGTGCACATTCAGTGTAAATTTTATTTTAAATATCTTTT	180
318	DB	CAGTGTACAGATCCTAATAAAGTGCACATTCAGTGTAAATTTTATTTTAAATATCTTTT	377
181	QY	TTAATCCTATTTTCTTCCTCTTTTGGCTCAGTAAATTTTGTATGAACATTTTAAAGGACT	240
378	DB	TTAATCCTATTTTCTTCCTCTTTTGGCTCAGTAAATTTTGTATGAACATTTTAAAGGACT	437
241	QY	TATGGCATGTAAACATTAATTATATAAGTAAAGTCAATGTTTAAATTTTCTCTCGCT	300
438	DB	TATGGCATGTAAACATTAATTATATAAGTAAAGTCAATGTTTAAATTTTCTCTCGCT	497
301	QY	CCTTATGTATTTATTTTCAGAAATGAGCCGTGACATGCTCTACAGCATTTACCTACCGGTACC	360
498	DB	CCTTATGTATTTATTTTCAGAAATGAGCCGTGACATGCTCTACAGCATTTACCTACCGGTACC	557
361	QY	TCCAAAGTGTCCACATCCAGAGGGTGCTGCCCTGACTGGCAACACTGTCATCCACAAT	420
558	DB	TCCAAAGTGTCCACATCCAGAGGGTGCTGCCCTGACTGGCAACACTGTCATCCACAAT	617
421	QY	GACTTGGCGAGTCTTTTGTAGTGTCCAGTCTGCTTTTGACTATGTGTACCGCCCATCTTT	480
618	DB	GACTTGGCGAGTCTTTTGTAGTGTCCAGTCTGCTTTTGACTATGTGTACCGCCCATCTTT	677
481	QY	CAATGTCCAGATGGCCATCTTTGTTTGTAGCAACTGTGCGCCAAAGCTCACATGTTGTCCA	540
678	DB	CAATGTCCAGATGGCCATCTTTGTTTGTAGCAACTGTGCGCCAAAGCTCACATGTTGTCCA	737
541	QY	ACTTTGCGGGGCCCTTTTGGGATCCATTCGCAACTTTGGCTATGGAGAAAGTGCTTAATTC	600
738	DB	ACTTTGCGGGGCCCTTTTGGGATCCATTCGCAACTTTGGCTATGGAGAAAGTGCTTAATTC	797
601	QY	GTACTTTTCCCTGTAAATATGCGTCTTCTGGATGTGAAATAACTCTGCCACACACAGAA	660
798	DB	GTACTTTTCCCTGTAAATATGCGTCTTCTGGATGTGAAATAACTCTGCCACACACAGAA	857
661	QY	AAAGCAGACCATGAAGAGCTCTGTGAGTTTAGGCCCTTATTTCTGTGCGTGCCCTGGTGCT	720
858	DB	AAAGCAGACCATGAAGAGCTCTGTGAGTTTAGGCCCTTATTTCTGTGCGTGCCCTGGTGCT	917
721	QY	TCCTGTAAATGGCAAGGCTCTCTGGATGTGTAATGCCCATCTGTATGTCATCAGCATPAAG	780
918	DB	TCCTGTAAATGGCAAGGCTCTCTGGATGTGTAATGCCCATCTGTATGTCATCAGCATPAAG	977
781	QY	TCCATTACAAACCCTACAGGGAGAGGATATAGTTTTTCTTGCTACAGACATTAATCTTCCT	840
978	DB	TCCATTACAAACCCTACAGGGAGAGGATATAGTTTTTCTTGCTACAGACATTAATCTTCCT	1037
841	QY	GGTGCTGTTGACTGGGTGATGATGCAGTCTCTGTTTTTGGCTTTCACTTCATGTTAGTCTTA	900
1038	DB	GGTGCTGTTGACTGGGTGATGATGCAGTCTCTGTTTTTGGCTTTCACTTCATGTTAGTCTTA	1097
901	QY	GAGAAACAGGAAAAATACGATGTGTCCAGCAGTTCCTTCCCAATCGTACAGCTGATAGGA	960
1098	DB	GAGAAACAGGAAAAATACGATGTGTCCAGCAGTTCCTTCCCAATCGTACAGCTGATAGGA	1157
961	QY	ACACGCAAGCAAGCTGAAAAATTTTGTCTTACCGACTTGAGCTAAATGGTCAATGGCGACGA	1020
1158	DB	ACACGCAAGCAAGCTGAAAAATTTTGTCTTACCGACTTGAGCTAAATGGTCAATGGCGACGA	1217

Qy	1021	TTGACTGGGAAGGACTCTCGATCTATTTCATGAAGGAATTCGCAACAGCCATTATGAAT	1080
Db	1218	TTGACTTTGGGAAGCGACTCTCGATCTATTTCATGAAGGAATTCGCAACAGCCATTATGAAT	1277
Qy	1081	AGCGACTGTCCTAGTCTTTGACACCGACGATTCGACAGCTTTTTCGAGAAAATGGCAATTTTA	1140
Db	1278	AGCGACTGTCCTAGTCTTTGACACCGATTCGACAGCTTTTTCGAGAAAATGGCAATTTTA	1337
Qy	1141	GGCATCAATGTAACCTATTTCATCTGTGTGAAATGGCAATCAAAACATTTTCTGGCCAGTGT	1200
Db	1338	GGCATCAATGTAACCTATTTCATCTGTGTGAAATGGCAATCAAAACATTTTCTGGCCAGTGT	1397
Qy	1201	TTAAACTTCAGTTTTCACAGAAAATAAGGCACCCATCTGTCTGCCAACTTAAAACTCTTT	1260
Db	1398	TTAAACTTCAGTTTTCACAGAAAATAAGGCACCCATCTGTCTGCCAACTTAAAACTCTTT	1457
Qy	1261	CGGTAGTGGGAAGC 1274	
Db	1458	CGGTAGTGGGAAGC 1471	

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RESULT 10
US-09-644-867-7203
; Sequence 7203, Application US/09644867
; GENERAL INFORMATION:
; APPLICANT: Holtzman, Douglas A.
; APPLICANT: Donovan, Michael J.
; APPLICANT: Leiby, Kevin R.
; APPLICANT: Culpepper, Janice A.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID MOLECULES AND USES
; TITLE OF INVENTION: THEREFOR
; FILE REFERENCE: 1600.1173-001
; CURRENT APPLICATION NUMBER: US/09/644,867
; CURRENT FILING DATE: 2000-08-28
; PRIOR APPLICATION NUMBER: 60/151,061
; PRIOR FILING DATE: 1999-08-27
; NUMBER OF SEQ ID NOS: 8090
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7203
; LENGTH: 2921
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(2921)
; OTHER INFORMATION: n = A,T,C or G
US-09-644-867-7203

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Query Match	100.0%;	Score 1274;	DB 29;	Length 2921;
Best Local Similarity	100.0%;	Pred. No. 1e-234;		
Matches 1274;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
Qy	1	TTTCTTTAGTGTGTTTATGGTCCATTTTCTATTTTAGCATTTATTATCTATGTAGTCTAT	60	
Db	479	TTTCTTTAGTGTGTTTATGGTCCATTTTCTATTTTAGCATTTATTATCTATGTAGTCTAT	538	
Qy	61	CCAAAGCAGATTAAAGGGAGTTCCACATGTTTCCGGAAACATTTTGAAGAGAGAGCTTATC	120	
Db	539	CCAAAGCAGATTAAAGGGAGTTCCACATGTTTCCGGAAACATTTTGAAGAGAGAGCTTATC	598	
Qy	121	CAGTGTACAGATCCTTAATAAGTGCACTTCAGTGTAAATTTTTATTTTTTTAAATATCTTTT	180	
Db	599	CAGTGTACAGATCCTTAATAAGTGCACTTCAGTGTAAATTTTTATTTTTTTAAATATCTTTT	658	
Qy	181	TTAATCCTATTTTTTCTTCTCTTTTGGCTCAGTAAATTTTGTATGAAACCTTTAAAGGACT	240	
Db	659	TTAATCCTATTTTTTCTTCTCTTTTGGCTCAGTAAATTTTGTATGAAACCTTTAAAGGACT	718	
Qy	241	TATGGCATGTAAACATTATTTATAAAGTAGTCATCGTTATTAATTAATTTTCTTCCTGCCT	300	
Db	719	TATGGCATGTAAACATTATTTATAAAGTAGTCATCGTTATTAATTAATTTTCTTCCTGCCT	778	

Db 1139 AAGCAGACCATGAAGAGCTCTGTGAGTTTAGGCTTTATTCCTGTCGGTCCCTGTGCT 1198
Qy 721 TCCTGTAATGGCAAGGCTCTCTGGATGCTGTAAATGCCCATCTGATGCATCAGCATAAG 780
Db 1199 TCCTGTAATGGCAAGGCTCTCTGGATGCTGTAAATGCCCATCTGATGCATCAGCATAAG 1258
Qy 781 TCATTTACAACCTACAGGAGAGGATATAGTTTTCTTGGCTACAGACATTAATCTTCCT 840
Db 1259 TCATTTACAACCTACAGGAGAGGATATAGTTTTCTTGGCTACAGACATTAATCTTCCT 1318
Qy 841 GGTGCTGTTGACTGGGTGATGATGCAGTCTGTGTTTGGCTTTTCACCTTCACTTTAGTCTTA 900
Db 1319 GGTGCTGTTGACTGGGTGATGATGCAGTCTGTGTTTGGCTTTTCACCTTCACTTTAGTCTTA 1378
Qy 901 GAGAAACAGGAAATACAGATGCTCACCAGAGTCTTTCGCAATCGTACAGCTGATAGGA 960
Db 1379 GAGAAACAGGAAATACAGATGCTCACCAGAGTCTTTCGCAATCGTACAGCTGATAGGA 1438
Qy 961 ACACGCAAGCAGCTGAAATTTTGTCTTACCAGCTTGAGCTAAATGGTCATAGGCGACGA 1020
Db 1439 ACACGCAAGCAGCTGAAATTTTGTCTTACCAGCTTGAGCTAAATGGTCATAGGCGACGA 1498
Qy 1021 TTGACTTGGAGCGACTCTCTCGATCTATTTCATGAAGGAATTGCAACAGCCATTATGAAT 1080
Db 1499 TTGACTTGGAGCGACTCTCTCGATCTATTTCATGAAGGAATTGCAACAGCCATTATGAAT 1558
Qy 1081 AGCGACTGTCTAGTCTTTGACACAGCATTGCAACAGCTTTTTCGAGAAATGGCAATTTA 1140
Db 1559 AGCGACTGTCTAGTCTTTGACACAGCATTGCAACAGCTTTTTCGAGAAATGGCAATTTA 1618
Qy 1141 GGCATCAATGTAATTTCCATGTTGGAATGGCAATTTTTCGCGCCAGTGT 1200
Db 1619 GGCATCAATGTAATTTCCATGTTGGAATGGCAATTTTTCGCGCCAGTGT 1678
Qy 1201 TTAAACTTCAGTTTCACAGAAATAGGCACCCATCTGCTGCCAACCTTAAACTCTTT 1260
Db 1679 TTAAACTTCAGTTTCACAGAAATAGGCACCCATCTGCTGCCAACCTTAAACTCTTT 1738
Qy 1261 CGGTAGGTGGAGC 1274
Db 1739 CGGTAGGTGGAGC 1752

RESULT 12

US-09-726-811-5469
; Sequence 5469, Application US/09726811
; GENERAL INFORMATION:
; APPLICANT: Gutierrez-Ramos, Jose-Carlos
; APPLICANT: Wen, Danyi
; TITLE OF INVENTION: NOVEL NUCLEIC ACID MOLECULES AND USES
; FILE REFERENCE: 1600.2027-001
; CURRENT APPLICATION NUMBER: US/09/726,811
; CURRENT FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: 60/168,136
; PRIOR FILING DATE: 1999-11-30
; NUMBER OF SEQ ID NOS: 5515
; SOFTWARE: Pstseq for Windows Version 4.0
; SEQ ID NO 5469
; LENGTH: 2921
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(2921)
; OTHER INFORMATION: n = A,T,C or G

US-09-726-811-5469

Query Match

Best Local Similarity 100.0%; Score 1274; DB 33; Length 2921;

Matches 1274; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTTCTTTAGTTGTTTATGCTCCATTTTCTTATTTTACATTTTATTTCTATGTAAGTCTAT 60
Db 479 TTTCTTTAGTTGTTTATGCTCCATTTTCTTATTTTAGCATTTTATTTCTATGTAAGTCTAT 538
Qy 61 CCAGACCATTAAGGAGTTCACATGTTTCCGGAACATTTTGAAGAGAGAGCTTATC 120
Db 539 CCAGACCATTAAGGAGTTCACATGTTTCCGGAACATTTTGAAGAGAGAGCTTATC 598
Qy 121 CAGTGTACAGATCCCTAATAAGTGACATTCAGTGTAAATTTTATTTTAAATATCTTTT 180
Db 599 CAGTGTACAGATCCCTAATAAGTGACATTCAGTGTAAATTTTATTTTAAATATCTTTT 658
Qy 181 TTAATCTATTTTCTTCTCTTTTGTCTCAGTAAATTTTGTATGAAACTTTTAAAGGACT 240
Db 659 TTAATCTATTTTCTTCTCTTTTGTCTCAGTAAATTTTGTATGAAACTTTTAAAGGACT 718
Qy 241 TATGCAATGTAACATTTATTAAGTAAGTATGTTTATTAATTTTCTCTCCCT 300
Db 719 TATGCAATGTAACATTTATTAAGTAAGTATGTTTATTAATTTTCTCTCCCT 778
Qy 301 CCTTATGTTATTTTTCAGAAATGAGCCGTACAGCTGTACAGCATTTACCTACCGGTACC 360
Db 779 CCTTATGTTATTTTTCAGAAATGAGCCGTACAGCTGTACAGCATTTACCTACCGGTACC 838
Qy 361 TCGAAGTGTCCACATCCAGAGGGTCCCTGCTGACCTGGCAAACTGATGCAACAAT 420
Db 839 TCGAAGTGTCCACATCCAGAGGGTCCCTGCTGACCTGGCAAACTGATGCAACAAT 898
Qy 421 GACTTGGCGAGTCTTTTTCAGTGTCCAGTCTGCTTGTGACTGTGTTTACCGCCATCTT 480
Db 899 GACTTGGCGAGTCTTTTTCAGTGTCCAGTCTGCTTGTGACTGTGTTTACCGCCATCTT 958
Qy 481 CAATGTACAGTGGGCATCTTGTGTTAGCAACTGTGCGCCAAAGCTCACATGTTCTCCA 540
Db 959 CAATGTACAGTGGGCATCTTGTGTTAGCAACTGTGCGCCAAAGCTCACATGTTCTCCA 1018
Qy 541 ACTTGGCGGGGCCCTTTGGGATCCATTTGCAACTGTTGGCTATGGAGAAAGTGGCTAATCA 600
Db 1019 ACTTGGCGGGGCCCTTTGGGATCCATTTGCAACTGTTGGCTATGGAGAAAGTGGCTAATCA 1078
Qy 601 GTACTTTTCCCTGTAAATATGGTCTTCTGATGTGAATTAACCTGCGCACACAGAA 660
Db 1079 GTACTTTTCCCTGTAAATATGGTCTTCTGATGTGAATTAACCTGCGCACACAGAA 1138
Qy 661 AAAGCAGACCATTAAGAGCTCTGTGAGTTTAGGCCCTTATTCCTGTCGGTCCCTGTGCT 720
Db 1139 AAAGCAGACCATTAAGAGCTCTGTGAGTTTAGGCCCTTATTCCTGTCGGTCCCTGTGCT 1198
Qy 721 TCCTGTAATGGCAAGGCTCTCTGATGCTGTAATGCCCATCTGATGCATCAGCATAAG 780
Db 1199 TCCTGTAATGGCAAGGCTCTCTGATGCTGTAATGCCCATCTGATGCATCAGCATAAG 1258
Qy 781 TCCTGTAATGGCAAGGCTCTCTGATGCTGTAATGCCCATCTGATGCATCAGCATAAG 840
Db 1259 TCCTGTAATGGCAAGGCTCTCTGATGCTGTAATGCCCATCTGATGCATCAGCATAAG 1318
Qy 841 GGTGCTGTTGACTGGGTGATGATGAGTCTGCTGTTTGGCTTTTCACTTCACTTTAGTCTTA 900
Db 1319 GGTGCTGTTGACTGGGTGATGATGAGTCTGCTGTTTGGCTTTTCACTTCACTTTAGTCTTA 1378
Qy 901 GAGAAACAGGAAATACAGATGCTCACCAGAGTCTTTCGCAATCGTACAGCTGATAGGA 960
Db 1379 GAGAAACAGGAAATACAGATGCTCACCAGAGTCTTTCGCAATCGTACAGCTGATAGGA 1438
Qy 961 ACACGCAAGCAGCTGAAATTTTGTCTTACCAGCTTGAGCTAAATGGTCATAGGCGACGA 1020
Db 1439 ACACGCAAGCAGCTGAAATTTTGTCTTACCAGCTTGAGCTAAATGGTCATAGGCGACGA 1498
Qy 1021 TTGACTTGGAGAGGACTCTCTCGATCTATTTCATGAAGGAATTGCAACAGCCATTATGAAT 1080
Db 1499 TTGACTTGGAGAGGACTCTCTCGATCTATTTCATGAAGGAATTGCAACAGCCATTATGAAT 1558
Qy 1081 AGCGACTGTCTAGTCTTTGACACAGCATTGCAACAGCTTTTTCGAGAAATGGCAATTTA 1140

Db	1559	ACGCACTGCTAGTCTTTTGACACCAAGCATGACAGCTTTTTCGAGAAATGGCAATTTA	1618	
Qy	1141	GCATCAATGTAACATTTTCCATGTTTGAATGGCAATCAAAATTTTCTGGCCAGTGT	1200	
Db	1619	GCATCAATGTAACATTTTCCATGTTTGAATGGCAATCAAAATTTTCTGGCCAGTGT	1678	
Qy	1201	TTAAACATTCAGTTTTCACAGAAATTAAGGACCCCATCTGTCTGCGCAACCTAAACCTCTTT	1260	
Db	1679	TTAAACATTCAGTTTTCACAGAAATTAAGGACCCCATCTGTCTGCGCAACCTAAACCTCTTT	1738	
Qy	1261	CGTAGGTGGAAGC	1274	
Db	1739	CGTAGGTGGAAGC	1752	
RESULT 13				
US-09-785-276A-22959				
; Sequence 22959, Application US/09785276A				
; GENERAL INFORMATION:				
; APPLICANT: Schlegel, Robert				
; APPLICANT: Endege, Wilson				
; APPLICANT: Monahan, John				
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR				
; TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY OF				
; TITLE OF INVENTION: HUMAN PROSTATE CANCER				
; FILE REFERENCE: MRI-007B				
; CURRENT APPLICATION NUMBER: US/09/785,276A				
; CURRENT FILING DATE: 2001-02-16				
; PRIOR APPLICATION NUMBER: 60/183,319				
; PRIOR FILING DATE: 2000-02-17				
; PRIOR APPLICATION NUMBER: 60/189,862				
; PRIOR FILING DATE: 2000-03-16				
; PRIOR APPLICATION NUMBER: 60/207,454				
; PRIOR FILING DATE: 2000-05-25				
; PRIOR APPLICATION NUMBER: 60/211,314				
; PRIOR FILING DATE: 2000-06-09				
; PRIOR APPLICATION NUMBER: 60/219,007				
; PRIOR FILING DATE: 2000-07-18				
; PRIOR APPLICATION NUMBER: 60/255,281				
; PRIOR FILING DATE: 2000-12-13				
; NUMBER OF SEQ ID NOS: 62232				
; SOFTWARE: Fast-SEQ for Windows Version 4.0				
; SEQ ID NO 22959				
; LENGTH: 2924				
; TYPE: DNA				
; ORGANISM: Homo sapiens				
; FEATURE:				
; NAME/KEY: misc feature				
; LOCATION: 1..57..2923, 2924				
; OTHER INFORMATION: n = A,T,C or G				
US-09-785-276A-22959				
Query Match 100.0%; Score 1274; DB 34; Length 2924;				
Best Local Similarity 100.0%; Pred. No. 1e-234;				
Matches 1274; Conservative 0; Mismatches 0; Indels 0; Gaps 0;				
Qy	1	TTTCTTTAGTTGTTATGGTCCATTTTCTATTTTAGCATTTATTTCTATGAGTCTAT	60	
Db	480	TTTCTTTAGTTGTTATGGTCCATTTTCTATTTTAGCATTTATTTCTATGAGTCTAT	539	
Qy	61	CCAAGACGATTAAAGGAGTCCACATGTTTTCGGAAACATTTTGAAGAGAGAGCTTATC	120	
Db	540	CCAAGACGATTAAAGGAGTCCACATGTTTTCGGAAACATTTTGAAGAGAGAGCTTATC	599	
Qy	121	CAGTGTACAGATCCTAATAAGTGCAATTCAGTGAATTTTAAATATCTTTT	180	
Db	600	CAGTGTACAGATCCTAATAAGTGCAATTCAGTGAATTTTAAATATCTTTT	659	
Qy	181	TTAATCCTATTTTCTTCTCTTTTGTCTCAGTAAATTTTGTATGAAACTTTAAAGGACT	240	
Db	660	TTAATCCTATTTTCTTCTCTTTTGTCTCAGTAAATTTTGTATGAAACTTTAAAGGACT	719	

RESULT 14
US-09-785-276A-25457
; Sequence 25457, Application US/09785276A
; GENERAL INFORMATION:
; APPLICANT: Schlegel, Robert
; APPLICANT: Endege, Wilson
; APPLICANT: Monahan, John
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
; TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY OF
; FILE REFERENCE: HUMAN PROSTATE CANCER
; FILE REFERENCE: MRI-007B
; CURRENT APPLICATION NUMBER: US/09/785,276A
; CURRENT FILING DATE: 2001-02-16
; PRIOR APPLICATION NUMBER: 60/183,319
; PRIOR FILING DATE: 2000-02-17
; PRIOR APPLICATION NUMBER: 60/189,862
; PRIOR FILING DATE: 2000-03-16
; PRIOR APPLICATION NUMBER: 60/207,454
; PRIOR FILING DATE: 2000-05-25
; PRIOR APPLICATION NUMBER: 60/211,314
; PRIOR FILING DATE: 2000-06-09
; PRIOR APPLICATION NUMBER: 60/219,007
; PRIOR FILING DATE: 2000-07-18
; PRIOR APPLICATION NUMBER: 60/255,281
; PRIOR FILING DATE: 2000-12-13
; NUMBER OF SEQ ID NOS: 62232
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 25457
; LENGTH: 2924
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 1, 57, 2923, 2924
; OTHER INFORMATION: n = A,T,C or G
US-09-785-276A-25457.

Query Match 100.0%; Score 1274; DB 34; Length 2924;
Best Local Similarity 100.0%; Pred. No. 1e-234;
Matches 1274; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTTCTTACGTTGTTATGTCCTCAATTTTCTATTTAGCATTTATTTCTATGCTAGTCTAT 60
DB 480 TTTCTTACGTTGTTATGTCCTCAATTTTCTATTTAGCATTTATTTCTATGCTAGTCTAT 539

QY 61 CCAAGACGATTAAAGGAGTTCACATGTTTCCGGAACAATTTGAAAGAGAGCTTATC 120
DB 540 CCAAGACGATTAAAGGAGTTCACATGTTTCCGGAACAATTTGAAAGAGAGCTTATC 599

QY 121 CAGGTACAGATCCTAATAAAGTGCACATTCAGTGTAAATTTATTTTAAATATCTTTT 180
DB 600 CAGGTACAGATCCTAATAAAGTGCACATTCAGTGTAAATTTATTTTAAATATCTTTT 659

QY 181 TTAATCCTATTTTCTCTCTCTTTTCTCAGTAAATTTTGTATGAACCTTAAAGGACT 240
DB 660 TTAATCCTATTTTCTCTCTCTTTTCTCAGTAAATTTTGTATGAACCTTAAAGGACT 719

QY 241 TATGCGATGTAACATTTATTTATAAAGTAAAGTCAATGTTTATTAATTTTCTCTGCGCT 300
DB 720 TATGCGATGTAACATTTATTTATAAAGTAAAGTCAATGTTTATTAATTTTCTCTGCGCT 779

QY 301 CCTATGTTATTTATTTTCAAGAAATGAGCGGTGACATGCTGACAGCAATTTACCTACCGGTACC 360
DB 780 CCTATGTTATTTATTTTCAAGAAATGAGCGGTGACATGCTGACAGCAATTTACCTACCGGTACC 839

QY 361 TGAAGTGTCCACATCCAGAGGGTCCCTGCGCTGACATGCGGACCAATCTGATCCCAAT 420
DB 840 TGAAGTGTCCACATCCAGAGGGTCCCTGCGCTGACATGCGGACCAATCTGATCCCAAT 899

QY 421 GACTTGGCGAGTCTTTTTCAGTGTCCAGTCTGCTTTGACTATGTTTACCGCCATCTTT 480
DB 900 GACTTGGCGAGTCTTTTTCAGTGTCCAGTCTGCTTTGACTATGTTTACCGCCATCTTT 959

QY 481 CAATGTCAGATGGCCATCTTGTGTAGCAACTGTGCGCCCAAGCTCACATGTTGTCCA 540
DB 960 CAATGTCAGATGGCCATCTTGTGTAGCAACTGTGCGCCCAAGCTCACATGTTGTCCA 1019

QY 541 ACTTGGCGGGGCCCTTTGGGATCCATTTCGCAACTTGGCTATGGAGAAAGTGGCTAATTC 600
DB 1020 ACTTGGCGGGGCCCTTTGGGATCCATTTCGCAACTTGGCTATGGAGAAAGTGGCTAATTC 1079

QY 601 GTACTTTTCCCTGTAAATATATCGTCTTCTGGATGTGAATAAATCTCTGCCACACAGAA 660
DB 1080 GTACTTTTCCCTGTAAATATATCGTCTTCTGGATGTGAATAAATCTCTGCCACACAGAA 1139

QY 661 AAAGCAGACCATGAAGAGCTCTGTGAGTTAGCCCTTATCTCTGCGCCCTGGTGT 720
DB 1140 AAAGCAGACCATGAAGAGCTCTGTGAGTTAGCCCTTATCTCTGCGCCCTGGTGT 1199

QY 721 TCTGTAAATGCAAGGCTCTCTGGATGTGTAAATGCCCATCTGATGATCAGCATAAG 780
DB 1200 TCTGTAAATGCAAGGCTCTCTGGATGTGTAAATGCCCATCTGATGATCAGCATAAG 1259

QY 781 TCCATTACAAACCTACAGGAGAGATATAGTTTTTCTTGTACAGACATTAATCTTCCT 840
DB 1260 TCCATTACAAACCTACAGGAGAGATATAGTTTTTCTTGTACAGACATTAATCTTCCT 1319

QY 841 GGTGCTGTTGACTGGGTGATGATGCTCTGTTTGGCTTTTCACTTATGTTAGTCTTA 900
DB 1320 GGTGCTGTTGACTGGGTGATGATGCTCTGTTTGGCTTTTCACTTATGTTAGTCTTA 1379

QY 901 GAGAAACAGGAAATAACATGATGTCACAGAGAGTCTTCGCAATCGTACAGCTGATAG 960
DB 1380 GAGAAACAGGAAATAACATGATGTCACAGAGAGTCTTCGCAATCGTACAGCTGATAG 1439

QY 961 ACACGCAAGCAAGCTGAAATTTTGTCTTACCGACTTTGAGCTAAATGCTCATAGCGACGA 1020
DB 1440 ACACGCAAGCAAGCTGAAATTTTGTCTTACCGACTTTGAGCTAAATGCTCATAGCGACGA 1499

QY 1021 TTGACTTGGGAAAGCGACTCTCTCGATCTATTCATGAAGAAATTCGCAACAGCCATTAAT 1080
DB 1500 TTGACTTGGGAAAGCGACTCTCTCGATCTATTCATGAAGAAATTCGCAACAGCCATTAAT 1559

QY 1081 AGCGACTGTCTAGTCTTTTGACACACAGCATTGACAGCTTTTTCGAGAAATGCAATTTA 1140
DB 1560 AGCGACTGTCTAGTCTTTTGACACACAGCATTGACAGCTTTTTCGAGAAATGCAATTTA 1619

QY 1141 GGCATCAATGTAATTTTCCATGTTTGAATGGAATGCAATCAAACTTTTCTGCGCAGTGT 1200
DB 1620 GGCATCAATGTAATTTTCCATGTTTGAATGGAATGCAATCAAACTTTTCTGCGCAGTGT 1679

QY 1201 TTAATACTTCAGTTTTCAGAGAAATAAGGACCCATCTCTGCGCAACCTTAAACTCTTT 1260
DB 1680 TTAATACTTCAGTTTTCAGAGAAATAAGGACCCATCTCTGCGCAACCTTAAACTCTTT 1739

QY 1261 CGGTAGGTGGAAGC 1274
DB 1740 CGGTAGGTGGAAGC 1753

RESULT 15
US-09-785-276A-28822
; Sequence 28822, Application US/09785276A
; GENERAL INFORMATION:
; APPLICANT: Schlegel, Robert
; APPLICANT: Endege, Wilson
; APPLICANT: Monahan, John
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
; TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY OF
; FILE REFERENCE: HUMAN PROSTATE CANCER
; FILE REFERENCE: MRI-007B
; CURRENT APPLICATION NUMBER: US/09/785,276A
; CURRENT FILING DATE: 2001-02-16
; PRIOR APPLICATION NUMBER: 60/183,319
; PRIOR FILING DATE: 2000-02-17
; PRIOR APPLICATION NUMBER: 60/189,862

;; PRIOR FILING DATE: 2000-03-16
;; PRIOR APPLICATION NUMBER: 60/207,454
;; PRIOR FILING DATE: 2000-05-25
;; PRIOR APPLICATION NUMBER: 60/211,314
;; PRIOR FILING DATE: 2000-06-09
;; PRIOR APPLICATION NUMBER: 60/219,007
;; PRIOR FILING DATE: 2000-07-18
;; PRIOR APPLICATION NUMBER: 60/255,281
;; PRIOR FILING DATE: 2000-12-13
;; NUMBER OF SEQ ID NOS: 62332
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO: 28822
;; LENGTH: 2924
;; TYPE: DNA
;; ORGANISM: Homo sapiens
;; FEATURE:
;; NAME/KEY: misc feature
;; LOCATION: 1, 57, 2923, 2924
;; OTHER INFORMATION: n = A,T,C or G
US-09-785-276A-28822

Query Match 100.0%; Score 1274; DB 34; Length 2924;
Best Local Similarity 100.0%; Pred. No. 1e-234;
Matches 1274; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	TTTCTTTAGTGTATGTTGTCATTTTCTATTTAGCATTTTATTTCTATGTAGTCTAT	60
DB	480	TTTCTTTAGTGTATGTTGTCATTTTCTATTTAGCATTTTATTTCTATGTAGTCTAT	539
QY	61	CAAAGACGATTAAAGGAGTTCACATGTTTTCGGAACATTTTGAAGAGAGCTTATC	120
DB	540	CAAAGACGATTAAAGGAGTTCACATGTTTTCGGAACATTTTGAAGAGAGCTTATC	599
QY	121	CAGTGACAGATCCTAATAAGTGACATTCAGTGTAATTTTATTTTATATCTTTT	180
DB	600	CAGTGACAGATCCTAATAAGTGACATTCAGTGTAATTTTATTTTATATCTTTT	659
QY	181	TTAATCCTATTTTCTCTCTTTTCTCAGTAAATTTTGTATGAACTTTAAAGGACT	240
DB	660	TTAATCCTATTTTCTCTCTTTTCTCAGTAAATTTTGTATGAACTTTAAAGGACT	719
QY	241	TATGGCATGTAACATTTATTAAGTAAGTCAATGTTATTAATTTTCTCTGCTT	300
DB	720	TATGGCATGTAACATTTATTAAGTAAGTCAATGTTATTAATTTTCTCTGCTT	779
QY	301	CCTTATGTTATTTTTCAGAAATGAGCGTTCAGCTGCTACAGCATTTACTACCGTACC	360
DB	780	CCTTATGTTATTTTTCAGAAATGAGCGTTCAGCTGCTACAGCATTTACTACCGTACC	839
QY	361	TGCAAGTGTCCACATCCCAAGAGGTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	420
DB	840	TGCAAGTGTCCACATCCCAAGAGGTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	899
QY	421	GACTGGCGAGTCTTTTGTAGTGTCCAGTCTGCTGCTGCTGCTGCTGCTGCTGCT	480
DB	900	GACTGGCGAGTCTTTTGTAGTGTCCAGTCTGCTGCTGCTGCTGCTGCTGCTGCT	959
QY	481	CAATGTCAGAGTGGCCATCTTTTGTAGTGTCCAGTCTGCTGCTGCTGCTGCTGCT	540
DB	960	CAATGTCAGAGTGGCCATCTTTTGTAGTGTCCAGTCTGCTGCTGCTGCTGCTGCT	1019
QY	541	ACTTGGCGGGCCCTTTGGGATCCATTCGCAACTTGGCTATGAGAAAGTGGTAAATCA	600
DB	1020	ACTTGGCGGGCCCTTTGGGATCCATTCGCAACTTGGCTATGAGAAAGTGGTAAATCA	1079
QY	601	GTACTTTTCCCTGTAAATATGCTCTTCTGGATGGAATACTCTGCCACACACAGAA	660
DB	1080	GTACTTTTCCCTGTAAATATGCTCTTCTGGATGGAATACTCTGCCACACACAGAA	1139
QY	661	AAAGCAGACCATGAAGAGCTCTGTAGTGTAGGCTTATTCCTGTCGCTGCTGCTGCT	720
DB	1140	AAAGCAGACCATGAAGAGCTCTGTAGTGTAGGCTTATTCCTGTCGCTGCTGCTGCT	1199

QY	721	TCCTGTAAATGGCAAGGCTCTCTGATGCTGTAAATGCCCATCTGATGATCAGATAAG	780
DB	1200	TCCTGTAAATGGCAAGGCTCTCTGATGCTGTAAATGCCCATCTGATGATCAGATAAG	1259
QY	781	TCCATTACAACCCCTACAGGAGAGGATATAGTTTCTTGTCTACAGACATTAATCTTCT	840
DB	1260	TCCATTACAACCCCTACAGGAGAGGATATAGTTTCTTGTCTACAGACATTAATCTTCT	1319
QY	841	GGTGTCTGTGACTGGGTGATGATGATGATGATGATGATGATGATGATGATGATGAT	900
DB	1320	GGTGTCTGTGACTGGGTGATGATGATGATGATGATGATGATGATGATGATGATGAT	1379
QY	901	GAGAAACAGGAAAAATACGATGGTCCAGCAGTTCCTGCAATCGTACAGCTGATAGGA	960
DB	1380	GAGAAACAGGAAAAATACGATGGTCCAGCAGTTCCTGCAATCGTACAGCTGATAGGA	1439
QY	961	ACAGCAAGCAAGCTGAAAAATTTTGTCTTACCGATTCGAGCTAAATGGTCATAGCGGAGA	1020
DB	1440	ACAGCAAGCAAGCTGAAAAATTTTGTCTTACCGATTCGAGCTAAATGGTCATAGCGGAGA	1499
QY	1021	TTGACTTGGGAAGCGACTCTCTCGATCTATTTCATGAAGAAATTCGAACAGCCATTAATGAAT	1080
DB	1500	TTGACTTGGGAAGCGACTCTCTCGATCTATTTCATGAAGAAATTCGAACAGCCATTAATGAAT	1559
QY	1081	AGCGACTGTCTAGTCTTTTGACACACAGCATTCGACAGCTTTTTCGAGAAAAATGGCAATTTA	1140
DB	1560	AGCGACTGTCTAGTCTTTTGACACACAGCATTCGACAGCTTTTTCGAGAAAAATGGCAATTTA	1619
QY	1141	GGCATCAATGTAACATTTTCCATGTTGAAATGGCAATCAAACTTTTCTGGCCAGTGT	1200
DB	1620	GGCATCAATGTAACATTTTCCATGTTGAAATGGCAATCAAACTTTTCTGGCCAGTGT	1679
QY	1201	TTAAAACTTCAGTTTTCACAGAAAAATAGGCAACCCATCTGTCTGCAACCTAAAACTCTTT	1260
DB	1680	TTAAAACTTCAGTTTTCACAGAAAAATAGGCAACCCATCTGTCTGCAACCTAAAACTCTTT	1739
QY	1261	CGGTAGGTGGAAGC 1274	
DB	1740	CGGTAGGTGGAAGC 1753	

Search completed: April 25, 2005, 00:27:40
Job time : 5412 secs

Db	1261	CAGTGTACAGATCCTTAATAAAGTGCCACATTCAGTGTAAATTTATATTTTTTAATAATATCTTTT	1320
Qy	181	TTAATCCTATTTTTTCTTCTCTTTTGTCTCAGTAAATTTTGTATGAACCTTTAAAGGACT	240
Db	1321	TTAATCCTATTTTTTCTTCTCTTTTGTCTCAGTAAATTTTGTATGAACCTTTAAAGGACT	1380
Qy	241	TATGGCATGTAAACATTAATTTATAAAGTAAGTCATGGTTATAATTAATTTTCTCCTGCCT	300
Db	1381	TATGGCATGTAAACATTAATTTATAAAGTAAGTCATGGTTATAATTAATTTTCTCCTGCCT	1440
Qy	301	CCTTATGTATTTATTTTCAGAAATGAGCCGTACAGCTGTACAGCATTAACCTACCGGTACC	360
Db	1441	CCTTATGTATTTATTTTCAGAAATGAGCCGTACAGCTGTACAGCATTAACCTACCGGTACC	1500
Qy	361	TCGAAGTGTCCACATCCCGAGAGGGTCCCTGCCTGACTGGGCAACAAGTCATCCACCAAT	420
Db	1501	TCGAAGTGTCCACATCCCGAGAGGGTCCCTGCCTGACTGGGCAACAAGTCATCCACCAAT	1560
Qy	421	GACTTGGCGAGTCCTTTTGTAGTGTCCAGTCTGTCTTTGACTATGTGTACCGGCCCATTCCT	480
Db	1561	GACTTGGCGAGTCCTTTTGTAGTGTCCAGTCTGTCTTTGACTATGTGTACCGGCCCATTCCT	1620
Qy	481	CAATGTTCAGAGTGGCCATCTTTTGTAGCAACTGTGCGCCCAAGCTCACATGTTGTCCA	540
Db	1621	CAATGTTCAGAGTGGCCATCTTTTGTAGCAACTGTGCGCCCAAGCTCACATGTTGTCCA	1680
Qy	541	ACTTGGCGGGCCCTTTTGGGATCCATTCGCAACTTGGCTATGGAGAAAGTGGCTAATTTCA	600
Db	1681	ACTTGGCGGGCCCTTTTGGGATCCATTCGCAACTTGGCTATGGAGAAAGTGGCTAATTTCA	1740
Qy	601	GTACTTTTCCCCTCTAAATATGCGCTCTCTGGATGTGAAATAACTCTGCCACACACAGAA	660
Db	1741	GTACTTTTCCCCTCTAAATATGCGCTCTCTGGATGTGAAATAACTCTGCCACACACAGAA	1800
Qy	661	AAAGCAGACCATGAAGAGCTCTGTAGTTAGGSCCTTAATTCCTGTCCGTGCCCTGGTGCT	720
Db	1801	AAAGCAGACCATGAAGAGCTCTGTAGTTAGGSCCTTAATTCCTGTCCGTGCCCTGGTGCT	1860
Qy	721	TCCTGTAAATGGCAAGGCTCTCTCGATGCTGTAAATGCCCCCATCTGATGSCATCAGCATAAAG	780
Db	1861	TCCTGTAAATGGCAAGGCTCTCTCGATGCTGTAAATGCCCCCATCTGATGSCATCAGCATAAAG	1920
Qy	781	TCCATTAACAACCTACAGGGAGAGGATATAGTTTTTTCTTGCTACAGACATTAATCTTCCT	840
Db	1921	TCCATTAACAACCTACAGGGAGAGGATATAGTTTTTTCTTGCTACAGACATTAATCTTCCT	1980
Qy	841	GGTGCTGTGACTGGGTGATCATGATGCAGTCTCTGTTTTGGCTTTTCACTTCATGTTAGTCTTA	900
Db	1981	GGTGCTGTGACTGGGTGATGATGCAGTCTCTGTTTTGGCTTTTCACTTCATGTTAGTCTTA	2040
Qy	901	GAGAAACAGGAAAAATACGATGGTCCACAGCAGTCTTCGCAATCGTACAGCTGATAGGA	960
Db	2041	GAGAAACAGGAAAAATACGATGGTCCACAGCAGTCTTCGCAATCGTACAGCTGATAGGA	2100
Qy	961	ACACCCAGCAGCTGAAAAATTTTGTTCACCGCTTGAGCTTAAATGTCATAGCGCAGCA	1020
Db	2101	ACACCCAGCAGCTGAAAAATTTTGTTCACCGCTTGAGCTTAAATGTCATAGCGCAGCA	2160
Qy	1021	TTGACTTTGGGAGCGACTCCTCGATCTATTATGAAGAAATTCGAAAGCAATTTATGAAT	1080
Db	2161	TTGACTTTGGGAGCGACTCCTCGATCTATTATGAAGAAATTCGAAAGCAATTTATGAAT	2220
Qy	1081	ACGGACTGTCTAGTCTTTTGAACACAGCAGTATGCACAGCTTTTTCGAGAAAAATGGCAATTTA	1140
Db	2221	ACGGACTGTCTAGTCTTTTGAACACAGCAGTATGCACAGCTTTTTCGAGAAAAATGGCAATTTA	2280
Qy	1141	GGCATCAATGTAACTAATTTTCAATGTGTGAAATGGCAATCAAAATTTTCTGGCCAGTGT	1200
Db	2281	GGCATCAATGTAACTAATTTTCAATGTGTGAAATGGCAATCAAAATTTTCTGGCCAGTGT	2340
Qy	1201	TTAAAACTTCAGTTTTCAGAAAAATAAGCACCCTATCTGTCTGCCACCTAAACTCTTTT	1260
Db	2341	TTAAAACTTCAGTTTTCAGAAAAATAAGCACCCTATCTGTCTGCCACCTAAACTCTTTT	2400

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QY      1261  CGGTAGGTGGAAGC  1274
      |||||
      |||||
Db      2401  CGGTAGGTGGAAGC  2414

RESULT 2
US-60-660-850-81
; Sequence 81, Application US/60660850
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; APPLICANT: Ming-Yi Chiang
; APPLICANT: Lex M. Cowser
; APPLICANT: Nicholas M. Dean
; APPLICANT: Kenneth W. Dobie
; APPLICANT: Susan M. Freier
; APPLICANT: Ravi Jain
; APPLICANT: Erich Koller
; APPLICANT: Eric G. Marcusson
; APPLICANT: Robert McKay
; APPLICANT: Brett P. Monia
; APPLICANT: Donna T. Ward
; APPLICANT: Jacqueline Wyatt
; TITLE OF INVENTION: COMPOSITIONS AND
; FILE REFERENCE: DPTK-0079US.L
; CURRENT APPLICATION NUMBER: US/60/61
; CURRENT FILING DATE: 2005-03-10
; NUMBER OF SEQ ID NOS: 2619
; SOFTWARE: PatentSeq version 1.0
; SEQ ID NO 81
; LENGTH: 972
; TYPE: DNA
; ORGANISM: Homo sapiens
US-60-660-850-81

```

Query Match	99.7%	Score	1270.8	DB	12	Length	2972
Best Local Similarity	99.8%	Pred. No.	6.1e-271				
Matches	1272	Conservative	0	Mismatches	2	Indels	0
Gaps	0						
QY	1	TTTTCTTAGTGTGTTTATGGTCCATTTTCTATTTTAGCATTTATTTCTATGTAGTCTAT	60				
DB	741	TTTCTTTAGTGTGTTATGGTCCATTTTCTATTTTAGCATTTATTTCTATGTAGTCTAT	800				
QY	61	CCAAAGACGATTAAGGGAGTTTCCACATGTTTTCCGGAACTTTTGGAAAAAGAGAGCTTATC	120				
DB	801	CCAAAGACGATTAAGGGAGTTTCCACATGTTTTCCGGAACTTTTGGAAAAAGAGAGCTTATC	860				
QY	121	CAGTGTACAGATCCTTAATAAAGTGCCACATTCAGTGTAAATTTTATTTTTTAAATATCTTTT	180				
DB	861	CAGTGTACAGATCCTTAATAAAGTGCCACATTCAGTGTAAATTTTATTTTTTAAATATCTTTT	920				
QY	181	TTAATCCTATTTTCTTCCTCTTTTGTCTCAGTAAATTTTGTATGAAACTTTTAAAAAGGACT	240				
DB	921	TTAATCCTATTTTCTTCCTCTTTTGTCTCAGTAAATTTTGTATGAAACTTTTAAAAAGGACT	980				
QY	241	TATGGCATGTAAACATTTATTTATAAAGTAAGTCACTGTTATAATTTTCTCCTGCCT	300				
DB	981	TATGGCATGTAAACATTTATTTATAAAGTAAGTCACTGTTATAATTTTCTCCTGCCT	1040				
QY	301	CCTTATGTATTATTTTCAGAAATGAGCGGTGAGCTGTACAGCAATTTACCTACCGGTACC	360				
DB	1041	CCTTATGTATTATTTTCAGAAATGAGCGGTGAGCTGTACAGCAATTTACCTACCGGTACC	1100				
QY	361	TCGAAGTGTCCACCATCCAGAGGGTGCTGCCCTGACTGSCAACACTGCATCCAACAAT	420				
DB	1101	TCGAAGTGTCCACCATCCAGAGGGTGCTGCCCTGACTGSCAACACTGCATCCAACAAT	1160				
QY	421	GACTTTGGCGAGTCTTTTGGAGTCCAGTCTGTCTTTGACTATGTGTTACCGCCCATCTTT	480				
DB	1161	GACTTTGGCGAGTCTTTTGGAGTCCAGTCTGTCTTTGACTATGTGTTACCGCCCATCTTT	1220				
QY	481	CAATGTCAGAGTGGCCATCTTTGTTGTAGAACTGTGTCGCCCAAGCTCAGATGTTGTCCA	540				

Db 1221 CAATGTCAGAGTGGCCATCTGTTGTAGCAACTGTGCCCCAAAGCTCAATGTTGTCCA 1280
Qy 541 ACTTGGCGGGCCCTTTGGGATCCATTGCGCAACTTGGCTATGAGAAAGTGGCTAATTCA 600
Db 1281 ACTTGGCGGGCCCTTTGGGATCCATTGCGCAACTTGGCTATGAGAAAGTGGCTAATTCA 1340
Qy 601 GTACTTTTCCCTGTAATAATGCGTCTCTGGAGTGTGAATAACTCTGCCACACAGAA 660
Db 1341 GTACTTTTCCCTGTAATAATGCGTCTCTGGAGTGTGAATAACTCTGCCACACAGAA 1400
Qy 661 AAAGCAGACCATGAAGAGCTCTGTAGTGTAGGCTTATTCCTGTGCGTCCCTGGTGCT 720
Db 1401 AAAGCAGACCATGAAGAGCTCTGTAGTGTAGGCTTATTCCTGTGCGTCCCTGGTGCT 1460
Qy 721 TCTGTAAATGGCAAGGCTCTGTGATGTGTAAATGCCCATCTGATGCATCAGCATAAG 780
Db 1461 TCTGTAAATGGCAAGGCTCTGTGATGTGTAAATGCCCATCTGATGCATCAGCATAAG 1520
Qy 781 TCCATTACACCCCTACAGGAGAGGATATAGTGTGCTGCTACAGACATTAATCTTCCT 840
Db 1521 TCCATTACACCCCTACAGGAGAGGATATAGTGTGCTGCTACAGACATTAATCTTCCT 1580
Qy 841 GGTGCTGTGACTGGGTGATGATGCAGTCTGTTTGGCTTTCACCTTCATGTTAGTCTTA 900
Db 1581 GGTGCTGTGACTGGGTGATGATGCAGTCTGTTTGGCTTTCACCTTCATGTTAGTCTTA 1640
Qy 901 GAGAAACAGGAAATAACGATGTCACAGCAGTCTTTCGCAATCGTACAGCTGATAGGA 960
Db 1641 GAGAAACAGGAAATAACGATGTCACAGCAGTCTTTCGCAATCGTACAGCTGATAGGA 1700
Qy 961 ACACGCAAGCAAGCTGAAATTTTGTCTTACCGACTTGGAGTAAATGGTATAGGCGACGA 1020
Db 1701 ACACGCAAGCAAGCTGAAATTTTGTCTTACCGACTTGGAGTAAATGGTATAGGCGACGA 1760
Qy 1021 TTGACTTGGAGAGCACTCTCGATCTATTATGAGAGGAATGCAACAGCCATTATGAAT 1080
Db 1761 TTGACTTGGAGAGCACTCTCGATCTATTATGAGAGGAATGCAACAGCCATTATGAAT 1820
Qy 1081 AGCGACTGTCTAGTCTTTGACACAGCAATGACAGCTTTTTCGAGAAATGGCAATTTA 1140
Db 1821 AGCGACTGTCTAGTCTTTGACACAGCAATGACAGCTTTTTCGAGAAATGGCAATTTA 1880
Qy 1141 GGCAATCAATGTAATTTCCATGTTGAAATGGCAATCAAAATTTTTCGCGCAGTGT 1200
Db 1881 GGCAATCAATGTAATTTCCATGTTGAAATGGCAATCAAAATTTTTCGCGCAGTGT 1940
Qy 1201 TTAATACTTCAGTTTCACAGAAATAAGGACCCATCTGCTGCCAACCTTAAACTCTTT 1260
Db 1941 TTAATACTTCAGTTTCACAGAAATAAGGACCCATCTGCTGCCAACCTTAAACTCTTT 2000
Qy 1261 CGGTAGGTGGAAGC 1274
Db 2001 CGGTAGGTGGAAGC 2014

RESULT 3
US-10-955-054A-69

; Sequence 69, Application US/10955054A
; GENERAL INFORMATION:
; APPLICANT: PUSZTAI, LAJOS
; APPLICANT: SYMMANS, W. FRASER
; APPLICANT: HESS, KENNETH R.
; APPLICANT: AYERS, MARK
; APPLICANT: SPEC. JAMES
; TITLE OF INVENTION: MULTIGENE PREDICTORS OF RESPONSE TO CHEMOTHERAPY
; FILE REFERENCE: UTX:8800S
; CURRENT APPLICATION NUMBER: US/10/955,054A
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 195
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 69
; LENGTH: 2240

; TYPE: DNA
; ORGANISM: Homo sapiens
; US-10-955-054A-69
Query Match 33.5%; Score 427.4; DB 7; Length 2240;
Best Local Similarity 73.7%; Pred. No. 5.7e-85;
Matches 558; Conservative 0; Mismatches 196; Indels 3; Gaps 1;
Qy 416 ACAATGACTTTGGGAGTCTTTTGGAGTGTCCAGTGTCTGCTTTGACTATGTGTACCGCCCA 475
Db 738 ACCACGAGTGCACCTCGCTCTTCGAGTGTCCGCTCTGCTTTGACTATGTCTCTGCTCCTA 797
Qy 476 TTCTTCAATGTCAAGTGGCCATCTTGTGTGTAGCAACTGTGCGCCCAAAAGCTCACATGTT 535
Db 798 TTCTGCAGTGCCAGGCGGGCACCTGGTGTGTAAACCAATGCCGCCAGAAAGTTGAGTGTCT 857
Qy 536 GTCCAACTTTCGGGGCCCTTTGGGATC---CATTCGCAACTTGGCTATGGAGAAAGTGG 592
Db 858 GCCGAGCTGCGAGGGGCGCTTGACGCCCAGCATCAGGAAACCTGGCTATGGAGAGGTGG 917
Qy 593 CTAAATTCAGTACTTTTCCCTGTAAATATGCGTCTTCTGATGTGAAATAAATCTCTCCAC 652
Db 918 CCTCGGCACTCTGTTTCCCTGTAGTATGCCACACGCGGCTGTTCCCTGACCTGCACC 977
Qy 653 ACACAGAAAAGCAGACCATGAGAGCTCTGTAGTGTAGGCTTATTCCTGTCCGTGCC 712
Db 978 ATACGGAGAAACAGAAACATATGAACATATGTAATACCGCCCTACTCTCTGCCCATGTC 1037
Qy 713 CTGTGCTTCTGTAAATGGCAAGGCTCTCTGATGCTGTAAATGCCCATCTCATGATCATC 772
Db 1038 CTGTGCTTCTGTAAATGGCAAGGCTCTCTGAGTGTGAGTGTGATGTCCATCTCATGACG 1097
Qy 773 AGCATAAGTCCATTACAACTTACAGGGAGAGGATATAGTCTTTTCTGTACAGACATTA 832
Db 1098 CCCACAAGAGCATTACCACTTACAGGAAGAGACATCGTCTTTCTAGCTACAGACATTA 1157
Qy 833 ATCTTCTGCTGCTGTTGATCGGGTGTATGATGATGATGATGATGATGATGATGATGATGAT 892
Db 1158 ACTTGCAGGGCTGTGCGACTGGGTGATGATGATGATGATGATGATGATGATGATGATGAT 1217
Qy 893 TAGTCTTACAGAAACAGGAAATAACGATGTTTCCAGCAGTCTTTCGCAATCGTACAGC 952
Db 1218 TGTGCTGAGAAACAGGAAAGTACGAAAGGCCACGAGAGTTTTCGCAATCGTCTGCTC 1277
Qy 953 TGATAGGAAACAGCAAGCAAGCTGAAATTTTGTCTTACCGACTTGTAGCTTAAATGCTCAT 1012
Db 1278 TCATTGGCAACCCGCAAGCAAGCCGAGAACTTTTGTCTTACAGCTGGAGTTGAATGGAA 1337
Qy 1013 GCGCAGATGATGATGCGGAGGAGCTCTCTGATCTTATTCATGAGGAATGCAACAGCCA 1072
Db 1338 GCGGAGATGATGATGCGGAGGAGCCACGCGCTCGATTCATGATGATGATGATGATGATG 1397
Qy 1073 TTATGAATAGCAGTCTGTAGTCTTTGACACAGCAGATTCACAGCTTTTTCAGAGAAATG 1132
Db 1398 TCATGAACAGCAGCTGCTTGTTCGACAGCAGCATACATCTTTTTCAGATATG 1457
Qy 1133 GCAATTTAGGCAATCAATGTAACTATTTTCCATGTGTTG 1169
Db 1458 GGAACCTTGGAAATCAATGTACTATTTCTACATGTTG 1494

RESULT 4

US-60-655-875-88907
; Sequence 88907, Application US/60655875
; GENERAL INFORMATION:
; APPLICANT: Boukharov, Andrey
; APPLICANT: Du, Zijiang
; APPLICANT: Guo, Liang
; APPLICANT: Kovalic, David
; APPLICANT: Lu, Maolong
; APPLICANT: McGarter, James
; APPLICANT: Miller, Nancy
; APPLICANT: Williams, Deryck

```

; APPLICANT: Vaudin, Mark
; APPLICANT: Wu, Wei
; TITLE OF INVENTION: METHODS FOR GENETIC CONTROL OF HETERODERA INFESTATIONS
; TITLE OF INVENTION: IN PLANTS AND COMPOSITIONS THEREOF
; FILE REFERENCE: 38-21(53885)
; CURRENT APPLICATION NUMBER: US/60/655,875
; NUMBER OF SEQ ID NOS: 171306
; TYPE: DNA
; ORGANISM: Heterodera glycines
; FEATURE:
; OTHER INFORMATION: SCN-specific regions: Sequence locations=1-791
; US-60-655-875-96609

Query Match      16.8%; Score 214.6; DB 12; Length 791;
Best Local Similarity 63.9%; Pred. No. 4e-38;
Matches 325; Conservative 0; Mismatches 184; Indels 0; Gaps 0;

QY 412 TCACAACATGACTTGGCGAGTCTTTTGGAGTCCAGTCTGCTTTGACTATGCTTTGACTATGCTTTACCG 471
Db 258 TCAAAATCTGAAATTTCTGTGAGCTTCGAATGTCGGTTTGTCTTGTATGATGCTTCCG 317

QY 472 CCATTTCTCAATGTCCAGAGTGGCCATCTTTTGTAGCAACTGTGCGCCAAAGCTCACA 531
Db 318 CCATATCTGCAATGTCATCGGTCATCTGGTTTGTGGAATTTGCTGCTTAAAGTCACT 377

QY 532 TGTGTCCAACTTGGCGGGCCCTTTGGGATCAATTCGCAACTTGGCTATGAGAAAGTG 591
Db 378 GCTTGCCGACATGTCCAGGTCCAAATTCGAGCATAGAAATCTTGGAAATGGAGAAAT 437

QY 592 GCTAATTCAGTACTTTCCCTCTAATATGCTCTTCTGGATGTGAATACTCTGCCA 651
Db 438 GCAGCAAGCGCTGCAATTTCCATGCAATTTGCTCAATTCGCGGGTGCAACCCAAATCTTTTAT 497

QY 652 CACACAGAAAAGCAGACCATGAGAGCTCTGTGAGTTTAGGCTTTATTCCTGTCGGTGC 711
Db 498 CATCATGAGAAATTTAGACAGAGAGATTTGGAGTTTCGCTTTACCAATGCCCTTGT 557

QY 712 CTTGGTCTTCTGTAATGGAAGCTCTCTGGATGCTGTATGCCCCATCTGATGCAT 771
Db 558 CTTGGAGCTTCTTGCAATGGCAAGGAGTCTGGCAGATGTGATGAGCCATCTAATGAAA 617

QY 772 CAGCATAGTCCATTCAACCTACAGGAGAGATATAGTTTCTGCTACAGACATT 831
Db 618 TTGCACAAATCAATCAACATTTTGCAAGGGAAGACATTTGTTTCTGCAACTGACATC 677

QY 832 AATCTTCTCGTGTCTGTGACTGGGTGATGATGAGTCTCTGTTTGGCTTTCACTTCATG 891
Db 678 AACCTCCTGGGCTGTGCGATTGGGTAATGATGCAATCGTGCTACAAAGCCTTTTTCATG 737

QY 892 TTAGTCTTAGAGAAACAGGAAATACGA 920
Db 738 CTCGTCTTGGAAGCAAGAACAAACAAGA 766

RESULT 5
US-60-655-875-96609
; Sequence 96609, Application US/60655875
; GENERAL INFORMATION:
; APPLICANT: Boukharov, Andrey
; APPLICANT: Du, Zijing
; APPLICANT: Guo, Liang
; APPLICANT: Kovalic, David
; APPLICANT: Lu, Maolong
; APPLICANT: McCarter, James
; APPLICANT: Miller, Nancy
; APPLICANT: Williams, Deryck
; APPLICANT: Vaudin, Mark
; APPLICANT: Wu, Wei
; TITLE OF INVENTION: METHODS FOR GENETIC CONTROL OF HETERODERA INFESTATIONS
; TITLE OF INVENTION: IN PLANTS AND COMPOSITIONS THEREOF

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; FILE REFERENCE: 38-21(53885)
; CURRENT APPLICATION NUMBER: US/60/655,875
; CURRENT FILING DATE: 2005-02-24
; NUMBER OF SEQ ID NOS: 171306
; SEQ ID NO 96609
; LENGTH: 481
; TYPE: DNA
; ORGANISM: Heterodera glycines
; FEATURE:
; OTHER INFORMATION: SCN-specific regions: Sequence locations=1-481
; US-60-655-875-96609

Query Match      11.6%; Score 148; DB 12; Length 481;
Best Local Similarity 61.8%; Pred. No. 1.8e-23;
Matches 235; Conservative 0; Mismatches 145; Indels 0; Gaps 0;

QY 412 TCACAACATGACTTGGCGAGTCTTTTGGAGTCCAGTCTGCTTTGACTATGCTTTACCG 471
Db 99 TCAAAATCTGAAATTTCTGTGAGCTTCGAATGTCGGTTTGTCTTGTATGATGCTTTCCG 158

QY 472 CCATTTCTCAATGTCCAGAGTGGCCATCTTTTGTAGCAACTGTGCGCCAAAGCTCACA 531
Db 159 CCATATCTGCAATGTCATCGGTCATCTGGTTTGTGGAATTTGCTGCTTAAAGTCACT 218

QY 532 TGTGTCCAACTTGGCGGGCCCTTTGGGATCCATTCGCAACTTGGCTATGAGAAAGTG 591
Db 219 GCTTGCCGACATGTCCAGGTCCAAATTCGAGCATAGAAATCTTGGAAATGGAGAAAT 278

QY 592 GCTAATTCAGTACTTTTCCCTGTAAATATGCTCTTCTGGATGTGAATACTCTGCCA 651
Db 279 GCAGCAAGCTGCAATTTCCATGCAATTTGCTCAATTCGCGGGTGCAACCCAAATCTTTTAT 338

QY 652 CACACAGAAAAGCAGACCATGAGAGCTCTGTGAGTTTAGGCTTTATTCCTGCTCGTGC 711
Db 339 CATCATGAGAAATTTGACACAGAGATTTGGAGTTTTCGCTTACCAATGCCCTTGT 398

QY 712 CTTGGTCTTCTGTAATGGAAGCTCTCTGGATGCTGTATGCCCCATCTGATGCAT 771
Db 399 CTTGGAGCTTCTTGCAATGGCAAGGAGTCTGGCAGATGTGATGAGCCATCTAATGAAA 458

QY 772 CAGCATAGTCCATTACAAAC 791
Db 459 TTGCACAAATCAATCACAAC 478

RESULT 6
US-10-972-079-20102/c
; Sequence 20102, Application US/10972079
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: Denise, Sue K.
; APPLICANT: ROSENFELD, David
; APPLICANT: KERR, Richard
; APPLICANT: BATES, Stephen
; APPLICANT: HOLM, Tom
; TITLE OF INVENTION: METHODS & SYSTEMS FOR INFERRING TRAITS TO BREED & MANAGE NON-BEEF
; FILE REFERENCE: MM1110-2
; CURRENT APPLICATION NUMBER: US/10/972,079
; CURRENT FILING DATE: 2004-10-22
; PRIOR APPLICATION NUMBER: US 60/514,333
; PRIOR FILING DATE: 2003-10-24
; NUMBER OF SEQ ID NOS: 96631
; SOFTWARE: PatentIN version 3.1
; SEQ ID NO 20102
; LENGTH: 600
; TYPE: DNA
; ORGANISM: Chicken 19866894230253_1
; US-10-972-079-20102

Query Match      10.4%; Score 132.6; DB 7; Length 600;
Best Local Similarity 67.6%; Pred. No. 4.6e-20;
Matches 186; Conservative 0; Mismatches 89; Indels 0; Gaps 0;

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; OTHER INFORMATION: SCN-specific regions: Sequence locations=1-809
US-60-655-875-97115

Query Match      8.1%; Score 103.4; DB 12; Length 809;
Best Local Similarity 65.2%; Pred. No. 1.3e-13;
Matches 152; Conservative 0; Mismatches 81; Indels 0; Gaps 0;

QY 926 ACCAGCAGTTCTTCGCAATCGTACAGCTGATAGGAACACGCAAGACGAGCTGAAAAATTTTG 985
DB 800 ACCAAATGTTCTACGCAGTTGTTCAACTAATTTGGGACCAAAAAGGAGCGGAAAAATTTG 741

QY 986 CTTACCGACTTGAGCTAAATGGTTCATAGGCGAGCATTGACTCTGGAAGCGACTCCTCGAT 1045
DB 740 TTTTACAAATTTGGAATTTATCCAACAATCGGCGTGCATTTGCTGGGAAGCCAGTCCAGAA 681

QY 1046 CTATTTCATGAAGAAATTCGAACGCCATTATGAATAGCGACTGTCTAGTCTTTTGACACCA 1105
DB 680 GTATTACGAGGGGGTGCCTGCCGAATTTCTCAATCAGACTGTTTGGCTTTTGACACAA 621

QY 1106 GCATTGCACAGCTTTTTCGAGAAAATGGCAATTTAGGCATCAATGTAACTATT 1158
DB 620 ATCATGCGAATTTTTTTTGTCTGAAACGGGAATTTGGGAATAAATGTACTATT 568

RESULT 10
US-10-450-763-10677/c
; Sequence 10677, Application US/10450763
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc
; TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
; FILE REFERENCE: 790CIP3/US
; CURRENT APPLICATION NUMBER: US/10/450,763
; CURRENT FILING DATE: 2003-06-11
; PRIOR APPLICATION NUMBER: PCT/US01/08631
; PRIOR FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: 09/540,217
; PRIOR FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: 09/649,167
; PRIOR FILING DATE: 2000-08-23
; NUMBER OF SEQ ID NOS: 60736
; SOFTWARE: Custom
; SEQ ID NO 10677
; LENGTH: 4313
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURES:
; NAME/KEY: SIMILAR
; LOCATION: (13)..(519)
; OTHER INFORMATION: 75% homologous to Homo sapiens Spl40 protein, accession number
; OTHER INFORMATION: U63420, Smith-Waterman Score=622.
US-10-450-763-10677

Query Match      6.4%; Score 81.4; DB 8; Length 4313;
Best Local Similarity 64.9%; Pred. No. 1.3e-08;
Matches 137; Conservative 0; Mismatches 71; Indels 3; Gaps 1;

QY 416 ACAATGACTTGGCGAGTCTTTTGAAGTCTCCAGTCTGCTTTGACTATGTGTTACGCGCCA 475
DB 2411 ACCAGAGTGAACCTCGCTCTTCGAGTGTGCGGTCTGCTTTGACTATGTCTGCTCCTTA 2352

QY 476 TCTTCAATGTGAGAGTGGCCATCTTTGTTGTAGCAACTGTGCGCCAAAGCTCAATGTT 535
DB 2351 TTCTGAGTGGCAGCGCGGCACTTGGTGTGTAAACCAATGCCGCCAGAAAGTTGAGCTGCT 2292

QY 536 GTCCAACTTGGCGGGCCCTTTTGGCATC---CATTTGCAACTTGGCTATGGGAGAAAGTGG 592
DB 2291 GCCCGAGCTGCAGGGGGCCCTTGACGCCAGCATCAGGACCAGAAATGAGGAGAGGTGG 2232

QY 593 CTAATTCAGTACTTTTCCCTGTAAATATGC 623
DB 2231 CTTGGGAGTCTGTTTCCCGGCCAATGC 2201

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; SEQ ID NO 8838
; LENGTH: 2287
; TYPE: DNA
; ORGANISM: Heterodera glycines
US-655-875-8838

Query Match      5.1%; Score 64.4; DB 12; Length 2287;
Best Local Similarity 62.3%; Pred. No. 6.5e-05;
Matches 101; Conservative 0; Mismatches 61; Indels 0; Gaps 0;

QY 651 ACACAGAAAAAGCAGACCATGAGAGCTCTGTGAGTTTGTAGCGCTTATTCCTGTCCGTG 710
    |||||
Db 827 ATACTCAATAATTGGAATTTATTACTTGTGTTTACTTAGTCCCTACCAATGCCCTTG 886

QY 711 CCTGTGTCTCTCTGTAATGGAAGCTCTCTGATGCTGTAAATGCCCATCTGATGCA 770
    |||||
Db 887 TCCTGGAGCTTCTGCAAAATGGAAGGAGCTCTGGCAGATGTGATGAGCCATCTAATGAA 946

QY 771 TCAGCATAGTCCATTACACCTTACAGGAGGAGGATAGT 812
    |||||
Db 947 ATTGCACAAATCAATCACAACTTTGCAAGCAATTTTAAATT 988

RESULT 13
US-10-972-079-11909/c
; GENERAL INFORMATION: Application US/10972079
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: ROSENFELD, David
; APPLICANT: KERR, Richard
; APPLICANT: BATES, Stephen
; APPLICANT: HOLM, Tom
; TITLE OF INVENTION: METHODS & SYSTEMS FOR INFERRING TRAITS TO BREED & MANAGE NON-BEEH
; FILE REFERENCE: MM1110-2
; CURRENT APPLICATION NUMBER: US/10/972,079
; CURRENT FILING DATE: 2004-10-22
; PRIOR APPLICATION NUMBER: US 60/514,333
; PRIOR FILING DATE: 2003-10-24
; NUMBER OF SEQ ID NOS: 96631
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 11909
; LENGTH: 600
; TYPE: DNA
; ORGANISM: Chicken 19866894215157_1
US-10-972-079-11909

Query Match      4.4%; Score 56.2; DB 7; Length 600;
Best Local Similarity 58.0%; Pred. No. 0.0033;
Matches 119; Conservative 0; Mismatches 83; Indels 3; Gaps 1;

QY 668 ACCATGAAGAGCTCTGTGAGTTTGTAGGCTTATTCCTGTGCGTCCCTGGTGTCTCTGTA 727
    |||||
Db 202 ACCATGAAGAGTGCAGACCCCGAGTGGTTCCTTGCAGGTGCTGCTTCTCTGCC 143

QY 728 AATGCAAGGCTCTCTGGATGCTGTAATGCCCATCTGATGCCATCAGCATAGTCCATTA 787
    |||||
Db 142 CATGGGAGGCACTTGGAGTGTGTGTCCTCCACCTGAGG---CAAATCACCAGCATCA 86

QY 788 CAACCTACAGGAGGAGATATAGTTTCTGCTACAGACATTAATCTCTCGTGTGCTG 847
    |||||
Db 85 ACATCTTTCAGGGGGGAGAGATGTCTTCTGCGCCAGGACATGCACCTGCCCGCACCCA 26

QY 848 TTGACTGGGTGATGATGCAGTCTG 872
    |||||
Db 25 CGGACTGGATCATCATGCACTCTG 1

RESULT 14
US-10-517-441-265
; GENERAL INFORMATION: Application US/10517441
; Sequence 539, Application US/10517441
; GENERAL INFORMATION:
; APPLICANT: FOEKENS, John
; APPLICANT: HARBECK, Nadia
; APPLICANT: KOENIG, Thomas
; APPLICANT: MAIER, Sabine
; APPLICANT: MARTENS, John
```

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; APPLICANT: FOEKENS, John
; APPLICANT: HARBECK, Nadia
; APPLICANT: KOENIG, Thomas
; APPLICANT: MAIER, Sabine
; APPLICANT: MARTENS, John
; APPLICANT: MODEL, Fabian
; APPLICANT: NIMMERICH, Inko
; APPLICANT: RUJAN, Tamas
; APPLICANT: SCHMITT, Armin
; APPLICANT: SCHMITT, Manfred
; APPLICANT: LOOK, Maxime P.
; APPLICANT: MARX, Almut
; APPLICANT: HOEFER, Heinz
; TITLE OF INVENTION: Method and nucleic acids for the improved treatment of breast cell
; FILE REFERENCE: 47675-93
; CURRENT APPLICATION NUMBER: US/10/517,441
; CURRENT FILING DATE: 2004-12-11
; PRIOR APPLICATION NUMBER: PCT/EP2003/010881
; PRIOR FILING DATE: 2003-10-01
; PRIOR APPLICATION NUMBER: DE 10317955.0
; PRIOR FILING DATE: 2003-04-17
; PRIOR APPLICATION NUMBER: DE 10300096.8
; PRIOR FILING DATE: 2003-01-07
; PRIOR APPLICATION NUMBER: DE 10245779.4
; PRIOR FILING DATE: 2002-10-01
; NUMBER OF SEQ ID NOS: 2147
; SEQ ID NO 265
; LENGTH: 14147
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
US-10-517-441-265

Query Match      4.3%; Score 55.2; DB 8; Length 14147;
Best Local Similarity 48.4%; Pred. No. 0.0097;
Matches 153; Conservative 0; Mismatches 163; Indels 0; Gaps 0;

QY 1 TTTCTTTAGTTGTTTATGTCCTATTTCTATTTTATTTAGCATTTATTTCTATGTAGTCTAT 60
    |||||
Db 10843 TTGTTTTTTTTTTCGTTGTTTTTTTTTTTTCGAATTTATGTAGTTTTTTTTTTT 10902

QY 61 CCAAGACGATTAAAGGAGTTCACATGTTTCCGGAACATTTTGAAAGAGAGCTTATC 120
    |||||
Db 10903 TATGTTATTTGTAGTATTTTATGTTTGGGTTTTTATATATCGGTGCGTTTTTAT 10962

QY 121 CAGGTACAGATCCTTAATAAGTGCACATTCAGTGTAAATTTTATTTTATATCTTTT 180
    |||||
Db 10963 TGGTTTGTGTTTGTAGATATTTACAGAGTTAGTTTTTTTATTTTGTGTTTTTGT 11022

QY 181 TTAATCCTATTTTCTCTCTTTTCTCAGTAAATTTTGTATGAAACTTTAAAGAGACT 240
    |||||
Db 11023 TAGTGTGTTTTTTTGGCGATTTATTTTGTATTTTATGTAAGAGTAAATAGTTT 11082

QY 241 TAGGCATGTAACATTTATTAAGTAAAGTCAATGTTATTAATTTTCTCTGCTGCT 300
    |||||
Db 11083 TTTTGTGTTGATTTTTTTTTTATTAATTTTATTTATTTGACGTATTTTGTATATGTT 11142

QY 301 CCTATGATTTATTT 316
    |||||
Db 11143 TGTTTTTTTTTTATTT 11158

RESULT 15
US-10-517-441-539
; Sequence 539, Application US/10517441
; GENERAL INFORMATION:
; APPLICANT: FOEKENS, John
; APPLICANT: HARBECK, Nadia
; APPLICANT: KOENIG, Thomas
; APPLICANT: MAIER, Sabine
; APPLICANT: MARTENS, John
```


GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: April 24, 2005, 22:53:26 ; Search time 758 Seconds
(without alignments)
9949,539 Million cell updates/sec

Title: US-10-679-246-1

Perfect score: 1274

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Scoring table: OLIGO_NUC

Gapop 60.0 , Gapext 60.0

Searched: 4390206 seqs, 2959870667 residues

Word size : 15

Total number of hits satisfying chosen parameters: 17572

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

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12: Geneseqn2004as:*

13: Geneseqn2004bs:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1274	100.0	1274	4	Aac67281 Human Sia
2	1274	100.0	2924	5	Abv28804 Human pro
3	1274	100.0	2924	5	Abv25468 Human pro
4	1274	100.0	2924	5	Abv22970 Human pro
5	1274	100.0	6107	4	Aal05382 Human rep
6	1274	100.0	6107	4	Ab198246 Human tes
7	1223	96.0	2829	11	Adm01584 Human cdn
8	1223	96.0	2829	13	AdS34362
9	1104	86.7	2128	13	AdS34361
10	1041	81.7	2440	11	AdI31262 Human cdn
11	958	75.2	1540	13	AdS34365
12	958	75.2	2048	13	AdS34360
13	957	75.1	2454	13	AdS34359
14	947	74.3	1886	13	AdS34363
15	881	69.2	4090	10	AdF81381
16	838	65.8	2034	13	AdS34364
17	780	61.2	1884	2	Aat64820 Tumour su
18	581	45.6	3128	10	AdI40343 Human pur
19	356	27.9	1535	3	Aac98856 Human pan
20	203	15.9	466	4	Aai87326 Human pol

Abv38421	Human pro	5	ABV38421	405	12.5	159	C	21
Abv08519	Human pro	5	ABV08519	277	12.1	154	C	22
Abv43789	Human pro	5	ABV43789	417	10.9	139	C	23
Abv48461	Human pro	5	ABV48461	473	10.0	128	C	24
Abv13828	Human pro	5	ABV13828	411	9.3	118	C	25
Abv34940	Human pro	5	ABV34940	441	9.3	118	C	26
Abv04659	Human pro	5	ABV04659	438	6.7	85	C	27
Abi99429	Mouse isc	1968	6	1968	6.0	77	C	28
Abx44846	Bovine ES	8	ABX44846	360	4.9	62	C	29
Abv18678	Human pro	4	ABV18678	426	4.1	52	C	30
Aal01548	Human rep	222	4	222	2.6	33	C	31
Ab196986	Human tes	222	4	222	2.6	33	C	32
Abi99430	Mouse isc	2198	6	2198	2.4	30	C	33
Adf54673	Human SIA	33	10	ADP54673	1.9	24	C	34
AbS69096	Novel mur	226	6	ABSG69096	1.8	23	C	35
Adf54668	Human SIA	21	10	ADF54668	1.6	21	C	36
Adf54669	Human SIA	21	10	ADF54669	1.6	21	C	37
Ach28397	Human adu	442	9	ACH28397	1.6	21	C	38
Ach28129	Human adu	477	9	ACH28129	1.6	21	C	39
Ad114958	Human gla	1094	12	ADL14958	1.6	21	C	40
Ad114957	Human gla	1150	12	ADL14957	1.6	21	C	41
Adel13891	Human opt	46951	10	ADE13891	1.6	21	C	42
Aac67288	Human SIA	28	4	AAC67288	1.6	20	C	43
AcS55739	Human sig	257	10	ACS55739	1.6	20	C	44
Ad155595	Human pol	257	12	ADI55595	1.6	20	C	45
Ab108593	Drosophil	834	4	ABL08593	1.6	20	C	46
Adr25256	Breast ca	975	13	ADR25256	1.6	20	C	47
Acc50292	Breast ca	2240	8	ACC50292	1.6	20	C	48
Adp13401	Renal cel	2240	12	ADP13401	1.6	20	C	49
Ad14122	Human NF-	2240	13	ADR14122	1.6	20	C	50
Adp54830	Human PRO	2240	13	ADP54830	1.6	20	C	51
Acc50293	Breast ca	2502	8	ACC50293	1.6	20	C	52
Ab119804	Drosophil	2961	4	ABL19804	1.6	20	C	53
Ab108592	Drosophil	3157	4	ABL08592	1.6	20	C	54
Aq75209	ALI-1 (ac	8342	2	AAQ75209	1.6	20	C	55
Aat63333	MLL gene	8391	2	AAI63333	1.6	20	C	56
Aaq3478	MLL gene	8392	2	AAQ3478	1.6	20	C	57
Aaa99882	Human MLL	8392	2	AAA99882	1.6	20	C	58
Continuation (10 o		110000	13	ABD32966_09	1.6	20	C	59
Aac67289	Human SIA	19	4	AC67289	1.5	19	C	60
Abv01160	Human pro	231	5	ABV01160	1.5	19	C	61
Abd11499	Pseudomon	345	11	ABD11499	1.5	19	C	62
Abv40469	Human pro	447	5	ABV40469	1.5	19	C	63
Abv31500	Human pro	447	5	ABV31500	1.5	19	C	64
Abv47042	Human pro	470	5	ABV47042	1.5	19	C	65
Adg56323	Novel can	547	13	ADG56323	1.5	19	C	66
Ach79377	Human gn	564	12	ACH79377	1.5	19	C	67
Acn62684	Cotton de	567	13	ACN62684	1.5	19	C	68
Aal04022	Human rep	605	4	AAL04022	1.5	19	C	69
Aal04020	Human rep	605	4	AAL04020	1.5	19	C	70
Aas40419	DNA encod	605	5	AAS40419	1.5	19	C	71
Aas40417	DNA encod	605	5	AAS40417	1.5	19	C	72
Adj09623	Human pro	605	11	ADJ09623	1.5	19	C	73
Adj09625	Human pro	605	11	ADJ09625	1.5	19	C	74
Abd11398	Pseudomon	636	11	ABD11398	1.5	19	C	75
Abv10329	Human pro	850	5	ABV10329	1.5	19	C	76
Adc79411	Human G p	1014	6	ADC79411	1.5	19	C	77
Abq88091	Human GPC	1015	6	ABQ88091	1.5	19	C	78
Aaq87727	Human aux	1473	2	AAQ87727	1.5	19	C	79
Aat28393	Human cyt	1473	2	AAT28393	1.5	19	C	80
Ado35351	Novel mou	1662	12	ADO35351	1.5	19	C	81
Ad12649	Human ENZ	1795	8	ADA12649	1.5	19	C	82
ACA34434	Prokaryot	1806	8	ACA34434	1.5	19	C	83
Aas00019	Pseudomon	1884	4	AAS00019	1.5	19	C	84
Aas00017	Pseudomon	1884	4	AAS00017	1.5	19	C	85
Aas00018	Pseudomon	1884	4	AAS00018	1.5	19	C	86
AAL40123	Isoprenol	1884	6	AAL40123	1.5	19	C	87
ABD11213	Pseudomon	1920	11	ABD11213	1.5	19	C	88
AB107583	Drosophil	1951	4	AB107583	1.5	19	C	89
Adi31729	Human cdn	1995	11	ADI31729	1.5	19	C	90
Adq39097	Human SNP	1995	13	ADQ39097	1.5	19	C	91
Ada71685	Rice gene	2000	8	ADA71685	1.5	19	C	92
Aat11379	Cytochrom	2009	2	AAT11379	1.5	19	C	93

94	19	1.5	2009	2	AAV44155	Human cyt	18	1.4	498	2	AAT63116	Human sol
95	19	1.5	2188	13	ACN41238	Human dia	18	1.4	501	2	AAT63112	Human sol
96	19	1.5	2191	13	ACN41233	Human dia	18	1.4	504	2	AAQ36621	Soluble K
97	19	1.5	2239	13	ACN41232	Human dia	18	1.4	506	2	AAV07350	Stem cell
98	19	1.5	2258	2	AAV11380	Cytochrom	18	1.4	506	2	AAV07364	Stem cell
99	19	1.5	2258	2	AAV44158	Human cyt	18	1.4	506	2	AAV07349	Stem cell
100	19	1.5	2258	6	ABN95871	Gene #236	18	1.4	506	2	AAV07348	Stem cell
101	19	1.5	2258	11	ADI31669	Human CDN	18	1.4	506	2	AAV07360	Stem cell
102	19	1.5	2268	6	ABS65367	ABSE5367 Clostridi	18	1.4	506	2	AAV07365	Stem cell
103	19	1.5	2271	4	AAI65841	Nucleotid	18	1.4	506	2	AAV07359	Stem cell
104	19	1.5	2271	6	ABS65378	ABSE5378 Clostridi	18	1.4	506	2	AAV07351	Stem cell
105	19	1.5	2297	13	ACN41236	Human dia	18	1.4	506	2	AAV07353	Stem cell
106	19	1.5	2341	13	ACN41235	Human dia	18	1.4	506	2	AAV07347	Stem cell
107	19	1.5	2349	13	ACN41234	Human dia	18	1.4	506	2	AAV07354	Stem cell
108	19	1.5	2389	13	ACN41231	Human dia	18	1.4	506	2	AAV07352	Stem cell
109	19	1.5	2502	10	ADD29610	Human tum	18	1.4	506	2	AAV07366	Stem cell
110	19	1.5	3001	3	AAH51808	Chromosom	18	1.4	506	2	AAV07367	Stem cell
111	19	1.5	3127	4	ABL09644	Drosophil	18	1.4	506	2	AAV07346	Stem cell
112	19	1.5	3662	13	ADT05448	Haemophil	18	1.4	506	2	AAV07357	Stem cell
113	19	1.5	3991	4	ABL07926	Drosophil	18	1.4	506	2	AAV07344	Stem cell
114	19	1.5	4026	4	ABL07582	Drosophil	18	1.4	506	2	AAV07355	Stem cell
115	19	1.5	4372	4	ABL07954	Drosophil	18	1.4	506	2	AAV07356	Stem cell
116	19	1.5	4515	11	ABD11433	Pseudomon	18	1.4	506	2	AAV07345	Stem cell
117	19	1.5	4821	13	ADT05416	Haemophil	18	1.4	506	2	AAV07361	Stem cell
118	19	1.5	6131	6	ABQ67024	Human ang	18	1.4	506	2	AAV07362	Stem cell
119	19	1.5	6621	3	AAV70188	Human che	18	1.4	506	2	AAV07336	Stem cell
120	19	1.5	6641	6	ABN80003	Human imm	18	1.4	507	2	AAV07334	Stem cell
121	19	1.5	7597	6	ABL33013	Human imm	18	1.4	507	2	AAV07335	Stem cell
122	19	1.5	7728	6	ABL32077	Human che	18	1.4	507	2	AAV07339	Stem cell
123	19	1.5	7728	6	ABK40072	Human imm	18	1.4	507	2	AAV07337	Stem cell
124	19	1.5	9983	6	ABL32116	Signal tr	18	1.4	507	2	AAV07333	Stem cell
125	19	1.5	13249	6	ABK31176	Chemical	18	1.4	507	2	AAV07338	Stem cell
126	19	1.5	13249	6	ABL70131	Human imm	18	1.4	507	2	AAV07340	Stem cell
127	19	1.5	17211	6	ABL32654	Human imm	18	1.4	507	2	AAV07341	Stem cell
128	19	1.5	17211	6	ABL33729	Human imm	18	1.4	507	2	AAV07340	Stem cell
129	19	1.5	17721	5	ABK31176	Human ner	18	1.4	512	2	AAV073617	Human ste
130	19	1.5	20320	5	ABK31176	Human DNA	18	1.4	512	2	AAV073617	Human ste
131	19	1.5	32187	5	ABS32249	Novel hum	18	1.4	512	2	AAV073617	Human ste
132	19	1.5	32187	6	ABS67552	Novel hum	18	1.4	512	2	AAV073617	Human ste
133	19	1.5	33053	6	ABQ67006	Human ang	18	1.4	512	2	AAV073617	Human ste
134	19	1.5	43991	12	ADJ12398	DNA fragm	18	1.4	555	5	AAF68445	Human gen
135	19	1.5	58822	9	ADA02540	Human TCO	18	1.4	555	5	AAF68445	Human gen
136	19	1.5	58822	10	ADJ72278	Human TCO	18	1.4	555	8	ABK38356	cDNA enco
137	19	1.5	58822	10	ADJ95788	Human TCO	18	1.4	555	8	ABK38356	cDNA enco
138	19	1.5	88607	12	ADQ97648	Mouse can	18	1.4	555	8	ACA10685	Human lun
139	19	1.5	110000	2	AAT42063_13	Continuation (14 o	18	1.4	555	10	ABX99636	Lung canc
140	19	1.5	110000	2	AAT42063_14	Continuation (15 o	18	1.4	555	12	ADH45899	Human lun
141	19	1.5	110000	6	ABQ67195_2	Continuation (3 of	18	1.4	555	13	ADJ19818	Human lun
142	19	1.5	110000	6	ABQ67195_2	Continuation (15 o	18	1.4	555	13	ADJ19818	Human lun
143	19	1.5	139904	6	ABK83562	Human CDN	18	1.4	555	13	ADJ19818	Human lun
144	19	1.5	157875	6	ABK99972	Human CAD	18	1.4	555	13	ADJ19818	Human lun
145	19	1.5	190000	10	ADL13752	Osteoarth	18	1.4	555	13	ADJ19818	Human lun
146	19	1.5	349980	13	ADT05648	Haemophil	18	1.4	555	13	ADJ19818	Human lun
147	19	1.5	349980	13	ADT05737	Haemophil	18	1.4	555	13	ADJ19818	Human lun
148	18	1.4	79	10	ADG89226	Cancer de	18	1.4	555	13	ADJ19818	Human lun
149	18	1.4	179	9	ADA60133	Soybean s	18	1.4	555	13	ADJ19818	Human lun
150	18	1.4	253	9	ADA60359	Soybean s	18	1.4	555	13	ADJ19818	Human lun
151	18	1.4	270	10	ADA60324	Soybean s	18	1.4	555	13	ADJ19818	Human lun
152	18	1.4	342	5	ABV07858	Human pro	18	1.4	555	13	ADJ19818	Human lun
153	18	1.4	345	4	AAK55429	Human imm	18	1.4	555	13	ADJ19818	Human lun
154	18	1.4	354	10	ACF67717	Phototrab	18	1.4	555	13	ADJ19818	Human lun
155	18	1.4	381	8	ABX52492	Bovine ES	18	1.4	555	13	ADJ19818	Human lun
156	18	1.4	403	9	ADN60433	Soybean s	18	1.4	555	13	ADJ19818	Human lun
157	18	1.4	404	6	ABN64918	Human can	18	1.4	555	13	ADJ19818	Human lun
158	18	1.4	406	4	AAK60241	Human imm	18	1.4	555	13	ADJ19818	Human lun
159	18	1.4	412	5	ABV61290	Human pro	18	1.4	555	13	ADJ19818	Human lun
160	18	1.4	432	3	AAK43694	Arabidops	18	1.4	555	13	ADJ19818	Human lun
161	18	1.4	435	3	AAK43694	Arabidops	18	1.4	555	13	ADJ19818	Human lun
162	18	1.4	451	3	AAK27380	Human sec	18	1.4	555	13	ADJ19818	Human lun
163	18	1.4	495	2	AAV07332	Stem cell	18	1.4	555	13	ADJ19818	Human lun
164	18	1.4	495	2	AAV07332	Stem cell	18	1.4	555	13	ADJ19818	Human lun
165	18	1.4	498	2	AAT63111	Human sol	18	1.4	555	13	ADJ19818	Human lun
166	18	1.4	498	2	AAT63111	Human sol	18	1.4	555	13	ADJ19818	Human lun

C 240	18	1.4	820	12	ADP99315	Adp99315 Human ste	313	18	1.4	2834	3	AAC59739	Aac59739 Human sec
C 241	18	1.4	822	6	ABV78250	Abv78250 Human ste	314	18	1.4	2951	8	ABT18167	Abt18167 Aspergill
C 242	18	1.4	822	6	ABZ35826	Abz35826 Human ste	C 315	18	1.4	2969	8	ABX10380	Abx10380 DNA encod
C 243	18	1.4	822	6	ABX10069	Abx10069 Human ste	316	18	1.4	2979	8	ABT19773	Abt19773 Aspergill
C 244	18	1.4	822	6	ABL191791	Abt191791 Human pol	317	18	1.4	2996	8	ABT19787	Abt19787 Aspergill
C 245	18	1.4	828	6	ABQ19340	Abq19340 Oligonucle	318	18	1.4	2996	8	ABT19981	Abt19981 Aspergill
C 246	18	1.4	828	6	ABQ19341	Abq19341 Oligonucle	C 319	18	1.4	3052	6	ABK83776	Abk83776 Human CDN
C 247	18	1.4	860	8	ADA69923	Ada69923 Rice gene	320	18	1.4	3243	10	ADB63141	Adb63141 Human CDN
C 248	18	1.4	863	11	ACN82158	Acn82158 Breast ca	C 321	18	1.4	3303	6	AAH54402	Aah54402 S. epider
C 249	18	1.4	864	2	AAQ20845	Aaq20845 Encodes h	C 322	18	1.4	3304	6	ABK83988	Abk83988 Human CDN
C 250	18	1.4	889	9	ACC84605	Acc84605 Human gto	C 323	18	1.4	3304	12	ADP43839	Adp43839 Human DNA
C 251	18	1.4	906	2	AAQ42808	Aaq42808 Human IL-	C 324	18	1.4	3310	6	ABK76552	Abk76552 cDNA enco
C 252	18	1.4	912	2	AAQ42809	Aaq42809 Human MGF	C 325	18	1.4	3310	13	ACN37823	Acn37823 Tumour-as
C 253	18	1.4	935	11	ACN90584	Acn90584 Breast ca	C 326	18	1.4	3310	13	ADR97393	Adr97393 Human XFC
C 254	18	1.4	942	9	ADA32208	Ada32208 DNA encod	C 327	18	1.4	3357	5	AAH54452	Aah54452 S. epider
C 255	18	1.4	945	6	ABQ20416	Abq20416 Oligonucle	328	18	1.4	3402	2	AAH54452	Aah54452 S. epider
C 256	18	1.4	945	6	ABQ20417	Abq20417 Oligonucle	C 329	18	1.4	3462	2	AZ77533	Aaz77533 Human ova
C 257	18	1.4	951	8	ABT18761	Abt18761 Aspergill	C 330	18	1.4	3614	11	ADN95698	Adn95698 Human BEC
C 258	18	1.4	979	8	ABT18567	Abt18567 Aspergill	331	18	1.4	3668	4	AAH54402	Aah54402 S. epider
C 259	18	1.4	996	8	ABT20577	Abt20577 Aspergill	C 332	18	1.4	3806	6	ABT73857	Abt73857 Human SCF
C 260	18	1.4	996	8	ABT20383	Abt20383 Aspergill	C 333	18	1.4	3807	4	AAH41340	Aah41340 Human ste
C 261	18	1.4	1024	10	ABZ83697	Abz83697 Toxicolog	C 334	18	1.4	3807	4	AAH41340	Aah41340 Human ste
C 262	18	1.4	1059	2	AAT63113	Aat63113 Human sol	C 335	18	1.4	3807	4	AAH41340	Aah41340 Human ste
C 263	18	1.4	1078	12	ADO62584	Ado62584 Transcrip	C 336	18	1.4	3807	5	AAH23898	Aah23898 Human gen
C 264	18	1.4	1088	2	AAQ11543	Aaq11543 Human Ste	C 337	18	1.4	3807	5	AAH23898	Aah23898 Human gen
C 265	18	1.4	1088	2	AAT04891	Aat04891 Human SCF	C 338	18	1.4	3807	5	AAH23898	Aah23898 Human gen
C 266	18	1.4	1088	3	AAH13715	Aah13715 Human SCF	C 339	18	1.4	3807	5	AAH23898	Aah23898 Human gen
C 267	18	1.4	1088	4	AAH41345	Aah41345 Human SCF	C 340	18	1.4	3807	10	ADP52471	Adp52471 Human ste
C 268	18	1.4	1088	4	AAH41345	Aah41345 Human SCF	C 341	18	1.4	3807	10	ADP52471	Adp52471 Human ste
C 269	18	1.4	1088	4	AAH41345	Aah41345 Human SCF	C 342	18	1.4	4063	2	AAQ11540	Aaq11540 Human Ste
C 270	18	1.4	1088	5	AAH23902	Aah23902 Human SCF	C 343	18	1.4	4100	4	AAH54798	Aah54798 S. epider
C 271	18	1.4	1088	5	AAH23902	Aah23902 Human SCF	C 344	18	1.4	4335	8	ACA36923	Acc36923 Prokaryot
C 272	18	1.4	1088	5	AAH23902	Aah23902 Human SCF	C 345	18	1.4	4699	6	AAH41340	Aah41340 Human ste
C 273	18	1.4	1088	5	AAH23902	Aah23902 Human SCF	C 346	18	1.4	4736	3	AAH41340	Aah41340 Human ste
C 274	18	1.4	1088	6	AAH23902	Aah23902 Human SCF	C 347	18	1.4	5204	6	ABL32900	Abt32900 Human imm
C 275	18	1.4	1088	6	AAH23902	Aah23902 Human SCF	C 348	18	1.4	5263	6	ABL32900	Abt32900 Human imm
C 276	18	1.4	1088	10	ADP52490	Adp52490 Human ste	C 349	18	1.4	5416	4	ABL32900	Abt32900 Human imm
C 277	18	1.4	1088	12	ADP99332	Adp99332 Human ste	C 350	18	1.4	5447	4	AAH41342	Aah41342 Human ste
C 278	18	1.4	1089	2	AAT63114	Aat63114 Human sol	C 351	18	1.4	5571	6	ABQ70974	Abq70974 Listeria
C 279	18	1.4	1155	5	AAH27499	Aah27499 DNA encod	C 352	18	1.4	5864	4	AAH41342	Aah41342 Human ste
C 280	18	1.4	1215	8	ACA25257	Acc25257 Prokaryot	C 353	18	1.4	5864	4	AAH41342	Aah41342 Human ste
C 281	18	1.4	1227	6	ABN66135	Abn66135 Streptoco	C 354	18	1.4	5864	4	AAH41342	Aah41342 Human ste
C 282	18	1.4	1227	13	ADS58417	Ads58417 Bacterial	C 355	18	1.4	5864	4	AAH41342	Aah41342 Human ste
C 283	18	1.4	1256	9	ADA50160	Ada50160 Human CAR	C 356	18	1.4	5864	5	AAH41342	Aah41342 Human ste
C 284	18	1.4	1272	2	AAT63110	Aat63110 Human sol	C 357	18	1.4	5864	5	AAH41342	Aah41342 Human ste
C 285	18	1.4	1321	2	AAT63110	Aat63110 Human sol	C 358	18	1.4	5864	5	AAH41342	Aah41342 Human ste
C 286	18	1.4	1321	13	ADS88050	Ads88050 Tumour tr	C 359	18	1.4	5864	10	ADP52475	Adp52475 Human ste
C 287	18	1.4	1383	12	ADN74714	Adn74714 Thale cre	C 360	18	1.4	5865	12	ADP99317	Adp99317 Human ste
C 288	18	1.4	1404	2	AAQ11542	Aaq11542 Human Ste	C 361	18	1.4	5865	12	ADP99317	Adp99317 Human ste
C 289	18	1.4	1404	2	AAT04890	Aat04890 Human SCF	C 362	18	1.4	5903	4	ABL32900	Abt32900 Human imm
C 290	18	1.4	1404	3	AAH13714	Aah13714 Human SCF	C 363	18	1.4	5976	4	AAH41342	Aah41342 Human ste
C 291	18	1.4	1404	4	AAH41344	Aah41344 Human SCF	C 364	18	1.4	5976	6	ABK34007	Abk34007 Human DNA
C 292	18	1.4	1404	4	AAH41344	Aah41344 Human SCF	C 365	18	1.4	5976	10	ADP54106	Adp54106 Pretreate
C 293	18	1.4	1404	4	AAH41344	Aah41344 Human SCF	C 366	18	1.4	5976	10	ADP54106	Adp54106 Pretreate
C 294	18	1.4	1404	5	AAH41344	Aah41344 Human SCF	C 367	18	1.4	5976	10	ADP54106	Adp54106 Pretreate
C 295	18	1.4	1404	5	AAH41344	Aah41344 Human SCF	C 368	18	1.4	5976	10	ADP54106	Adp54106 Pretreate
C 296	18	1.4	1404	6	AAH41344	Aah41344 Human SCF	C 369	18	1.4	5976	13	ADP54106	Adp54106 Pretreate
C 297	18	1.4	1404	6	AAH41344	Aah41344 Human SCF	C 370	18	1.4	5976	13	ADP54106	Adp54106 Pretreate
C 298	18	1.4	1404	10	ADP52488	Adp52488 Human ste	C 371	18	1.4	6049	6	ABL32229	Abt32229 Human imm
C 299	18	1.4	1404	12	ADP99330	Adp99330 Human ste	C 372	18	1.4	6078	4	ABL32229	Abt32229 Human imm
C 300	18	1.4	1405	10	ACA56718	Acc56718 Human ste	C 373	18	1.4	6222	6	ABL32693	Abt32693 Human imm
C 301	18	1.4	1405	11	ADN95541	Adn95541 Human BEC	C 374	18	1.4	6255	6	ABL32960	Abt32960 Human imm
C 302	18	1.4	1405	12	ADI56514	Adi56514 Human pol	C 375	18	1.4	6351	6	ABL33174	Abt33174 Human imm
C 303	18	1.4	1461	4	AAE32431	Aae32431 LHM18 (li	C 376	18	1.4	6365	6	ABL33174	Abt33174 Human imm
C 304	18	1.4	1559	2	AAQ74818	Aaq74818 Firefly 1	C 377	18	1.4	6487	9	ABL32124	Abt32124 Human imm
C 305	18	1.4	1735	6	ABK52200	Abk52200 cDNA enco	C 378	18	1.4	6533	6	ABL32124	Abt32124 Human imm
C 306	18	1.4	1832	6	ABK52200	Abk52200 cDNA enco	C 379	18	1.4	6533	6	ABL32124	Abt32124 Human imm
C 307	18	1.4	2000	8	ADA71913	Ada71913 Rice gene	C 380	18	1.4	7028	4	AAH46531	Aah46531 Tumour su
C 308	18	1.4	2063	2	AAQ74819	Aaq74819 Firefly 1	C 381	18	1.4	7625	6	ABL33430	Abt33430 Human imm
C 309	18	1.4	2166	4	AAH46531	Aah46531 Human dig	C 382	18	1.4	7703	4	AAH46531	Aah46531 Tumour su
C 310	18	1.4	2206	12	ADP04554	Adp04554 Sea squir	C 383	18	1.4	7703	4	AAH46531	Aah46531 Tumour su
C 311	18	1.4	2616	8	ACA30186	Acc30186 Prokaryot	C 384	18	1.4	7703	5	AAH46531	Aah46531 Tumour su
C 312	18	1.4	2793	4	AAF31892	Aaf31892 Human KAR	C 385	18	1.4	7703	6	ABN90335	Abn90335 Human liv

C 386	18	1.4	7703	6	ABN90294	Abn90294 Human liv	459	18	1.4	110000	10	ACF65385_1	Continuation (2 of
C 387	18	1.4	7703	11	ADJ15248	Adj15248 Human liv	C 460	18	1.4	110000	10	ACF65383_2	Continuation (3 of
C 388	18	1.4	7703	11	ADJ15207	Adj15207 Human liv	C 461	18	1.4	110000	10	ACF67367_03	Continuation (4 of
C 389	18	1.4	7759	4	AAK77916	AAk77916 Human imm	C 462	18	1.4	110000	10	ACF67367_00	Continuation (31 o
C 390	18	1.4	7781	6	ABL33168	AbL33168 Human imm	C 463	18	1.4	110000	12	ADJ77486_12	Continuation (13 o
C 391	18	1.4	7857	6	ABQ67075	Abq67075 Human ang	C 464	18	1.4	110000	12	ADJ25985_15	Continuation (16 o
C 392	18	1.4	8794	4	AAS30465	Aas30465 DNA encod	C 465	18	1.4	110000	12	ADN97989_15	Continuation (16 o
C 393	18	1.4	8794	4	AAS30465	Aas30465 DNA encod	C 466	18	1.4	110000	12	ADO50281_15	Continuation (16 o
C 394	18	1.4	8794	4	AAL06245	Aal06245 Human rep	C 467	18	1.4	110000	13	ABD32629_1	Continuation (2 of
C 395	18	1.4	8962	6	ABL32686	AbL32686 Human imm	C 468	18	1.4	110000	13	ABD32629_2	Continuation (3 of
C 396	18	1.4	9741	6	ABL33323	AbL33323 Human imm	C 469	18	1.4	122614	11	ACN44998	Acn44998 Human gen
C 397	18	1.4	10866	6	ABL33488	AbL33488 Human imm	C 470	18	1.4	122923	11	ACN44026	Acn44026 Human gen
C 398	18	1.4	11155	6	ABL34134	AbL34134 Human imm	C 471	18	1.4	143391	10	ADL13648	AdL13648 Osteoarth
C 399	18	1.4	11754	6	ABL32686	AbL32686 Human imm	C 472	18	1.4	143391	10	ADL13648	AdL13648 Osteoarth
C 400	18	1.4	11754	6	ABL58149	AbL58149 Human imm	C 473	18	1.4	149034	11	ADP65433	Adp65433 Human ABC
C 401	18	1.4	13079	5	ABAL7964	AbAL7964 Drosoephil	C 474	18	1.4	168575	4	AAH21613	Aah21613 Human hyp
C 402	18	1.4	13549	4	AAK72853	AAk72853 Human imm	C 475	18	1.4	183999	4	AAQ92831	Aaq92831 Human ABC
C 403	18	1.4	14540	4	AAK72853	AAk72853 Human imm	C 476	18	1.4	185695	8	AAQ77405	Aaq77405 Human THB
C 404	18	1.4	14987	6	ABL32630	AbL32630 Human che	C 477	18	1.4	201766	10	ADL13771	AdL13771 Osteoarth
C 405	18	1.4	15121	6	ABN80239	AbN80239 Human imm	C 478	18	1.4	243390	13	ABD33366	Abd33366 Human can
C 406	18	1.4	15387	6	ABL32185	AbL32185 Human imm	C 479	18	1.4	265118	5	AAH41227	Aah41227 Pyrococcu
C 407	18	1.4	15789	4	AAS33399	Aas33399 DNA encod	C 480	18	1.4	321491	11	ACN44202	Acn44202 Human gen
C 408	18	1.4	15789	4	AAS33399	Aas33399 DNA encod	C 481	18	1.4	321491	11	ACN44202	Acn44202 Human gen
C 409	18	1.4	15789	10	ADC46514	Adc46514 Human neo	C 482	17	1.3	20	12	ADQ81511	Adq81511 PCR prime
C 410	18	1.4	17213	6	ABL33482	AbL33482 Human imm	C 483	17	1.3	20	12	ADQ81511	Adq81511 PCR prime
C 411	18	1.4	17213	6	ABL33483	AbL33483 Human imm	C 484	17	1.3	25	2	AAQ32035	Aaq32035 Oligonucl
C 412	18	1.4	17596	6	AAK72852	AAk72852 Human imm	C 485	17	1.3	25	2	AAQ32035	Aaq32035 Oligonucl
C 413	18	1.4	17959	6	ABL32575	AbL32575 Human imm	C 486	17	1.3	51	4	AAH39640	Aah39640 Human SNP
C 414	18	1.4	17959	6	ABL54342	AbL54342 Chemical	C 487	17	1.3	141	13	ADS01678	AdS01678 Staphyloc
C 415	18	1.4	18283	6	ABL70502	AbL70502 Chemical	C 488	17	1.3	153	12	ADL87810	AdL87810 DNA up-re
C 416	18	1.4	18283	6	ABL70502	AbL70502 Chemical	C 489	17	1.3	165	8	ABX35880	Abx35880 Bovine ES
C 417	18	1.4	18663	4	AAK75859	AAk75859 Human gen	C 490	17	1.3	179	6	ABK29611	Abk29611 Colon ade
C 418	18	1.4	18663	4	AAK75859	AAk75859 Human gen	C 491	17	1.3	196	12	ADH00855	Adh00855 Kidney di
C 419	18	1.4	19332	2	AAT46159	Aat46159 Cagi locu	C 492	17	1.3	197	5	ABV61884	Abv61884 Human pro
C 420	18	1.4	21729	4	ABL06154	AbL06154 Drosoephil	C 493	17	1.3	201	13	ADO47767	Ado47767 Myocardia
C 421	18	1.4	24853	5	ABAL7904	AbAL7904 Human ner	C 494	17	1.3	206	8	ABZ09478	Abz09478 Human Oli
C 422	18	1.4	25967	5	ABAL7904	AbAL7904 Human ner	C 495	17	1.3	206	8	ABZ09478	Abz09478 Human Oli
C 423	18	1.4	27423	6	ABL04268	AbL04268 Drosoephil	C 496	17	1.3	221	8	ABX55916	Abx55916 Bovine ES
C 424	18	1.4	30781	6	ADA04672	Ada04672 Human LCK	C 497	17	1.3	222	8	ABX55916	Abx55916 Bovine ES
C 425	18	1.4	31842	9	ADA02966	Ada02966 Human LCK	C 498	17	1.3	228	3	AAK32552	Aak32552 Urogenita
C 426	18	1.4	31842	10	ADC85446	Adc85446 Human LCK	C 499	17	1.3	232	8	ABX39412	Abx39412 Bovine ES
C 427	18	1.4	31842	10	ADC85446	Adc85446 Human LCK	C 500	17	1.3	261	9	ADA60343	Ada60343 Soybean s
C 428	18	1.4	32212	5	ABAL7905	AbAL7905 Human ner	C 501	17	1.3	300	3	AAQ00854	Aaq00854 Human col
C 429	18	1.4	35962	8	ABZ09958	AbZ09958 Haematopo	C 502	17	1.3	309	3	AAQ00854	Aaq00854 Human col
C 430	18	1.4	35962	8	ABZ09958	AbZ09958 Haematopo	C 503	17	1.3	316	12	ADO41039	Ado41039 Human sec
C 431	18	1.4	36194	4	ABL20582	AbL20582 Drosoephil	C 504	17	1.3	316	12	ADO41039	Ado41039 Human sec
C 432	18	1.4	40862	6	ABL34072	AbL34072 Human imm	C 505	17	1.3	326	8	ABX36466	Abx36466 Bovine ES
C 433	18	1.4	41454	11	ACN44942	Acn44942 Human gen	C 506	17	1.3	329	4	AAK82346	Aak82346 Human imm
C 434	18	1.4	41540	11	ACN44328	Acn44328 Mouse gen	C 507	17	1.3	329	4	AAK82346	Aak82346 Human imm
C 435	18	1.4	41540	11	ACN44328	Acn44328 Mouse gen	C 508	17	1.3	347	3	AAK26666	Aak26666 Human sec
C 436	18	1.4	41966	11	ACN45050	Acn45050 Human gen	C 509	17	1.3	348	6	ABK81989	Abk81989 Human dys
C 437	18	1.4	43411	6	ABQ98169	Abq98169 Human ost	C 510	17	1.3	357	6	ABL84400	AbL84400 Human ova
C 438	18	1.4	47613	11	ACN44072	Acn44072 Mouse gen	C 511	17	1.3	360	4	AAK61733	Aak61733 Human imm
C 439	18	1.4	48551	6	AAS20800	Aas20800 Clostridi	C 512	17	1.3	363	10	ADF55057	Adf55057 SINE fami
C 440	18	1.4	56153	4	AAS46793	Aas46793 Tumour su	C 513	17	1.3	370	6	ABN17701	Abn17701 Human ORF
C 441	18	1.4	63411	12	ADQ97081	Adq97081 Mouse can	C 514	17	1.3	373	5	ADL45101	AdL45101 Human ova
C 442	18	1.4	64125	13	ABD33295	Abd33295 Human can	C 515	17	1.3	376	4	AAS39016	Aas39016 Novel hum
C 443	18	1.4	65559	11	ACN44408	Acn44408 Mouse gen	C 516	17	1.3	376	6	ABK80934	Abk80934 Bacillus
C 444	18	1.4	82938	6	ABV72623	Abv72623 Human tra	C 517	17	1.3	387	5	ABV13239	Abv13239 Human pro
C 445	18	1.4	82952	6	ABN85766	AbN85766 Arabidops	C 518	17	1.3	387	5	ABZ41154	Abz41154 N. gonorr
C 446	18	1.4	86264	9	AAAL62889	AaAL62889 Human alp	C 519	17	1.3	388	2	AAQ60440	Aaq60440 Human bra
C 447	18	1.4	89024	4	ABL15486	AbL15486 Drosoephil	C 520	17	1.3	394	6	ABQ97602	Abq97602 Human epo
C 448	18	1.4	90798	12	ADP68859	Adp68859 Human chr	C 521	17	1.3	397	2	AAV02144	Aav02144 Human sec
C 449	18	1.4	95269	6	ABQ67195_4	AbQ67195_4 Continuation (5 of	C 522	17	1.3	397	2	AAV02144	Aav02144 Human sec
C 450	18	1.4	100000	4	AAK95248_12	AAK95248_12 Continuation (13 o	C 523	17	1.3	397	2	AAV02144	Aav02144 Human sec
C 451	18	1.4	100000	4	AAK96733_12	AAK96733_12 Continuation (13 o	C 524	17	1.3	408	5	ABV19135	Abv19135 Human pro
C 452	18	1.4	100000	6	ABN71527_04	AbN71527_04 Continuation (5 of	C 525	17	1.3	408	5	ABV19135	Abv19135 Human pro
C 453	18	1.4	100000	6	ABT00010_12	AbT00010_12 Continuation (13 o	C 526	17	1.3	418	9	ACH49073	Ach49073 Human leu
C 454	18	1.4	100000	6	ABQ8336_15	AbQ8336_15 Continuation (16 o	C 527	17	1.3	421	5	ABV34358	Abv34358 Human pro
C 455	18	1.4	100000	6	ABQ69245_13	AbQ69245_13 Continuation (14 o	C 528	17	1.3	423	8	ABX46087	Abx46087 Bovine ES
C 456	18	1.4	100000	6	ABQ67195_3	AbQ67195_3 Continuation (4 of	C 529	17	1.3	424	9	ACH30557	Ach30557 Human tes
C 457	18	1.4	100000	6	ABT01503_12	AbT01503_12 Continuation (13 o	C 530	17	1.3	427	4	AAI80439	Aai80439 Human pol
C 458	18	1.4	100000	6	ABA03041_13	AbA03041_13 Continuation (14 o	C 531	17	1.3	428	5	ABV19036	Abv19036 Human pro

532	17	1.3	429	6	ABL85657	Ab185657 Human ova	c 605	17	1.3	542	6	ABK38527	Abk38527 cDNA enco
533	17	1.3	431	8	ABX33663	Aax24526 Bovine ES	c 606	17	1.3	542	8	ACA10856	Aca10856 Human lun
534	17	1.3	434	2	AAX24526	Aax24526 Human lun	c 607	17	1.3	542	8	ABX99807	Abx99807 Lung canc
535	17	1.3	434	3	AAC65765	Ab148984 Human lun	c 608	17	1.3	542	10	ADH46070	Adh46070 Human lun
536	17	1.3	434	6	ABL48984	Abq92170 Human lun	c 609	17	1.3	542	12	ADH71822	Adh71822 Human lun
537	17	1.3	434	3	ABQ92170	Abq92170 Human lun	c 610	17	1.3	542	13	ADJ19889	Adj19889 Human lun
538	17	1.3	434	9	ADA28585	Ada28585 Human lun	c 611	17	1.3	543	4	AAH09850	Aah09850 Human cDN
539	17	1.3	434	10	ADH53345	Adh53345 Human lun	c 612	17	1.3	543	3	AAH04604	Aah04604 Partial c
540	17	1.3	434	10	ADH36680	Adh36680 Human lun	c 613	17	1.3	549	3	ACN56233	Acn56233 Cotton an
541	17	1.3	434	12	ADM56483	Adm56483 Human lun	c 614	17	1.3	555	13	ABZ34947	Abz34947 Human gen
542	17	1.3	434	12	ADH89527	Adh89527 Human lun	c 615	17	1.3	560	6	ACH72974	Ach72974 Human gen
543	17	1.3	436	6	ABL79054	Ab179054 Human ova	c 616	17	1.3	560	13	ACN47472	Acn47472 Cotton pr
544	17	1.3	437	2	AAX24574	Aax24574 Human lun	c 617	17	1.3	567	6	ABN69156	Abn69156 Streptoco
545	17	1.3	437	2	ACAC5813	Aac5813 Human lun	c 618	17	1.3	569	12	ACH72974	Ach72974 Human gen
546	17	1.3	437	5	ABV13143	Abv13143 Human pro	c 619	17	1.3	579	6	ABK27492	Abk27492 DNA enco
547	17	1.3	437	6	ABL49032	Ab149032 Human lun	c 620	17	1.3	579	12	ADN13642	Adn13642 Human pro
548	17	1.3	437	6	ABQ92218	Abq92218 Human lun	c 621	17	1.3	587	6	ABT10415	Abt10415 Human bre
549	17	1.3	437	9	ADA28633	Ada28633 Human lun	c 622	17	1.3	593	4	AAI18216	Aai18216 Human bre
550	17	1.3	437	10	ADH53593	Adh53593 Human lun	c 623	17	1.3	596	10	ADB51391	Adb51391 Primary r
551	17	1.3	437	10	ADH36728	Adh36728 Human lun	c 624	17	1.3	596	10	ADH41220	Adh41220 Toxicity
552	17	1.3	437	12	ADM56531	Adm56531 Human lun	c 625	17	1.3	598	6	ABQ40682	Abq40682 Oligonucl
553	17	1.3	437	12	ADH89575	Adh89575 Human lun	c 626	17	1.3	598	6	ABQ40683	Abq40683 Oligonucl
554	17	1.3	438	2	AAV88097	Aav88097 EST clone	c 627	17	1.3	600	13	ACN60364	Acn60364 Cotton gy
555	17	1.3	444	5	ADL63766	Adl63766 Human ova	c 628	17	1.3	612	13	ADQ53137	Adq53137 Novel can
556	17	1.3	451	5	ABV48913	Abv48913 Human pro	c 629	17	1.3	612	13	ADQ53137	Adq53137 Novel can
557	17	1.3	464	5	ABV34263	Abv34263 Human pro	c 630	17	1.3	634	5	ABV48815	Abv48815 Human pro
558	17	1.3	465	5	ABV43124	Abv43124 Human pro	c 631	17	1.3	644	12	ADO41040	Ado41040 Human cDN
559	17	1.3	466	4	AAI10076	Aai10076 Probe #9	c 632	17	1.3	647	3	AAZ46044	Aaz46044 Partial c
560	17	1.3	466	4	ABAS1705	Abas1705 Human foe	c 633	17	1.3	654	6	ABQ60427	Abq60427 Human col
561	17	1.3	466	4	AAI13134	Aai13134 Probe #10	c 634	17	1.3	655	5	ASB29050	Asb29050 cDNA enco
562	17	1.3	466	4	ABR21543	Ab21543 Probe #9	c 635	17	1.3	655	5	ABSG68190	Absg68190 cDNA enco
563	17	1.3	466	4	AAK25453	Aak25453 Human bon	c 636	17	1.3	655	10	ADC25184	Adc25184 Human cDN
564	17	1.3	466	4	AAK00018	Aak00018 Human bra	c 637	17	1.3	665	6	ABQ25763	Abq25763 Oligonucl
565	17	1.3	466	4	ABSG2020	Absg2020 Human liv	c 638	17	1.3	665	6	ABQ25762	Abq25762 Oligonucl
566	17	1.3	466	5	AAI00019	Aai00019 Probe #10	c 639	17	1.3	668	3	AAC51405	Aac51405 Arabidops
567	17	1.3	466	6	ABSG0018	Absg0018 Human gen	c 640	17	1.3	670	5	ABV47977	Abv47977 Human pro
568	17	1.3	474	5	AAST74547	Aas74547 DNA enco	c 641	17	1.3	671	3	AAAC35330	Aac35330 Arabidops
569	17	1.3	474	5	AAST68037	Aas68037 DNA enco	c 642	17	1.3	676	6	ABL99764	Ab199764 Human sec
570	17	1.3	474	5	AAST78435	Aas78435 DNA enco	c 643	17	1.3	690	6	ABT09295	Abt09295 Phase-1 R
571	17	1.3	478	8	ABX49267	Abx49267 Bovine ES	c 644	17	1.3	690	12	ADH22945	Adh22945 Liver inf
572	17	1.3	479	8	ACH16122	Ach16122 Human adu	c 645	17	1.3	690	13	ADR91259	Adr91259 Spleen ne
573	17	1.3	480	10	ADH82183	Adh82183 Arabidops	c 646	17	1.3	737	3	AAAC45974	Aac45974 Arabidops
574	17	1.3	480	5	ABV03974	Abv03974 Human pro	c 647	17	1.3	737	3	AAI96771	Aai96771 Human neu
575	17	1.3	482	5	ACH36684	Ach36684 Human end	c 648	17	1.3	740	3	AAAC39897	Aac39897 Arabidops
576	17	1.3	483	9	ADQ55308	Adq55308 Novel can	c 649	17	1.3	753	13	ADR313351	Adr313351 Stress re
577	17	1.3	488	13	ADQ55308	Adq55308 Novel can	c 650	17	1.3	756	9	ADB12302	Adb12302 Alloococ
578	17	1.3	489	4	ABA08868	Ab08868 Human sec	c 651	17	1.3	758	4	ABN93445	Abn93445 Human gen
579	17	1.3	489	9	ACH22149	Ach22149 Human adu	c 652	17	1.3	759	5	AAAC67568	Aac67568 DNA enco
580	17	1.3	490	5	AAST93417	Aas93417 cDNA enco	c 653	17	1.3	760	3	AAAO1744	Aao01744 Human col
581	17	1.3	490	5	AAST83837	Aas83837 DNA enco	c 654	17	1.3	771	4	AAH04267	Aah04267 Human cDN
582	17	1.3	494	4	AAI14563	Aai14563 Probe #44	c 655	17	1.3	775	6	ABQ69382	Abq69382 Listeria
583	17	1.3	494	4	ABA56289	Abas56289 Human foe	c 656	17	1.3	775	2	AAAX04327	Aax04327 Human sec
584	17	1.3	494	4	ABA25928	Abas25928 Probe #43	c 657	17	1.3	789	6	ABQ67690	Abq67690 Listeria
585	17	1.3	494	4	AAK04469	Aak04469 Human bra	c 658	17	1.3	792	4	AAD07860	Aad07860 Human sec
586	17	1.3	494	4	ABSG29624	Absg29624 Human liv	c 659	17	1.3	795	1	AAAN30099	Aan30099 Sequence
587	17	1.3	497	6	ABN65647	Abn65647 Human can	c 660	17	1.3	801	6	ABN67075	Abn67075 Streptoco
588	17	1.3	500	5	AAST93393	Aas93393 Mammary e	c 661	17	1.3	809	2	AAAX39878	Aax39878 Gastric c
589	17	1.3	500	10	ACD93923	Adc93923 Human col	c 662	17	1.3	811	3	AAAC41551	Aac41551 Arabidops
590	17	1.3	504	2	AAV88444	Aav88444 EST clone	c 663	17	1.3	819	10	ABZ41601	Abz41601 N. gonorr
591	17	1.3	507	2	AAV07342	Aav07342 Stem cell	c 664	17	1.3	822	3	AAZ53555	Aaz53555 Neisseria
592	17	1.3	514	6	ABN60635	Abn60635 Human can	c 665	17	1.3	832	6	ABQ68729	Abq68729 Listeria
593	17	1.3	518	4	AAAL02117	Aal02117 Human rep	c 666	17	1.3	836	6	AAI94704	Aai94704 Human neu
594	17	1.3	518	5	AAAS40208	Aas40208 DNA enco	c 667	17	1.3	836	8	ABT42804	Abt42804 Human neu
595	17	1.3	518	11	ADJ09203	Adj09203 Human pro	c 668	17	1.3	847	3	AAAC36952	Aac36952 Arabidops
596	17	1.3	532	4	ABA62144	Abas62144 Human foe	c 669	17	1.3	880	4	AAH08682	Aah08682 Human cDN
597	17	1.3	532	4	AAI42092	Aai42092 Probe #10	c 670	17	1.3	899	6	ABZ16683	Abz16683 Arabidops
598	17	1.3	532	4	AAK36364	Aak36364 Human bon	c 671	17	1.3	900	6	ABT05894	Abt05894 Human pro
599	17	1.3	532	4	AAK10462	Aak10462 Human bra	c 672	17	1.3	901	10	ADD48893	Add48893 Rat gene
600	17	1.3	532	4	ABSG36042	Absg36042 Human liv	c 673	17	1.3	912	3	AAA40492	Aaa40492 Human fet
601	17	1.3	536	4	AAK92600	Aak92600 Human cDN	c 674	17	1.3	913	2	AAV02297	Aav02297 Human sec
602	17	1.3	536	12	ADL29027	Adl29027 3' end of	c 675	17	1.3	934	4	AAI91423	Aai91423 Human pol
603	17	1.3	539	12	ADN12940	Adn12940 Human pro	c 676	17	1.3	937	5	ABV28411	Abv28411 Human pro
604	17	1.3	542	5	AAF68616	Aaf68616 Human lun	c 677	17	1.3	937	5	ABV22590	Abv22590 Human pro

c 678	17	1.3	940	6	ABQ36731	Abq36731 Oligonuc1	c 751	17	1.3	1780	8	ABZ23175	Abz23175 Polynucle
679	17	1.3	940	6	ABQ36730	Abq36730 Oligonuc1	c 752	17	1.3	1780	12	ADF11374	Adf11374 Human CAR
680	17	1.3	944	6	ABN59830	Abn59830 Novel hum	c 753	17	1.3	1824	6	ABK87939	Abk87939 Human arg
c 681	17	1.3	957	12	ADO35876	Ado35876 Novel mou	c 754	17	1.3	1824	12	ADJ58909	Adj58909 Human arg
c 682	17	1.3	984	10	ADC12713	Adc12713 Human GPC	755	17	1.3	1841	4	AAS25856	Aas25856 Human cDN
c 683	17	1.3	1011	6	ABK47820	Abk47820 Borrelia	756	17	1.3	1841	8	ABX73897	Abx73897 Human nov
c 684	17	1.3	1011	6	ABK47874	Abk47874 DNA encod	c 757	17	1.3	1849	8	ABZ23176	Abz23176 Polynucle
c 685	17	1.3	1011	6	ABK47821	Abk47821 Borrelia	c 758	17	1.3	1849	12	ADF11376	Adf11376 Human CAR
c 686	17	1.3	1011	6	ABK47873	Abk47873 DNA encod	c 759	17	1.3	1861	6	ABS73880	Abs73880 Human cDN
c 687	17	1.3	1011	12	ADN36407	Adn36407 Human gen	c 760	17	1.3	1872	6	ABQ68034	Abq68034 Listeria
c 688	17	1.3	1014	2	AAX30166	Aax30166 Human sec	c 761	17	1.3	1872	6	ABQ69949	Abq69949 Listeria
c 689	17	1.3	1024	3	AAZ97200	Aaz97200 Human pro	c 762	17	1.3	1872	8	ACA36328	Acc36328 Prokaryot
c 690	17	1.3	1024	3	AAZ97201	Aaz97201 Human pro	763	17	1.3	1886	6	ABQ54218	Abq54218 Human ova
c 691	17	1.3	1067	13	ADR62195	Adr62195 Cotton cD	764	17	1.3	1927	2	AAZ11963	Aaz11963 Human Hel
c 692	17	1.3	1113	3	AAZ53582	Aaz53582 Neisseria	765	17	1.3	1945	3	AAZ23436	Aaz23436 cDNA enco
c 693	17	1.3	1113	3	AAZ53581	Aaz53581 Neisseria	766	17	1.3	1973	4	AAO30303	Aao30303 Human dia
c 694	17	1.3	1127	6	ABQ41716	Abq41716 Oligonuc1	767	17	1.3	1984	6	ABL34634	AbL34634 Human met
c 695	17	1.3	1127	6	ABQ41717	Abq41717 Oligonuc1	768	17	1.3	1984	6	ABL70613	AbL70613 Chemical
c 696	17	1.3	1155	6	ABQ52090	Abq52090 Oligonuc1	769	17	1.3	1984	7	ADS99895	AdS99895 Bisulphit
c 697	17	1.3	1155	6	ABQ52091	Abq52091 Oligonuc1	770	17	1.3	1984	10	ADB54175	AdB54175 Pretreat
c 698	17	1.3	1175	6	ABZ17416	Abz17416 Arabidops	771	17	1.3	1984	10	ADB54303	AdB54303 Pretreat
c 699	17	1.3	1177	4	ABF82507	Abf82507 Human bre	772	17	1.3	1984	10	ADE37766	AdE37766 Human che
c 700	17	1.3	1263	6	ABL92690	AbL92690 Chlamydia	773	17	1.3	1984	10	ADE37776	AdE37776 Human che
c 701	17	1.3	1263	8	ACA30972	Acc30972 Prokaryot	774	17	1.3	1984	13	ADS89325	AdS89325 Oligonuc1
c 702	17	1.3	1264	3	AAO50438	Aao50438 Arabidops	775	17	1.3	1984	13	ADS89559	AdS89559 Oligonuc1
c 703	17	1.3	1266	3	AAO39994	Aao39994 Arabidops	776	17	1.3	1992	2	AAZ90717	Aaz90717 Human cw2
c 704	17	1.3	1266	10	ADQ43767	Adq43767 Chlamydia	777	17	1.3	1992	4	AAZ59252	Aaz59252 Human cDN
c 705	17	1.3	1291	6	ABQ40886	Abq40886 Oligonuc1	778	17	1.3	1992	6	ABA90921	AbA90921 Human pol
c 706	17	1.3	1291	6	ABQ40887	Abq40887 Oligonuc1	779	17	1.3	2000	6	ABZ16607	AbZ16607 Arabidops
c 707	17	1.3	1300	6	ABQ70486	Abq70486 Listeria	780	17	1.3	2000	6	ABZ15190	AbZ15190 Arabidops
c 708	17	1.3	1345	4	AAZ26136	Aaz26136 Human cDN	781	17	1.3	2000	6	ABZ15745	AbZ15745 Arabidops
c 709	17	1.3	1345	8	ABX73477	Abx73477 Human nov	782	17	1.3	2000	6	ABZ16098	AbZ16098 Arabidops
c 710	17	1.3	1350	6	ABN70749	Abn70749 Streptoco	783	17	1.3	2000	8	ADA68878	Ada68878 Arabidops
c 711	17	1.3	1356	6	ABK85745	Abk85745 DNA encod	c 784	17	1.3	2000	8	ADA73155	Ada73155 Rice gene
c 712	17	1.3	1356	8	ACA40044	Acc40044 Prokaryot	c 785	17	1.3	2046	4	AAI82495	Aai82495 Human pol
c 713	17	1.3	1362	12	ADN05427	Adn05427 Antipsori	c 786	17	1.3	2076	12	ADQ64842	AdQ64842 Novel hum
c 714	17	1.3	1362	12	ADQ20966	Adq20966 Human sof	c 787	17	1.3	2103	4	ABL01933	AbL01933 Drosophil
c 715	17	1.3	1393	3	AAO41244	Aao41244 Arabidops	788	17	1.3	2113	5	AAC88071	Aac88071 Human FLE
c 716	17	1.3	1410	2	AAZ34489	Aaz34489 Human LYS	789	17	1.3	2133	12	ADN73160	Adn73160 Thale cre
c 717	17	1.3	1459	2	AAV58646	Aav58646 Prostate	c 790	17	1.3	2133	8	ABZ23170	AbZ23170 Polynucle
c 718	17	1.3	1459	2	AAV61251	Aav61251 cDNA sequ	c 791	17	1.3	2160	12	ADP13415	Adp13415 Renal cel
c 719	17	1.3	1459	3	AAA06409	Aaa06409 Human imm	c 792	17	1.3	2169	6	ADQ37232	AdQ37232 Human dys
c 720	17	1.3	1459	3	ABH71314	Abh71314 Human pro	c 793	17	1.3	2172	12	ADQ63131	AdQ63131 Novel hum
c 721	17	1.3	1459	4	AAH93525	Aah93525 Human pro	c 794	17	1.3	2208	6	ABA90866	AbA90866 Facillus
c 722	17	1.3	1459	4	AAH63617	Aah63617 Human pro	c 795	17	1.3	2223	3	AAZ46024	Aaz46024 cDNA enco
c 723	17	1.3	1459	4	AAH02590	Aah02590 Prostate	c 796	17	1.3	2224	10	ADG32769	AdG32769 Human DNA
c 724	17	1.3	1459	4	AAH48439	Aah48439 Human pro	c 797	17	1.3	2224	13	ADS88619	AdS88619 Human hou
c 725	17	1.3	1459	5	ACA59426	Acc59426 Prostate	c 798	17	1.3	2229	6	AAI41491	Aai41491 Drug meta
c 726	17	1.3	1459	5	AAI10168	Aai10168 Human pro	c 799	17	1.3	2239	11	ACN88657	Acn88657 Breast ca
c 727	17	1.3	1459	6	ABL94989	AbL94989 Human P70	800	17	1.3	2259	11	ADI31470	AdI31470 Bacterial
c 728	17	1.3	1459	6	ABH58698	Abh58698 Prostate	c 801	17	1.3	2265	13	ADS51500	AdS51500 Human cDN
c 729	17	1.3	1459	8	ACQ95153	Acc95153 Prostate	c 802	17	1.3	2284	4	AAH18021	Aah18021 Human cDN
c 730	17	1.3	1459	10	ADBI3624	Adbi3624 Human pro	c 803	17	1.3	2315	4	ABL25202	AbL25202 Drosophil
c 731	17	1.3	1459	10	ADG26040	Adg26040 Human pro	c 804	17	1.3	2358	13	ACN38982	Acn38982 Tumour-as
c 732	17	1.3	1463	4	AAI26658	Aai26658 Human bre	805	17	1.3	2412	10	ABE59152	AbE59152 Toxicity-
c 733	17	1.3	1463	6	ABO75922	AbO75922 CHD activ	c 806	17	1.3	2412	12	ADP72905	AdP72905 Renal Cox
c 734	17	1.3	1504	3	AAZ15922	AAZ15922 Arabidops	c 807	17	1.3	2433	4	AAH17262	Aah17262 Human cDN
c 735	17	1.3	1527	3	AAZ70121	Aaz70121 Plasmodiu	c 808	17	1.3	2446	10	ADA53324	AdA53324 Human cod
c 736	17	1.3	1527	9	ADA31054	Ada31054 DNA encod	c 809	17	1.3	2446	12	ADN06067	Adn06067 Antipsori
c 737	17	1.3	1537	4	ACA85080	Acc85080 Atheroscl	c 810	17	1.3	2508	4	AAI41026	Aai41026 cDNA enco
c 738	17	1.3	1537	11	ADM29568	Adm29568 Human ath	c 811	17	1.3	2510	5	AAF93772	Aaf93772 Human cDN
c 739	17	1.3	1537	6	AAH59407	Aah59407 Human sec	812	17	1.3	2516	5	AAH42501	Aah42501 Human cDN
c 740	17	1.3	1585	3	AAH51290	Aah51290 Human REM	c 813	17	1.3	2523	4	AAH16955	Aah16955 Human cDN
c 741	17	1.3	1597	3	AAH59784	Aah59784 Human sec	c 814	17	1.3	2537	2	AAV44866	Aav44866 Clone CT5
c 742	17	1.3	1597	5	AAF24170	Aaf24170 Human sec	c 815	17	1.3	2546	2	AAV48463	Aav48463 Human cDN
c 743	17	1.3	1668	8	ACA23158	Acc23158 Prokaryot	c 816	17	1.3	2546	5	AAH98463	Aah98463 Human sec
c 744	17	1.3	1674	10	ADE58172	AdE58172 Rat gene	c 817	17	1.3	2547	4	AAO08315	Aao08315 Human sec
c 745	17	1.3	1690	4	AAO07817	Aao07817 Human sec	c 818	17	1.3	2591	10	ADA53243	AdA53243 Human cod
c 746	17	1.3	1711	3	AAH59844	Aah59844 Human cDN	c 819	17	1.3	2591	6	ABK35492	AbK35492 Human end
c 747	17	1.3	1741	4	AAH13927	Aah13927 Human cDN	c 820	17	1.3	2595	6	ABK39858	Abk39858 Human all
c 748	17	1.3	1767	5	AAH29126	Aah29126 cDNA enco	c 821	17	1.3	2595	6	ABK94408	Abk94408 DNA encod
c 749	17	1.3	1767	6	ABS68266	Abs68266 cDNA enco	c 822	17	1.3	2616	6	ABS54139	AbS54139 Mouse cDN
c 750	17	1.3	1767	10	ADC25260	Adc25260 Human cDN	c 823	17	1.3	2637	10	ADI22007	Adi22007 Novel hum

824	17	1.3	2648	10	ACA92448	Ac92448 DNA encod	897	17	1.3	4105	13	ADR87642	Adt87642 Human End
825	17	1.3	2660	6	ABQ54750	Abq54750 Human ova	898	17	1.3	4141	10	ADE57243	Ades7243 Rat gene
826	17	1.3	2708	10	ADD90222	Novel hum	899	17	1.3	4179	4	ABL25562	Ab125562 Drosophil
827	17	1.3	2708	10	ADG90041	Adg90041 Human cdn	900	17	1.3	4182	6	AAD37230	Aad37230 Human dys
828	17	1.3	2727	4	AAI58340	Human pol	901	17	1.3	4202	12	ADQ22606	Adq22606 Human sof
829	17	1.3	2727	5	ADQ98548	DNA encod	902	17	1.3	4230	6	ABQ70965	Abq70965 Listeria
830	17	1.3	2727	9	ADB48308	Novel hum	903	17	1.3	4310	3	AAC77525	Aac77525 Human ORF
831	17	1.3	2760	6	ABN66563	Streptoco	904	17	1.3	4313	5	AAS74873	Aas74873 DNA encod
832	17	1.3	2828	4	AAK94249	Human ful	905	17	1.3	4385	8	ABQ83347	Abq83347 Human KLK
833	17	1.3	2828	12	ADL30823	Full leng	906	17	1.3	4415	6	ABL33907	Ab133907 Human imm
834	17	1.3	2844	3	ABX05212	Human nov	907	17	1.3	4415	6	ABL34603	Ab134603 Human met
835	17	1.3	2865	3	AAZ28209	Non-malto	908	17	1.3	4415	6	ABL70424	Ab170424 Chemicall
836	17	1.3	2898	6	ABK87938	Human arg	909	17	1.3	4415	7	ADS9864	Ads9864 Complemen
837	17	1.3	2898	12	ADU58907	Human arg	910	17	1.3	4415	10	ADF76792	Adf76792 Novel hum
838	17	1.3	2921	4	AAI60126	Human pol	911	17	1.3	4415	12	ADN05936	Adn05936 Antipsori
839	17	1.3	2930	4	ABL20678	Drosophil	912	17	1.3	4415	12	ADO20315	Ado20315 Human PRO
840	17	1.3	2933	5	AA874797	DNA encod	913	17	1.3	4415	12	ADO20317	Ado20317 Human PRO
841	17	1.3	2940	11	ADN95667	Human BEC	914	17	1.3	4415	13	ADP55594	Adp55594 Human PRO
842	17	1.3	2941	10	ADW71105	Human met	915	17	1.3	4498	6	AAD37258	Aad37258 Adeno-ass
843	17	1.3	2952	10	ADA54019	Human cod	916	17	1.3	4617	12	ADQ20862	Adq20862 Human sof
844	17	1.3	2954	8	ABZ23169	Polynucle	917	17	1.3	4618	4	ABK42604	Abk42604 Genomic s
845	17	1.3	2954	12	ADQ83535	Human tum	918	17	1.3	4618	9	ADB60760	Adb60760 Connectiv
846	17	1.3	2954	13	ADQ84715	Human tum	919	17	1.3	4705	10	ADF74747	Adf74747 Murine dn
847	17	1.3	2954	13	ACN40459	Tumour-as	920	17	1.3	4707	12	ADQ28629	Adq28629 Human col
848	17	1.3	3025	4	AAI65200	Human neu	921	17	1.3	4718	4	AAH98223	Aah98223 Human EST
849	17	1.3	3031	3	AAAG4722	C. tracho	922	17	1.3	4718	10	ADI21512	Adi21512 Novel hum
850	17	1.3	3031	3	AAH56225	Chlamydia	923	17	1.3	4740	3	AAA95896	Aaa95896 Human KLK
851	17	1.3	3031	6	ABL92454	Chlamydia	924	17	1.3	4765	12	ADJ64312	Adj64312 Cartilage
852	17	1.3	3037	3	AA874986	Human ORF	925	17	1.3	4778	2	AA796562	Aat96562 Human neu
853	17	1.3	3081	6	ABQ74346	Human PNI	926	17	1.3	4825	6	AAD37257	Aad37257 Adeno-ass
854	17	1.3	3088	2	AAQ13727	Drosophil	927	17	1.3	4839	3	AAC47635	Aac47635 Arabidops
855	17	1.3	3096	4	ABL10095	Plasmodiu	928	17	1.3	4848	6	AAD37263	Aad37263 Adeno-ass
856	17	1.3	3100	10	AAAD51702	Human nuc	929	17	1.3	4869	4	AAH18396	Aah18396 Human cdn
857	17	1.3	3104	3	AAA28215	Non-malto	930	17	1.3	4869	5	AAI93855	Aai93855 Human sto
858	17	1.3	3128	8	ABZ10017	Haematopo	931	17	1.3	4877	13	ADI61640	Adi61640 Human cdn
859	17	1.3	3128	8	ABZ10163	Haematopo	932	17	1.3	4898	12	ADQ25276	Adq25276 Human sof
860	17	1.3	3136	3	AAAO9386	Human DNA	933	17	1.3	4932	6	ABK46137	Abk46137 cDNA enco
861	17	1.3	3136	4	AAO08154	Mammalian	934	17	1.3	4933	8	AAI57279	Aai57279 KIAA0644
862	17	1.3	3143	4	ABL22778	Drosophil	935	17	1.3	4933	10	ACC72792	Acc72792 Human can
863	17	1.3	3215	11	ACN88795	Breast ca	936	17	1.3	4933	11	ADN95166	Adn95166 Human BEC
864	17	1.3	3224	3	AAA75848	Sequence	937	17	1.3	4933	11	ADN95093	Adn95093 Human LFC
865	17	1.3	3303	6	ABZ22372	Signal pa	938	17	1.3	4933	12	ADQ21195	Adq21195 Human sof
866	17	1.3	3361	10	ADB62810	Human cdn	939	17	1.3	4941	13	ADP25678	Adp25678 Breast ca
867	17	1.3	3369	1	AAAN81690	Atrial na	940	17	1.3	4941	12	ADP09634	Adp09634 Rice cinn
868	17	1.3	3388	13	ADRO6827	Full leng	941	17	1.3	4949	12	ADQ25090	Adq25090 Human sof
869	17	1.3	3391	4	ABL01932	Drosophil	942	17	1.3	4966	6	AAD37256	Aad37256 Adeno-ass
870	17	1.3	3531	6	ABD37238	Human dys	943	17	1.3	4990	6	AAD37262	Aad37262 Adeno-ass
871	17	1.3	3531	8	ABX63123	Human cdn	944	17	1.3	5060	6	AAD37264	Aad37264 Adeno-ass
872	17	1.3	3737	4	ABLI1603	Drosophil	945	17	1.3	5079	6	AAS94937	Aas94937 Human DNA
873	17	1.3	3755	12	ADJ76120	Marker ge	946	17	1.3	5127	4	AA545425	Aas45425 Chemicall
874	17	1.3	3778	13	ADRO8277	Full leng	947	17	1.3	5149	6	AAD37255	Aad37255 Adeno-ass
875	17	1.3	3778	13	ADRO8277	Full leng	948	17	1.3	5174	13	ADT05447	Adt05447 Haemophil
876	17	1.3	3812	2	AA742219	Drosophil	949	17	1.3	5244	6	ABK40013	Abk40013 Human che
877	17	1.3	3812	2	AA779605	TATA-bind	950	17	1.3	5276	6	ABLI32151	Ab132151 Human imm
878	17	1.3	3825	6	ABK72928	Bacillus	951	17	1.3	5276	12	ADN05527	Adn05527 Antipsori
879	17	1.3	3837	12	ADJ12448	DNA fragm	952	17	1.3	5303	6	ABL33493	Ab133493 Human imm
880	17	1.3	3857	4	AAH54116	S. epide	953	17	1.3	5303	6	ABL32870	Ab132870 Human imm
881	17	1.3	3858	6	AAAD37237	Human dys	954	17	1.3	5303	6	ADP33339	Adp33339 Brassica
882	17	1.3	3941	8	ADA83888	Human MUC	955	17	1.3	5313	6	ABL32763	Ab132763 Human imm
883	17	1.3	3941	13	ADQ08265	Mucin 3B	956	17	1.3	5317	6	ABL32609	Ab132609 Human imm
884	17	1.3	3972	12	ADQ63887	Novel hum	957	17	1.3	5339	6	ABK81998	Abk81998 DNA encod
885	17	1.3	3999	6	AAD37234	Human dys	958	17	1.3	5365	6	ABL32047	Ab132047 Human imm
886	17	1.3	4011	12	ADO03170	Corn orth	959	17	1.3	5365	6	ABL70118	Ab170118 Chemicall
887	17	1.3	4079	10	ACA56659	Human eig	960	17	1.3	5365	6	AA661050	Aa661050 Human gen
888	17	1.3	4097	8	ABX05211	Human nov	961	17	1.3	5366	4	ABL03676	Ab103676 Drosophil
889	17	1.3	4097	8	ABX05211	Human nov	962	17	1.3	5439	6	ABL33403	Ab133403 Human imm
890	17	1.3	4105	3	AAA34583	ETA recep	963	17	1.3	5462	6	ABK81999	Abk81999 DNA encod
891	17	1.3	4105	3	AAA38341	Human end	964	17	1.3	5464	6	ABL33916	Ab133916 Human imm
892	17	1.3	4105	6	ABZ35259	Human gen	965	17	1.3	5464	6	ABK31452	Abk31452 Signal tr
893	17	1.3	4105	6	ABV94238	Breast ca	966	17	1.3	5464	6	ABL70429	Ab170429 Chemicall
894	17	1.3	4105	8	ABZ42662	Human end	967	17	1.3	5471	4	ABL10094	Ab110094 Drosophil
895	17	1.3	4105	12	ADF42785	Human end	968	17	1.3	5551	6	ABL70157	Ab170157 Chemicall
896	17	1.3	4105	12	ADQ18007	Human sof	969	17	1.3	5551	6	AA661099	Aa661099 Human gen

Ab133258 Human imm
Adq64971 Novel hum
Abd84161 Gene expr
Ab132374 Human imm
Abk333931 Human DNA
Ab134486 Human met
Adq99747 Bisulphit
Ada20366 Prostate
Ad844173 Human ren
Abk94926 Human nov
Abk94980 Human nov
Ab133704 Human imm
Ab134162 Human imm
Abn80073 Human che
Ab133355 Human che
Abk40023 Human che
Abk28382 DNA trans
Ab133338 Human imm
Aad06794 Human dys
Ab132383 Human imm
Aas61404 Human gen
Aas61404 Human gen
Aas61404 Human gen
Aas61405 Human gen
Ab133646 Human imm
Ab129649 Drosophil
Ade84205 Human lym
Ade84129 Human lym
Ab133944 Human imm
Ab111602 Drosophil
Ab132373 Human imm
Aas45335 Chemicall

ALIGNMENTS

RESULT 1
AAC67281
ID AAC67281 standard; cDNA; 1274 BP.
AC AAC67281;
09-APR-2001 (first entry)
Human Siah-1alpha coding sequence SEQ ID NO: 1.
Human; protein degradation; siah-mediated degradation protein; SMPD;
SCF-complex protein; SCP; siah-1 interacting protein; SIP;
KW Skpl-associated F-box protein; SAF-1; SAF-2; SAD; cancer; cell division;
KW Skpl-associated destruction-box protein; inflammatory disease; ss.
OS Homo sapiens.
XX
XX WO200077207-A2.
XX
XX 21-DEC-2000.
XX
XX 09-JUN-2000; 2000WO-US015873.
XX
XX 11-JUN-1999; 99US-00330517.
XX
XX (BURN-) BURNHAM INST.
XX Reed JC, Matsuzawa S;
XX WPI; 2001-071273/08.
XX P-PSDB; AAB35157.
XX
XX Siah-Mediated Degradation Protein, useful for drug screening, for
XX therapeutic applications and for functional genomics.
XX
XX Claim 5; Page 95-97; 121pp; English.
XX

The present invention provides the protein and coding sequences of several siah-mediated degradation proteins and SCF-complex proteins. These are designated siah-1alpha, Siah-1 interacting protein (SIP), which encodes two proteins due to alternative splicing (SIP-L and SIP-S), Skpl-associated F-box protein-lalpha and beta and -2 (SAF-lalpha, SAF-lbeta and SAF-2) and Skpl-associated destruction-box protein (SAD). The proteins and their coding sequences are useful in the diagnosis and treatment of cancers, disorders where too little cell division occurs such as bone marrow aplasia, immunodeficiencies and inflammatory diseases including sepsis, fibrosis, arthritis and graft versus host disease

Sequence 1274 BP; 336 A; 273 C; 253 G; 412 T; 0 U; 0 Other;

Query Match	100.0%;	Score 1274;	DB 4;	Length 1274;
Best Local Similarity	100.0%;	Pred. No. 0;		
Matches 1274;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

QY 1 TTTCTTTAGTTGTTTATGGTCCATTTTCTATTATTAGCATTTTATTCTATGTAGTCTAT 60
Db 1 TTTCTTTAGTTGTTTATGGTCCATTTTCTATTATTAGCATTTTATTCTATGTAGTCTAT 60

QY 61 CCAAGACGATTAAGGGAGTTTCCACATGTTTCCGGAACATTTTGAAGAAGAGAGCTTATC 120
Db 61 CCAAGACGATTAAGGGAGTTTCCACATGTTTCCGGAACATTTTGAAGAAGAGAGCTTATC 120

QY 121 CAGTGTACAGATCCTTAATAAGTCACATTCAGTGTAAATTTTATTATTTTAAATATCTTTT 180
Db 121 CAGTGTACAGATCCTTAATAAGTCACATTCAGTGTAAATTTTATTATTTTAAATATCTTTT 180

QY 181 TTAATCTTATTTTCTTCT 240
Db 181 TTAATCTTATTTTCT 240

QY 241 TATGCATGTAAACATTAATTTTATAAGTAAGTCATGTTTATAATTTTCTCTCTCTCTCT 300
Db 241 TATGCATGTAAACATTAATTTTATAAGTAAGTCATGTTTATAATTTTCTCTCTCTCTCT 300

QY 301 CCTATGTATTTTATTTTCAAAATAGCCGTGAGTGTCTAGCATTTACCTACCGGTACC 360
Db 301 CCTATGTATTTTATTTTCAAAATAGCCGTGAGTGTCTAGCATTTACCTACCGGTACC 360

QY 361 TCGAAGTGTCCACCATCCAGAGGGTGCCTGCCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 420
Db 361 TCGAAGTGTCCACCATCCAGAGGGTGCCTGCCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 420

QY 421 GACTTGGCGAGTCTTTTTCAGTGTCCAGTGTCTGCTTGTGATGTGTTTACCGCCCATCTT 480
Db 421 GACTTGGCGAGTCTTTTTCAGTGTCCAGTGTCTGCTTGTGATGTGTTTACCGCCCATCTT 480

QY 481 CAATGTACAGATGGCCATCTTGTGTTAGCACTGTCGCCCAAGCTCAGATGTTGTCCA 540
Db 481 CAATGTACAGATGGCCATCTTGTGTTAGCACTGTCGCCCAAGCTCAGATGTTGTCCA 540

QY 541 ACTTGGCGGGCCCTTTGGGATCCATTCGCAACTTTGGCTATGAGAAAGTGGCTAATTCA 600
Db 541 ACTTGGCGGGCCCTTTGGGATCCATTCGCAACTTTGGCTATGAGAAAGTGGCTAATTCA 600

QY 601 GTACTTTTCCCTGTAAATATATCGTCTTCTGATGTGAATTAACCTCTGCCACACAGAA 660
Db 601 GTACTTTTCCCTGTAAATATATCGTCTTCTGATGTGAATTAACCTCTGCCACACAGAA 660

QY 661 AAGCAGACATGAAGAGCTCTGTCAGTTTACGCTTATTTCTGCTCCGCTCGCTGCTGCT 720
Db 661 AAGCAGACATGAAGAGCTCTGTCAGTTTACGCTTATTTCTGCTCCGCTCGCTGCTGCT 720

QY 721 TCCGTGTAATGGCAAGGCTCTCTGGATGCTGTAATGCCCATCTCTGATGATCAGCATTAAG 780
Db 721 TCCGTGTAATGGCAAGGCTCTCTGGATGCTGTAATGCCCATCTCTGATGATCAGCATTAAG 780

QY 781 TCCATTACACCCCTACAGGAGAGGATATAGTTTTTCTTCTGCTACAGACATTAATCTTCT 840
Db 781 TCCATTACACCCCTACAGGAGAGGATATAGTTTTTCTTCTGCTACAGACATTAATCTTCT 840

QY 841 GGTGCTGTTGACTGGGTGATGATGAGTCTCTGTTTGGCTTTCACTTCATGTTAGTCTTA 900
 DB |||||
 QY 841 GGTGCTGTTGACTGGGTGATGATGAGTCTCTGTTTGGCTTTCACTTCATGTTAGTCTTA 900
 DB |||||
 QY 901 GAGAAACAGGAAATACCATGTCACACGAGTCTTCGCAATCTGACGCTGATAGGA 960
 DB |||||
 QY 901 GAGAAACAGGAAATACCATGTCACACGAGTCTTCGCAATCTGACGCTGATAGGA 960
 DB |||||
 QY 961 ACACGCAAGAGCTGAAATTTTGGCTTACCGACTTGGAGCTAAATGGTCATAGGCGACGA 1020
 DB |||||
 QY 961 ACACGCAAGAGCTGAAATTTTGGCTTACCGACTTGGAGCTAAATGGTCATAGGCGACGA 1020
 DB |||||
 QY 1021 TTGACTTGGGAAGCGACTCTCGATCTATTCATGAAGGAATTGCAACAGCCATTATGAAT 1080
 DB |||||
 QY 1021 TTGACTTGGGAAGCGACTCTCGATCTATTCATGAAGGAATTGCAACAGCCATTATGAAT 1080
 DB |||||
 QY 1081 AGCGACTGTCAGTCTTTCACACGAGCTTTCGACAGCTTTTTCGAGAAATGCAATTTA 1140
 DB |||||
 QY 1081 AGCGACTGTCAGTCTTTCACACGAGCTTTCGACAGCTTTTTCGAGAAATGCAATTTA 1140
 DB |||||
 QY 1141 GGCATCAATGTAATTTCCATGTTGAAATGGCAATCAAACTTTTCTGCGCAGTGT 1200
 DB |||||
 QY 1141 GGCATCAATGTAATTTCCATGTTGAAATGGCAATCAAACTTTTCTGCGCAGTGT 1200
 DB |||||
 QY 1201 TTAAACTTCAGTTTCACAGAAATAAGGACCCATCTGTCTGCGCAACCTTAACTCTTT 1260
 DB |||||
 QY 1201 TTAAACTTCAGTTTCACAGAAATAAGGACCCATCTGTCTGCGCAACCTTAACTCTTT 1260
 DB |||||
 QY 1261 CGGTAGTGGAGC 1274
 DB |||||
 QY 1261 CGGTAGTGGAGC 1274
 DB |||||

RESULT 2

ID ABV28804 standard; cDNA; 2924 BP.
 AC ABV28804;
 XX
 DT 16-SEP-2002 (first entry)
 DE Human prostate expression marker cDNA 28795.
 KW Human; prostate cancer; cytostatic; carcinogen; pharmacodynamic marker;
 KW pharmacogenomic marker; gene; ss.
 OS Homo sapiens.
 XX
 PN WO200160860-A2.
 XX
 PD 23-AUG-2001.
 XX
 PF 20-FEB-2001; 2001WO-US045171.
 XX
 PR 17-FEB-2000; 2000US-0183619P.
 PR 16-MAR-2000; 2000US-0189862P.
 PR 25-MAY-2000; 2000US-0207854P.
 PR 09-JUN-2000; 2000US-0211314P.
 PR 18-JUL-2000; 2000US-0219407P.
 PR 13-DEC-2000; 2000US-0255281P.
 XX
 PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
 XX
 PI Schlegel R, Endege WO, Monahan JB;
 XX
 XX WPI; 2001-662795/76.
 XX
 PT Novel isolated nucleic acid molecule associated with cancerous state of
 PT prostate cells and correlating with presence of prostate cancer, useful
 PT for detecting presence of prostate cancer, stage of prostate cancer.
 XX
 PS Claim 1; Page 6058; 11750pp; English.

XX The invention relates to an isolated nucleic acid molecule (I) comprising
 CC a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the
 CC specification or its complement. (I) is useful for: (a) assessing whether
 CC a patient is afflicted with prostate cancer; (b) monitoring the
 CC progression of prostate cancer in a patient; (c) assessing the efficacy
 CC of a test compound to inhibit prostate cancer in a patient; (d) assessing
 CC the efficacy of a therapy for inhibiting prostate cancer in a patient;
 CC (e) selecting a composition for inhibiting prostate cancer in a patient;
 CC (f) assessing whether prostate cancer has metastasized in a patient; (g)
 CC assessing the aggressiveness or indolence of prostate cancer in a patient
 CC ; (I) is also useful as a pharmacodynamic or pharmacogenomic marker
 XX
 SQ Sequence 2924 BP; 871 A; 562 C; 562 G; 925 T; 0 U; 4 Other;
 Query Match 100.0%; Score 1274; DB 5; Length 2924;
 Best Local Similarity 100.0%; Pred No. 0;
 Matches 1274; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 TTTCTTTTGTGTTTATGCTCCATTTTCTATTTTATTTAGCATTTTATTTCTATGATGCTAT 60
 DB |||||
 QY 480 TTTCTTTTGTGTTTATGCTCCATTTTCTATTTTATTTAGCATTTTATTTCTATGATGCTAT 539
 DB |||||
 QY 61 CCAAGACGATTAAGGAGTTCACATGTTTCCGGAACATTTTGAAGAGAGCTTATC 120
 DB |||||
 QY 540 CCAAGACGATTAAGGAGTTCACATGTTTCCGGAACATTTTGAAGAGAGCTTATC 599
 DB |||||
 QY 121 CAGTGTACAGATCTTAATAAGTGACATTCAGTGTAAATTTTATTTTAAATATCTTT 180
 DB |||||
 QY 600 CAGTGTACAGATCTTAATAAGTGACATTCAGTGTAAATTTTATTTTAAATATCTTT 659
 DB |||||
 QY 181 TTAATCTTATTTTCTCTCTTTTGTCTCAGTAAATTTTGTATGAAACTTTTAAAGGACT 240
 DB |||||
 QY 660 TTAATCTTATTTTCTCTCTTTTGTCTCAGTAAATTTTGTATGAAACTTTTAAAGGACT 719
 DB |||||
 QY 241 TATGCGATGTAACATTTATTAATAAGTCAATGTTTATTAATTTTCTCTCTCTCT 300
 DB |||||
 QY 720 TATGCGATGTAACATTTATTAATAAGTCAATGTTTATTAATTTTCTCTCTCTCT 779
 DB |||||
 QY 301 CCTTATGTTATTTTTCAGATATGAGCGCTCAGATGCTACAGCATTTACTACCGGTACC 360
 DB |||||
 QY 780 CCTTATGTTATTTTTCAGATATGAGCGCTCAGATGCTACAGCATTTACTACCGGTACC 839
 DB |||||
 QY 361 TCGAAGTGTCCACCATCCAGAGGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 420
 DB |||||
 QY 840 TCGAAGTGTCCACCATCCAGAGGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 899
 DB |||||
 QY 421 GACTTGGCGAGTCTTTTGGAGTGTCCAGTCTGCTTTGACTATGTGTAGCGCCATCTTT 480
 DB |||||
 QY 900 GACTTGGCGAGTCTTTTGGAGTGTCCAGTCTGCTTTGACTATGTGTAGCGCCATCTTT 959
 DB |||||
 QY 481 CAATGTCAGAGTGGCCATCTTCTTTGTAGCAATTTGTCGCCCAAGCTCAGTGTCTTCCA 540
 DB |||||
 QY 960 CAATGTCAGAGTGGCCATCTTCTTTGTAGCAATTTGTCGCCCAAGCTCAGTGTCTTCCA 1019
 DB |||||
 QY 541 ACTTGGCGGGGCTTTGGGATCCATTCGCAACTTTGCTATGAGAGAAAGTGGCTAATTTCA 600
 DB |||||
 QY 1020 ACTTGGCGGGGCTTTGGGATCCATTCGCAACTTTGCTATGAGAGAAAGTGGCTAATTTCA 1079
 DB |||||
 QY 601 GTACTTTTCCCTGTAAATATATGCGTCTTCTGATGTGAATATCTCTGCCACACAGAA 660
 DB |||||
 QY 1080 GTACTTTTCCCTGTAAATATATGCGTCTTCTGATGTGAATATCTCTGCCACACAGAA 1139
 DB |||||
 QY 661 AAAGCAGACCATGAAGAGCTCTGAGTTTATGCGCTTATTTCTGCTGCTGCTGCTGCTGCT 720
 DB |||||
 QY 1140 AAAGCAGACCATGAAGAGCTCTGAGTTTATGCGCTTATTTCTGCTGCTGCTGCTGCTGCT 1199
 DB |||||
 QY 721 TCTCTGTAATGCAAGGCTCTCTGATGCTGTAATGCCCTCATCTGATGATCAGCATAAG 780
 DB |||||
 QY 1200 TCTCTGTAATGCAAGGCTCTCTGATGCTGTAATGCCCTCATCTGATGATCAGCATAAG 1259
 DB |||||
 QY 781 TCCATTACAAACCTTACAGGAGAGGATATAGTTTTTCTTGTGTACAGACATTAATCTTCT 840
 DB |||||

Db 1260 TCCATTACACCCCTACAGGAGAGATATAGTTTTCTTGCTACAGACATTAATCTTCCT 1319

Qy 841 GGTGCTGTTGACTGGGCTGATGATGAGTCCCTGTTTGGCTTTTCACTTCATGTTAGTCTTA 900

Db 1320 GGTGCTGTTGACTGGGCTGATGATGAGTCCCTGTTTGGCTTTTCACTTCATGTTAGTCTTA 1379

Qy 901 GAGAACAGGAAAAATACGATGGTACAGGAGTCTTTCGCAATCGTACAGCTGATAGGA 960

Db 1380 GAGAACAGGAAAAATACGATGGTACAGGAGTCTTTCGCAATCGTACAGCTGATAGGA 1439

Qy 961 ACACCAAGCAGCTGAAAAATTTCTACCGACTTGGAGTAAATGGTACATAGGCGACGA 1020

Db 1440 ACACCAAGCAGCTGAAAAATTTCTACCGACTTGGAGTAAATGGTACATAGGCGACGA 1499

Qy 1021 TTGACTTGGGAAGCGACTCTCGATCTATTCATGAAGAAATGCAACAGCCATTAATGAAT 1080

Db 1500 TTGACTTGGGAAGCGACTCTCGATCTATTCATGAAGAAATGCAACAGCCATTAATGAAT 1559

Qy 1081 AGCGACTGCTAGTCTTTGACACCGACTTGCAGCTTTTGGCAAGAAATGGCAATTTA 1140

Db 1560 AGCGACTGCTAGTCTTTGACACCGACTTGCAGCTTTTGGCAAGAAATGGCAATTTA 1619

Qy 1141 GGCATCAATGTAATCTATTTCCATGTTTGAATGGCAATCAAAATTTTCTGGCCAGTGT 1200

Db 1620 GGCATCAATGTAATCTATTTCCATGTTTGAATGGCAATCAAAATTTTCTGGCCAGTGT 1679

Qy 1201 TTAATACTTCAGTTTACAGAAATAAGGACCCATCTGTCTGCGCAACCTAAATCTTT 1260

Db 1680 TTAATACTTCAGTTTACAGAAATAAGGACCCATCTGTCTGCGCAACCTAAATCTTT 1739

Qy 1261 CGGTAGTGGAGC 1274

Db 1740 CGGTAGTGGAGC 1753

RESULT 3

ABV25468

ID ABV25468 standard; cDNA; 2924 BP.

XX AC ABV25468;

XX DT 16-SEP-2002 (first entry)

XX DE Human prostate expression marker cDNA 25459.

XX KW Human; prostate cancer; cytostatic; carcinogen; pharmacodynamic marker;

XX KW pharmacogenomic marker; gene; ss.

XX OS Homo sapiens.

XX PN WO200160860-A2.

XX PD 23-AUG-2001.

XX PP 20-FEB-2001; 2001WO-US005171.

XX PR 17-FEB-2000; 2000US-0183319P.

XX PR 16-MAR-2000; 2000US-0199862P.

XX PR 25-MAY-2000; 2000US-0207454P.

XX PR 09-JUN-2000; 2000US-0211314P.

XX PR 18-JUL-2000; 2000US-0219007P.

XX PR 13-DEC-2000; 2000US-0255281P.

XX PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.

XX PI Schlegel R, Endege WO, Monahan JE;

XX WPI; 2001-662795/76.

XX Novel isolated nucleic acid molecule associated with cancerous state of

PT prostate cells and correlating with presence of prostate cancer, useful

PT for detecting presence of prostate cancer, stage of prostate cancer.

XX Claim 1; Page 5054-5055; 11750pp; English.

PS The invention relates to an isolated nucleic acid molecule (I) comprising

CC a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the

CC specification or its complement. (I) is useful for: (a) assessing whether

CC a patient is afflicted with prostate cancer; (b) monitoring the efficacy

CC progression of prostate cancer in a patient; (c) assessing the efficacy

CC of a test compound to inhibit prostate cancer in a patient; (d) assessing

CC the efficacy of a therapy for inhibiting prostate cancer in a patient;

CC (e) selecting a composition for inhibiting prostate cancer of a compound; (g)

CC (f) assessing the prostate cell carcinogenic potential of a compound; (g)

CC determining whether prostate cancer has metastasized in a patient; (h)

CC assessing the aggressiveness or indolence of prostate cancer in a patient

CC ; (I) is also useful as a pharmacodynamic or pharmacogenomic marker

XX Sequence 2924 BP; 871 A; 562 C; 562 G; 925 T; 0 U; 4 Other;

SQ

Query Match 100.0%; Score 1274; DB 5; Length 2924;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 1274; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTTCTTTAGTTGTTTATGGTCCATTTTCTATTTTAGCATTTATTATTCTATGTAGTCTAT 60

Db 480 TTTCTTTAGTTGTTTATGGTCCATTTTCTATTTTAGCATTTATTATTCTATGTAGTCTAT 539

Qy 61 CCAAGACGATTAAGGAGTTCCACATGTTTTCGGAAACATTTTGAAGAGAGCTTATC 120

Db 540 CCAAGACGATTAAGGAGTTCCACATGTTTTCGGAAACATTTTGAAGAGAGCTTATC 599

Qy 121 CAGTGTACAGATCTCTAATAAAGTGCACATTCAGTGTAAATTTTATTATTTTAAATCTTTT 180

Db 600 CAGTGTACAGATCTCTAATAAAGTGCACATTCAGTGTAAATTTTATTATTTTAAATCTTTT 659

Qy 181 TTAATCTTATTTTCT 240

Db 660 TTAATCTTATTTTCT 719

Qy 241 TATGGCATGTAACATATTTTATAAAGTCAATGATGTTTATTAATTTTCTCTCTCTCTCT 300

Db 720 TATGGCATGTAACATATTTTATAAAGTCAATGATGTTTATTAATTTTCTCTCTCTCTCT 779

Qy 301 CCTTATGTTATTTTATTTTCAAGATGAGCGTCAAGTCTAGCAGATTAACCTACCGGTACC 360

Db 780 CCTTATGTTATTTTATTTTCAAGATGAGCGTCAAGTCTAGCAGATTAACCTACCGGTACC 839

Qy 361 TCGAAGTGTCCACCATCCAGAGGGTGCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 420

Db 840 TCGAAGTGTCCACCATCCAGAGGGTGCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 899

Qy 421 GACTTGGCGAGTCTTTTGGAGTGTCCAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 480

Db 900 GACTTGGCGAGTCTTTTGGAGTGTCCAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 959

Qy 481 CAATGTCCAGTGGCGCATCTCTGTTGTAGCACTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 540

Db 960 CAATGTCCAGTGGCGCATCTCTGTTGTAGCACTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1019

Qy 541 ACTTGGCGGGCGCTTTTGGGATCCATTCGCAATCTGGCTATGAGAAAGTGCCTAATTC 600

Db 1020 ACTTGGCGGGCGCTTTTGGGATCCATTCGCAATCTGGCTATGAGAAAGTGCCTAATTC 1079

Qy 601 GTACTTTTCCCTGTAAATATGCGTCTTCTGATGTGAATTAATCTGCTGCTGCTGCTGCTGCTGCT 660

Db 1080 GTACTTTTCCCTGTAAATATGCGTCTTCTGATGTGAATTAATCTGCTGCTGCTGCTGCTGCTGCT 1139

Qy 661 AAAGCAGACCATGAAGAGCTCTGTTGAGTTTAGGCTTTTCTGCTGCTGCTGCTGCTGCTGCTGCT 720

Db 1140 AAAGCAGACCATGAAGAGCTCTGTTGAGTTTAGGCTTTTCTGCTGCTGCTGCTGCTGCTGCTGCT 1199

Qy 721 TCTGTAAATGGCAAGGCTCTCTGATGCTGTAATGCCCTCCCTGATGATGATGATGATGATGATGAT 780

Db 1200 TCTGTAAATGGCAAGGCTCTCTGATGCTGTAATGCCCTCCCTGATGATGATGATGATGATGATGAT 1259

QY 781 TCCATTACCAACCTCAGGAGAGGATATAGTTTTCTTGCTACAGACATTAATCTTCT 840
DB 1260 TCCATTACCAACCTCAGGAGAGGATATAGTTTTCTTGCTACAGACATTAATCTTCT 1319
QY 841 GGTGCTGTTGACTGGGTGATGATGCTGCTGTTTGGCTTTCACATTCATGTTAGTCTTA 900
DB 1320 GGTGCTGTTGACTGGGTGATGATGCTGCTGTTTGGCTTTCACATTCATGTTAGTCTTA 1379
QY 901 GAGAAACAGGAAATACATGATGTCACCGAGCTTCTTCCCAATCGTACAGCTGATAGGA 960
DB 1380 GAGAAACAGGAAATACATGATGTCACCGAGCTTCTTCCCAATCGTACAGCTGATAGGA 1439
QY 961 ACACGACAGCTGAAATTTGCTTACCGACTTTCAGCTTAAATGGTCAATAGGCGACGA 1020
DB 1440 ACACGACAGCTGAAATTTGCTTACCGACTTTCAGCTTAAATGGTCAATAGGCGACGA 1499
QY 1021 TTGACTTGGGAAACGACTCTCGATCTATTTCATGAAGGAATGCAACAGCCATTATGAAT 1080
DB 1500 TTGACTTGGGAAACGACTCTCGATCTATTTCATGAAGGAATGCAACAGCCATTATGAAT 1559
QY 1081 AGCGACTGCTAGCTTTTGACACACGACTTTCAGCTTAAATGGTCAATAGGCGACGA 1140
DB 1560 AGCGACTGCTAGCTTTTGACACACGACTTTCAGCTTAAATGGTCAATAGGCGACGA 1619
QY 1141 GGCATCAATGTAATCTATTTCCATGTTGGAATGGCAATCAAACTTTCTGCCAGTGT 1200
DB 1620 GGCATCAATGTAATCTATTTCCATGTTGGAATGGCAATCAAACTTTCTGCCAGTGT 1679
QY 1201 TTAAACTTTCAGTTTTCACAGAAATGAAGGACCCATCTCTGCGCAACCTTAACTCTTT 1260
DB 1680 TTAAACTTTCAGTTTTCACAGAAATGAAGGACCCATCTCTGCGCAACCTTAACTCTTT 1739
QY 1261 CGGTAGTGGAGC 1274
DB 1740 CGGTAGTGGAGC 1753

RESULT 4

ABV22970
ID ABV22970 standard; cdna; 2924 BP.
XX AC ABV22970;
XX DT 13-SEP-2002 (first entry)
XX DE Human prostate expression marker cdna 22961.
XX KW Human; prostate cancer; cytostatic; carcinogen; pharmacodynamic marker;
XX KW pharmacogenomic marker; gene; ss.
XX OS Homo sapiens.
XX PN WO200160860-A2.
XX PD 23-AUG-2001.
XX PF 20-FEB-2001; 2001WO-US005171.
XX PR 17-FEB-2000; 2000US-0183319P.
XX PR 16-MAR-2000; 2000US-0189862P.
XX PR 25-MAY-2000; 2000US-0207454P.
XX PR 09-JUN-2000; 2000US-0211314P.
XX PR 18-JUL-2000; 2000US-0219007P.
XX PR 13-DEC-2000; 2000US-0255281P.
XX PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
XX PI Schlegel R, Endege WO, Monahan JB;
XX DR WPI; 2001-662795/76.
XX PT Novel isolated nucleic acid molecule associated with cancerous state of

PT prostate cells and correlating with presence of prostate cancer, useful
PT for detecting presence of prostate cancer, stage of prostate cancer.
XX Claim 1; Page 4080-4081; 11750pp; English.

XX The invention relates to an isolated nucleic acid molecule (I) comprising
CC a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the
CC specification or its complement. (I) is useful for: (a) assessing whether
CC a patient is afflicted with prostate cancer; (b) monitoring the
CC progression of prostate cancer in a patient; (c) assessing the efficacy
CC of a test compound to inhibit prostate cancer in a patient; (d) assessing
CC the efficacy of a therapy for inhibiting prostate cancer in a patient;
CC (e) selecting a composition for inhibiting prostate cancer in a patient;
CC (f) assessing the prostate cell carcinogenic potential of a compound; (g)
CC determining whether prostate cancer has metastasized in a patient; (h)
CC assessing the aggressiveness or indolence of prostate cancer in a patient
CC; (i) is also useful as a pharmacodynamic or pharmacogenomic marker
XX; (i) is also useful as a pharmacodynamic or pharmacogenomic marker
SQ Sequence 2924 BP; 871 A; 562 C; 562 G; 925 T; 0 U; 4 Other;

Query Match 100.0%; Score 1274; DB 5; Length 2924;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1274; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TTTCTTTAGTTGTTTATGCTCCATTTTCTATTTTAGCATTTATTTCTATGCTAT 60
DB 480 TTTCTTTAGTTGTTTATGCTCCATTTTCTATTTTAGCATTTATTTCTATGCTAT 539
QY 61 CCAAGACGATTAAGGAGTTCACATGTTTCCGGAACATTTTGAAGAGAGCTTATC 120
DB 540 CCAAGACGATTAAGGAGTTCACATGTTTCCGGAACATTTTGAAGAGAGCTTATC 599
QY 121 CAGTGTACAGATCCTTAATAAGTGCACATTCAGTGTAAATTTTATTTTAAATATCTTT 180
DB 600 CAGTGTACAGATCCTTAATAAGTGCACATTCAGTGTAAATTTTATTTTAAATATCTTT 659
QY 181 TTAATCCTATTTTCTCTCTTTTGTCTCAGTAAATTTTGTATGAACCTTAAAGGACT 240
DB 660 TTAATCCTATTTTCTCTCTTTTGTCTCAGTAAATTTTGTATGAACCTTAAAGGACT 719
QY 241 TATGCATGTAACATTTATTAAGTAAGTCAATGTTTATTAATTTTCTCTCTGCT 300
DB 720 TATGCATGTAACATTTATTAAGTAAGTCAATGTTTATTAATTTTCTCTCTGCT 779
QY 301 CTTATGATTTTATTTAGAAATAGCCGTACAGCTGCTACAGCATTTACCTACCGTACC 360
DB 780 CTTATGATTTTATTTAGAAATAGCCGTACAGCTGCTACAGCATTTACCTACCGTACC 839
QY 361 TCGAAGTGTCCACCATCCAGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 420
DB 840 TCGAAGTGTCCACCATCCAGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 899
QY 421 GACTTGGCGAGTCTTTTGGAGTCCAGTCTCTTTGACTGTGTGTGTGTGTGTGTGTGT 480
DB 900 GACTTGGCGAGTCTTTTGGAGTCCAGTCTCTTTGACTGTGTGTGTGTGTGTGTGTGT 959
QY 481 CAATGTACAGTGGCCATCTTTTGTAGCAATCTGTCGCCAAAGCTCAATGTTGTCCA 540
DB 960 CAATGTACAGTGGCCATCTTTTGTAGCAATCTGTCGCCAAAGCTCAATGTTGTCCA 1019
QY 541 ACTTCCCGGGCCCTTTGGATCCATTTGCAATCTTGGCTATGAGAGAAATGGCTAATTC 600
DB 1020 ACTTCCCGGGCCCTTTGGATCCATTTGCAATCTTGGCTATGAGAGAAATGGCTAATTC 1079
QY 601 GTACTTTTCCCTGTAAATATATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 660
DB 1080 GTACTTTTCCCTGTAAATATATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1139
QY 661 AAAGCAGACCATGAAGAGCTCTGTGAGTTTAGGCTTATTTCTGCTGCTGCTGCTGCTGCT 720
DB 1140 AAAGCAGACCATGAAGAGCTCTGTGAGTTTAGGCTTATTTCTGCTGCTGCTGCTGCTGCT 1199
QY 721 TCCTGTAATGGCAAGGCTCTCTGGAATGCTGTAAATGCTGCTGCTGCTGCTGCTGCTGCT 780

Db	1200	TCCTGTAATGGCAAGGCTCTCTGATGCTGTAATGGCCCACTGATGCATCAGCATTAAG	1259	PR	07-JUL-2000;	2000US-0216880P.
				PR	11-JUL-2000;	2000US-0217487P.
				PR	11-JUL-2000;	2000US-0217496P.
QY	781	TCATTACAACCTTACAGGAGAGATATAGTTTTTCTTGCTACAGACATTAATCTTCCT	840	PR	14-JUL-2000;	2000US-0218290P.
				PR	26-JUL-2000;	2000US-0220963P.
Db	1260	TCATTACAACCTTACAGGAGAGATATAGTTTTTCTTGCTACAGACATTAATCTTCCT	1319	PR	26-JUL-2000;	2000US-0220964P.
				PR	14-AUG-2000;	2000US-0224518P.
QY	841	GGTGTGTGACTGGGTGANGANGCAGCTCTGTTTTGGCTTTCATCTCATGTTAGTCTTA	900	PR	14-AUG-2000;	2000US-0224519P.
				PR	14-AUG-2000;	2000US-0225213P.
Db	1320	GGTGTGTGACTGGGTGANGANGCAGCTCTGTTTTGGCTTTCATCTCATGTTAGTCTTA	1379	PR	14-AUG-2000;	2000US-0225214P.
				PR	14-AUG-2000;	2000US-0225266P.
QY	901	GAGAACAGGAAATACAGTGTCCACAGCAGTTCTTCGCAATCGTACAGCTGATAGGA	960	PR	14-AUG-2000;	2000US-0225267P.
				PR	14-AUG-2000;	2000US-0225268P.
Db	1380	GAGAACAGGAAATACAGTGTCCACAGCAGTTCTTCGCAATCGTACAGCTGATAGGA	1439	PR	14-AUG-2000;	2000US-0225270P.
				PR	14-AUG-2000;	2000US-0225447P.
QY	961	ACACGACAGCAAGCTGAAATTTTGTCTTACCGACTTGAGCTAAATGGTCATAGGCGACGA	1020	PR	14-AUG-2000;	2000US-0225757P.
				PR	14-AUG-2000;	2000US-0225758P.
Db	1440	ACACGACAGCAAGCTGAAATTTTGTCTTACCGACTTGAGCTAAATGGTCATAGGCGACGA	1499	PR	14-AUG-2000;	2000US-0225759P.
				PR	18-AUG-2000;	2000US-0226279P.
QY	1021	TTGACTTGGGAAGCACTCTCGATCTATTCAATGAAGCAATTTGCAACAGCCATTATGAAT	1080	PR	22-AUG-2000;	2000US-0226681P.
				PR	22-AUG-2000;	2000US-0226868P.
Db	1500	TTGACTTGGGAAGCACTCTCGATCTATTCAATGAAGCAATTTGCAACAGCCATTATGAAT	1559	PR	22-AUG-2000;	2000US-0227182P.
				PR	23-AUG-2000;	2000US-0227009P.
QY	1081	AGCGACTGTCTAGTCTTTCACACACGACATTCACACAGCTTTTTCGAGAAATGGCAATTTA	1140	PR	30-AUG-2000;	2000US-0228924P.
				PR	01-SEP-2000;	2000US-0229287P.
Db	1560	AGCGACTGTCTAGTCTTTCACACACGACATTCACACAGCTTTTTCGAGAAATGGCAATTTA	1619	PR	01-SEP-2000;	2000US-0229343P.
				PR	01-SEP-2000;	2000US-0229344P.
QY	1141	GGCATCAATGTAACTATTTCCATGTGTGAAATGGCAATTCATTAATTTTGGCCAGTGT	1200	PR	01-SEP-2000;	2000US-0229345P.
				PR	05-SEP-2000;	2000US-0229509P.
Db	1620	GGCATCAATGTAACTATTTCCATGTGTGAAATGGCAATTCATTAATTTTGGCCAGTGT	1679	PR	05-SEP-2000;	2000US-0229513P.
				PR	06-SEP-2000;	2000US-0230437P.
QY	1201	TTAAACTTCAGTTTCACAGAAATTAAGCACCACCTGCTGCGCAACCTTAAACTCTTT	1260	PR	06-SEP-2000;	2000US-0230438P.
				PR	08-SEP-2000;	2000US-0231242P.
Db	1680	TTAAACTTCAGTTTCACAGAAATTAAGCACCACCTGCTGCGCAACCTTAAACTCTTT	1739	PR	08-SEP-2000;	2000US-0231243P.
				PR	08-SEP-2000;	2000US-0231244P.
QY	1261	CGGTAGTGGGAAGC 1274		PR	08-SEP-2000;	2000US-0231413P.
				PR	08-SEP-2000;	2000US-0231414P.
Db	1740	CGGTAGTGGGAAGC 1753		PR	08-SEP-2000;	2000US-0232080P.
				PR	08-SEP-2000;	2000US-0232081P.
				PR	12-SEP-2000;	2000US-0231968P.
				PR	14-SEP-2000;	2000US-0232397P.
				PR	14-SEP-2000;	2000US-0232398P.
				PR	14-SEP-2000;	2000US-0232399P.
				PR	14-SEP-2000;	2000US-0232400P.
				PR	14-SEP-2000;	2000US-0232401P.
				PR	14-SEP-2000;	2000US-0233063P.
				PR	14-SEP-2000;	2000US-0233064P.
				PR	14-SEP-2000;	2000US-0233065P.
				PR	21-SEP-2000;	2000US-0234223P.
				PR	21-SEP-2000;	2000US-0234274P.
				PR	25-SEP-2000;	2000US-0234997P.
				PR	25-SEP-2000;	2000US-0234998P.
				PR	25-SEP-2000;	2000US-0234999P.
				PR	26-SEP-2000;	2000US-0235484P.
				PR	27-SEP-2000;	2000US-0235834P.
				PR	27-SEP-2000;	2000US-0235836P.
				PR	29-SEP-2000;	2000US-0236272P.
				PR	29-SEP-2000;	2000US-0236368P.
				PR	29-SEP-2000;	2000US-0236369P.
				PR	29-SEP-2000;	2000US-0236370P.
				PR	29-SEP-2000;	2000US-0236802P.
				PR	02-OCT-2000;	2000US-0237037P.
				PR	02-OCT-2000;	2000US-0237038P.
				PR	02-OCT-2000;	2000US-0237039P.
				PR	02-OCT-2000;	2000US-0237040P.
				PR	13-OCT-2000;	2000US-0239935P.
				PR	13-OCT-2000;	2000US-0239937P.
				PR	20-OCT-2000;	2000US-0240960P.
				PR	20-OCT-2000;	2000US-0241221P.
				PR	20-OCT-2000;	2000US-0241785P.
				PR	20-OCT-2000;	2000US-0241786P.
				PR	20-OCT-2000;	2000US-0241787P.
				PR	20-OCT-2000;	2000US-0241808P.

RESULT 5
AAL05382
ID AAL05382 standard; DNA; 6107 BP.
XX AC AAL05382;
XX DT 21-NOV-2001 (first entry)
XX DE Human reproductive system related antigen DNA SEQ ID NO: 8070.
XX KW Human; reproductive system related antigen; reproductive system disorder;
XX OS cancer; gene therapy; ds.
XX OS Homo sapiens.
XX PN WO200155320-A2.
XX PD 02-AUG-2001.
XX PF 17-JAN-2001; 2001WO-US001339.
XX PF 31-JAN-2000; 2000US-0179065P.
XX PR 04-FEB-2000; 2000US-0180628P.
XX PR 24-FEB-2000; 2000US-0184664P.
XX PR 02-MAR-2000; 2000US-0186350P.
XX PR 16-MAR-2000; 2000US-0189874P.
XX PR 17-MAR-2000; 2000US-0190076P.
XX PR 18-APR-2000; 2000US-0198123P.
XX PR 19-MAY-2000; 2000US-0205515P.
XX PR 07-JUN-2000; 2000US-0209467P.
XX PR 28-JUN-2000; 2000US-0214886P.
XX PR 30-JUN-2000; 2000US-0215135P.
XX PR 07-JUL-2000; 2000US-0216647P.

QY	1081	AGCGACTGCTAGCTCTTTTGACACGACCATTTGCAAGCTTTTTCAGAAAAATGCAATTTA	1140
Db	4244	AGCGACTGCTAGCTCTTTTGACACGACCATTTGCAAGCTTTTTCAGAAAAATGCAATTTA	4303
QY	1141	GGCATCAATGTAAGTATTTTCATCTGTTGAATGGCAATCAATTTCTGCCAGTCT	1200
Db	4304	GGCATCAATGTAAGTATTTTCATCTGTTGAATGGCAATCAATTTCTGCCAGTCT	4363
QY	1201	TTAAACCTTCAGTTTCACAGAAATAGGACCATCTGCTGCCAACCTGAAAACTCTTT	1260
Db	4364	TTAAACCTTCAGTTTCACAGAAATAGGACCATCTGCTGCCAACCTGAAAACTCTTT	4423
QY	1261	CGGTAGGTGAAGC	1274
Db	4424	CGGTAGGTGAAGC	4437
RESULT 6			
ABL98246			
ID	ABL98246 standard; DNA; 6107 BP.		
XX	AC	ABL98246;	
XX	DT	21-JUN-2002 (first entry)	
XX	XX	Human testicular antigen encoding DNA fragment SEQ ID NO: 2898.	
XX	DE	Human; testicular antigen; testes; cancer; metastasis; immune disorder;	
XX	XX	reproductive system disorder; urinary system disorder; gene therapy;	
KW	KW	cardiovascular disorder; respiratory disorder; neurological disorder;	
KW	KW	gastrointestinal disease; infection; cytostatic; gene; ds.	
XX	XX	Homo sapiens.	
XX	OS	WO200155317-A2.	
XX	PN	02-AUG-2001.	
XX	PD	17-JAN-2001; 2001WO-US001329.	
XX	PF	31-JAN-2000; 2000US-0179065P.	
XX	XX	04-FEB-2000; 2000US-0180628P.	
PR	PR	24-FEB-2000; 2000US-0184664P.	
PR	PR	02-MAR-2000; 2000US-0186350P.	
PR	PR	16-MAR-2000; 2000US-0189874P.	
PR	PR	17-MAR-2000; 2000US-0190076P.	
PR	PR	18-APR-2000; 2000US-01981123P.	
PR	PR	19-MAY-2000; 2000US-0205515P.	
PR	PR	07-JUN-2000; 2000US-0209467P.	
PR	PR	28-JUN-2000; 2000US-0214886P.	
PR	PR	30-JUN-2000; 2000US-0215135P.	
PR	PR	07-JUL-2000; 2000US-0216647P.	
PR	PR	07-JUL-2000; 2000US-0216880P.	
PR	PR	11-JUL-2000; 2000US-0217487P.	
PR	PR	11-JUL-2000; 2000US-0217496P.	
PR	PR	14-JUL-2000; 2000US-0218290P.	
PR	PR	26-JUL-2000; 2000US-0220964P.	
PR	PR	14-AUG-2000; 2000US-0224518P.	
PR	PR	14-AUG-2000; 2000US-0224519P.	
PR	PR	14-AUG-2000; 2000US-0225213P.	
PR	PR	14-AUG-2000; 2000US-0225214P.	
PR	PR	14-AUG-2000; 2000US-0225266P.	
PR	PR	14-AUG-2000; 2000US-0225267P.	
PR	PR	14-AUG-2000; 2000US-0225268P.	
PR	PR	14-AUG-2000; 2000US-0225270P.	
PR	PR	14-AUG-2000; 2000US-0225447P.	
PR	PR	14-AUG-2000; 2000US-0225575P.	
PR	PR	14-AUG-2000; 2000US-0225756P.	
PR	PR	14-AUG-2000; 2000US-0225759P.	
PR	PR	18-AUG-2000; 2000US-0226279P.	
PR	PR	22-AUG-2000; 2000US-0226681P.	
PR	PR	22-AUG-2000; 2000US-0226868P.	
PR	PR	22-AUG-2000; 2000US-0227182P.	
PR	PR	23-AUG-2000; 2000US-0227709P.	
PR	PR	30-AUG-2000; 2000US-0228924P.	
PR	PR	01-SEP-2000; 2000US-0229287P.	
PR	PR	01-SEP-2000; 2000US-0229343P.	
PR	PR	01-SEP-2000; 2000US-0229344P.	
PR	PR	01-SEP-2000; 2000US-0229345P.	
PR	PR	05-SEP-2000; 2000US-0229509P.	
PR	PR	05-SEP-2000; 2000US-0229513P.	
PR	PR	06-SEP-2000; 2000US-0230437P.	
PR	PR	06-SEP-2000; 2000US-0230438P.	
PR	PR	08-SEP-2000; 2000US-0231242P.	
PR	PR	08-SEP-2000; 2000US-0231243P.	
PR	PR	08-SEP-2000; 2000US-0231413P.	
PR	PR	08-SEP-2000; 2000US-0231414P.	
PR	PR	08-SEP-2000; 2000US-0232080P.	
PR	PR	08-SEP-2000; 2000US-0232081P.	
PR	PR	12-SEP-2000; 2000US-0231968P.	
PR	PR	14-SEP-2000; 2000US-0232397P.	
PR	PR	14-SEP-2000; 2000US-0232398P.	
PR	PR	14-SEP-2000; 2000US-0232399P.	
PR	PR	14-SEP-2000; 2000US-0232400P.	
PR	PR	14-SEP-2000; 2000US-0232401P.	
PR	PR	14-SEP-2000; 2000US-0233063P.	
PR	PR	14-SEP-2000; 2000US-0233064P.	
PR	PR	14-SEP-2000; 2000US-0233065P.	
PR</			

PR 17-NOV-2000; 2000US-0249208P.
PR 17-NOV-2000; 2000US-0249209P.
PR 17-NOV-2000; 2000US-0249210P.
PR 17-NOV-2000; 2000US-0249211P.
PR 17-NOV-2000; 2000US-0249212P.
PR 17-NOV-2000; 2000US-0249213P.
PR 17-NOV-2000; 2000US-0249214P.
PR 17-NOV-2000; 2000US-0249215P.
PR 17-NOV-2000; 2000US-0249216P.
PR 17-NOV-2000; 2000US-0249217P.
PR 17-NOV-2000; 2000US-0249218P.
PR 17-NOV-2000; 2000US-0249244P.
PR 17-NOV-2000; 2000US-0249245P.
PR 17-NOV-2000; 2000US-0249264P.
PR 17-NOV-2000; 2000US-0249265P.
PR 17-NOV-2000; 2000US-0249297P.
PR 17-NOV-2000; 2000US-0249299P.
PR 17-NOV-2000; 2000US-0249300P.
PR 01-DEC-2000; 2000US-0250160P.
PR 01-DEC-2000; 2000US-0250391P.
PR 05-DEC-2000; 2000US-0251830P.
PR 05-DEC-2000; 2000US-0251988P.
PR 06-DEC-2000; 2000US-0256719P.
PR 06-DEC-2000; 2000US-0251479P.
PR 08-DEC-2000; 2000US-0251856P.
PR 08-DEC-2000; 2000US-0251868P.
PR 08-DEC-2000; 2000US-0251869P.
PR 08-DEC-2000; 2000US-0251989P.
PR 08-DEC-2000; 2000US-0251990P.
PR 11-DEC-2000; 2000US-0254097P.
PR 05-JAN-2001; 2001US-0259678P.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
XX Rosen CA, Barash SC, Ruben SM;
XX
XX WPI; 2001-483232/52.
XX
XX Nucleic acids encoding 973 human testicular antigen polypeptides, useful
XX for preventing, diagnosing and/or treating testicular cancer.
XX
XX Disclosure; SEQ ID NO 2898; 766pp; English.
XX
XX The present invention provides the protein and coding sequences of 973
XX human testicular antigens, and fragments of their genomic sequences. The
XX sequences can be used in the treatment of cardiovascular, urinary system,
XX reproductive system, immune, respiratory, neurological and
XX gastrointestinal disorders, infections, and particularly cancer,
XX especially testicular cancers. The present sequence is a DNA encoding a
XX protein fragment of the invention
XX
XX SQ Sequence 6107 BP; 1636 A; 1200 C; 1285 G; 1986 T; 0 U; 0 Other;
XX
XX Query Match 100.0%; Score 1274; DB 4; Length 6107;
XX Best Local Similarity 100.0%; Pred. No. 0;
XX Matches 1274; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 1 TTTCTTTAGTTGTTATGTTCCATTTTCTATTTTATTTAGCATTTATTTCTATGTTAGTCTAT 60
XX
XX 3164 TTTCTTTAGTTGTTATGTTCCATTTTCTATTTTATTTAGCATTTATTTCTATGTTAGTCTAT 3223
XX
XX 61 CCAAGACGATTAAAGGAGTCCACATGTTTCCGGAAACATTTTGAAGAGAGAGCTTATC 120
XX
XX 3224 CCAAGACGATTAAAGGAGTCCACATGTTTCCGGAAACATTTTGAAGAGAGAGCTTATC 3283
XX
XX 121 CAGTGACAGATCTTAATAAGTGACATTCAGTGTAAATTTATTTTATATATCTTTT 180
XX
XX 3284 CAGTGACAGATCTTAATAAGTGACATTCAGTGTAAATTTATTTTATATCTTTT 3343
XX
XX 181 TTAATCCTATTTTCTCTCTTTTCTCAGTAAATTTTGTATGAACCTTAAAGGACT 240
XX
XX 3344 TTAATCCTATTTTCTCTCTTTTCTCAGTAAATTTTGTATGAACCTTAAAGGACT 3403
XX

QY 241 TATGGCATGTAACATTTATTAAGTAAGTCATGGTTATTAATTTATTTTCTCTGCCT 300
DB 3404 TATGGCATGTAACATTTATTAAGTAAGTCATGGTTATTAATTTATTTTCTCTGCCT 3463
QY 301 CCTTATGTAATTTATTTTCAAAATGAGCGTCAGATGCTACAGCATTTACCTACCGGTACC 360
DB 3464 CCTTATGTAATTTATTTTCAAAATGAGCGTCAGATGCTACAGCATTTACCTACCGGTACC 3523
QY 361 TCGAAGTGTCCACCATCCAGAGGGTGCCTGCGCTGACTGGCACAACACTGCATCCAACAAT 420
DB 3524 TCGAAGTGTCCACCATCCAGAGGGTGCCTGCGCTGACTGGCACAACACTGCATCCAACAAT 3583
QY 421 GACTTGGCGAGTCTTTTTCAGATGTCAGTCTGCTTTGACTATGTTGTTACCGCCATCTTT 480
DB 3584 GACTTGGCGAGTCTTTTTCAGATGTCAGTCTGCTTTGACTATGTTGTTACCGCCATCTTT 3643
QY 481 CAATGTCAGAGTGGCCATCTTTGTTGTAGCAACTGCGCCAAAGCTCACATGTTGTCCA 540
DB 3644 CAATGTCAGAGTGGCCATCTTTGTTGTAGCAACTGCGCCAAAGCTCACATGTTGTCCA 3703
QY 541 ACTTGGCGGGGCCCTTTGGGATCCATTTCGCAACTTGGCTATGGAGAAAGTGGCTAATTC 600
DB 3704 ACTTGGCGGGGCCCTTTGGGATCCATTTCGCAACTTGGCTATGGAGAAAGTGGCTAATTC 3763
QY 601 GTACTTTTCCCTGTAAATATGCGTCTTCTGGATGTAATACTCTGCCACACACAGAA 660
DB 3764 GTACTTTTCCCTGTAAATATGCGTCTTCTGGATGTAATACTCTGCCACACACAGAA 3823
QY 661 AAAGCAGACCATGAAGAGCTCTGTGAGTTTTCAGCTTATTCCTGTCGCTCGCTGTTGCT 720
DB 3824 AAAGCAGACCATGAAGAGCTCTGTGAGTTTTCAGCTTATTCCTGTCGCTCGCTGTTGCT 3883
QY 721 TCCTGTAATGCAAGGCTCTCTGATGCTGTAATGCCCATCTGATGTCATCAGCATAAG 780
DB 3884 TCCTGTAATGCAAGGCTCTCTGATGCTGTAATGCCCATCTGATGTCATCAGCATAAG 3943
QY 781 TCATTAACACCTCAGGAGAGGATATAGTTTTTCTTGTCTACAGACATTAATCTTCT 840
DB 3944 TCATTAACACCTCAGGAGAGGATATAGTTTTTCTTGTCTACAGACATTAATCTTCT 4003
QY 841 GGTGCTGTTGACTGGGTGATGATGAGTCTGTTTGGCTTTTTCACATTCATGTTAGTCTTA 900
DB 4004 GGTGCTGTTGACTGGGTGATGATGAGTCTGTTTGGCTTTTTCACATTCATGTTAGTCTTA 4063
QY 901 GAGAAACAGGAAAAATACGATGCTCACACGAGTCTTTCGCAATCGTACAGCTGATAGGA 960
DB 4064 GAGAAACAGGAAAAATACGATGCTCACACGAGTCTTTCGCAATCGTACAGCTGATAGGA 4123
QY 961 ACAGGCAAGCAAGCTGAAAAATTTTGGCTTACCGACTGAGCTAAATGCTATAGGCGACGA 1020
DB 4124 ACAGGCAAGCAAGCTGAAAAATTTTGGCTTACCGACTGAGCTAAATGCTATAGGCGACGA 4183
QY 1021 TTGACTTTGGGAAGGACTCTCGATCTATTTCATGAAGGAATTCGCAAGCAATTTATGAAT 1080
DB 4184 TTGACTTTGGGAAGGACTCTCGATCTATTTCATGAAGGAATTCGCAAGCAATTTATGAAT 4243
QY 1081 AGCGACTGTCTAGTCTTTTCACACACGATTTGACAGCTTTTTCGAGAAAATGCAATTTA 1140
DB 4244 AGCGACTGTCTAGTCTTTTCACACACGATTTGACAGCTTTTTCGAGAAAATGCAATTTA 4303
QY 1141 GGCATCAATGTAATTTTCCATGTTGAAATGGAATGGAATGGAATGGAATGGAATGGAAT 1200
DB 4304 GGCATCAATGTAATTTTCCATGTTGAAATGGAATGGAATGGAATGGAATGGAATGGAAT 4363
QY 1201 TTAATCCTATTTTCTCTCTTTTCTCAGTAAATTTTGTATGAACCTTAAAGGACT 1260
DB 4364 TTAATCCTATTTTCTCTCTTTTCTCAGTAAATTTTGTATGAACCTTAAAGGACT 4423
QY 1261 CGTAGTGTGGAAGC 1274
DB 4424 CGTAGTGTGGAAGC 4437

XX ADS34362;
AC
XX
DT 02-DEC-2004 (first entry)
XX
XX POSH protein associated DNA #116.
DE
DE ds; gene; cytostatic; neurotropic; neuroprotective; antiparkinsonian;
KW anticonvulsant; antiviral; neuroleptic; central nervous system;
KW POSH polypeptide; POSH-associated protein; POSH-AP; HERPUDI1;
KW ubiquitin ligase; anti-viral agent; anti-apoptotic agent;
KW anti-cancer agent; secretory pathway trafficking inhibitor;
KW neurological disorder progression disorder; Alzheimer's disease;
KW Parkinson's disease; Huntington's disease; schizophrenia;
KW Niemann-Pick's disease.
XX
XX Homo sapiens.
XX
XX WO20040781130-A2
XX
XX 16-SEP-2004.
XX
XX 02-MAR-2004; 2004WO-US006308.
XX
XX 03-MAR-2003; 2003US-0451437P.
XX
XX 05-MAR-2003; 2003US-0452284P.
XX
XX 19-MAR-2003; 2003US-0455760P.
XX
XX 20-MAR-2003; 2003US-0456640P.
XX
XX 03-APR-2003; 2003US-0460526P.
XX
XX 04-APR-2003; 2003US-0460792P.
XX
XX 21-APR-2003; 2003US-0464285P.
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XX 09-MAY-2003; 2003US-0469462P.
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XX 15-MAY-2003; 2003US-0471378P.
XX
XX 20-MAY-2003; 2003US-0472327P.
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XX 30-MAY-2003; 2003US-0474706P.
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XX 03-JUN-2003; 2003US-0475825P.
XX
XX 17-JUN-2003; 2003US-0477317P.
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XX 19-JUN-2003; 2003US-0480615P.
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XX 19-JUN-2003; 2003US-0480376P.
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XX 08-AUG-2003; 2003US-0493850P.
XX
XX 28-AUG-2003; 2003US-0498633P.
XX
XX 16-SEP-2003; 2003US-0503931P.
XX
XX 10-NOV-2003; 2003WO-US035711.
XX
XX 05-FEB-2004; 2004WO-US003600.
XX
XX 02-MAR-2004; 2004US-0549896P.
XX
XX (PROT-) PROTEOLOGICS INC.
XX
XX Taglicht DN, Alroy I, Reiss Y, Yaar L, Ben-Avraham D, Tuvia S;
PI Greener T;
XX
XX WPI; 2004-662346/64.
XX
XX Isolated, purified or recombinant complex, useful for identifying an
PT antiviral, anti-apoptotic or anti-cancer, comprising POSH polypeptide and
PT POSH-associated protein (POSH-AP).
XX
XX Disclosure; SEQ ID NO 126; 374pp; English.
XX
XX The invention relates to an isolated, purified or recombinant complex (I)
CC comprising a POSH polypeptide and a POSH-associated protein (POSH-AP) (a)
CC or HERPUDI1 and a ubiquitin ligase (b). Methods using (I), (a) or (b) are
CC useful for identifying an agent that modulates an activity of a POSH
CC polypeptide or POSH-AP, for identifying an antiviral agent, an anti-
CC apoptotic agent, an anti-cancer agent, an agent that inhibits trafficking
CC of a protein through the secretory pathway, an agent that inhibits the
CC progression of a neurological disorder, an agent that modulates a POSH
CC function, an agent that modulates a HERPUDI1 function. The methods can be
CC used for treating a viral infection, for inhibiting an activity of a POSH
CC AP in a cell for treating a POSH-associated disease in a subject. The
CC POSH-associated disease is viral infection, POSH-associated cancer or
CC POSH-associated neurological disorder. The methods are useful for
CC treating or preventing POSH-associated neurological disorder in a subject

CC e.g. Alzheimer's disease, Parkinson's disease, Huntington's disease,
CC schizophrenia, Niemann-Pick's disease. This sequence corresponds to a
XX nucleic acid of the invention.
XX
XX Sequence 2829 BP; 756 A; 566 C; 553 G; 954 T; 0 U; 0 Other;
Query Match 96.0%; Score 1223; DB 13; Length 2829;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1273; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 TTTCTTTAGTGTGTTATGTCCTCAATTTCTATTATTTAGCATTTATTCTATGAGTCTAT 60
DB 1134 TTTCTTTAGTGTGTTATGTCCTCAATTTCTATTATTTAGCATTTATTCTATGAGTCTAT 1193
QY 61 CCAAGACGATTAAGGAGTTCACATGTTTTCGGAAACATTTTGAAGAGAGAGCTTATC 120
DB 1194 CCAAGACGATTAAGGAGTTCACATGTTTTCGGAAACATTTTGAAGAGAGAGCTTATC 1253
QY 121 CAGTGTACAGATCCTAATAAGTGCACATTCAGTGAATTTATTTTATATATCTTTT 180
DB 1254 CAGTGTACAGATCCTAATAAGTGCACATTCAGTGAATTTATTTTATATCTTTT 1313
QY 181 TTAATCTTATTTTCT 240
DB 1314 TTAATCTTATTTTCT 1373
QY 241 TATGCGATGTAACATTTATTAAGTAAGTCAATGTTTATTAATTTTCTCTCTCTCT 300
DB 1374 TATGCGATGTAACATTTATTAAGTAAGTCAATGTTTATTAATTTTCTCTCTCTCT 1433
QY 301 CCTTATGTTATTTATTTTTCAGAAATGAGCCGTGACATGCTGACAGCATTTACTACCGGTACC 360
DB 1434 CCTTATGTTATTTATTTTTCAGAAATGAGCCGTGACATGCTGACAGCATTTACTACCGGTACC 1493
QY 361 TCGAAGTGTCCACCATCCAGAGAGGTGCTGCCCTGACTGGCAGCACTGCATCCACAAAT 420
DB 1494 TCGAAGTGTCCACCATCCAGAGAGGTGCTGCCCTGACTGGCAGCACTGCATCCACAAAT 1553
QY 421 GACTTGGCGAGTCTTTTGGAGTGTCCAGTCTGCTTTGACTATGTTTACCGCCATCTT 480
DB 1554 GACTTGGCGAGTCTTTTGGAGTGTCCAGTCTGCTTTGACTATGTTTACCGCCATCTT 1613
QY 481 CAATGTACAGTGGCCATCTTGTGTTAGCAACATGTCGCCCAAGCTCACTGTTGTCCA 540
DB 1614 CAATGTACAGTGGCCATCTTGTGTTAGCAACATGTCGCCCAAGCTCACTGTTGTCCA 1673
QY 541 ACTTGGCGGGGCGCTTGGGATCCATTCGCACTTGGCTATCGAGAAAGTGGCTAATTC 600
DB 1674 ACTTGGCGGGGCGCTTGGGATCCATTCGCACTTGGCTATCGAGAAAGTGGCTAATTC 1733
QY 601 GTACTTTTCCCTGTAAATATATGCGTCTTCTGGATGTGAATAAATCTGCGCACACAGAA 660
DB 1734 GTACTTTTCCCTGTAAATATATGCGTCTTCTGGATGTGAATAAATCTGCGCACACAGAA 1793
QY 661 AAAGCAGACCATGAAGAGCTCTGTGAGTTTAGCCCTTATCTCTGCCCTGGCTGGTCT 720
DB 1794 AAAGCAGACCATGAAGAGCTCTGTGAGTTTAGCCCTTATCTCTGCCCTGGCTGGTCT 1853
QY 721 TCCTGTAATGCGAGGCTCTCTGATGCTGTAAATGCCCCCATCTGATGATGAGTAAAG 780
DB 1854 TCCTGTAATGCGAGGCTCTCTGATGCTGTAAATGCCCCCATCTGATGATGAGTAAAG 1913
QY 781 TCCTGTAATGCGAGGCTCTCTGATGCTGTAAATGCCCCCATCTGATGATGAGTAAAG 840
DB 1914 TCCTGTAATGCGAGGCTCTCTGATGCTGTAAATGCCCCCATCTGATGATGAGTAAAG 1973
QY 841 GGTGCTGTGAGTGGGTGATGATGAGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 900
DB 1974 GGTGCTGTGAGTGGGTGATGATGAGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 2033
QY 901 GAGAAACAGGAAATATGATGCTGACAGAGTCTTCCGCAATGCTACAGCTGATAGCA 960
DB 2034 GAGAAACAGGAAATATGATGCTGACAGAGTCTTCCGCAATGCTACAGCTGATAGCA 2093

QY 438 TGAGTGTCAAGTCTGCTTTGACTATGTTTACCGCCATTTCTTCAATGTCAGAGTGGCCA 497
DB |||||
DB 576 TGAGTGTCCAGTCTGCTTTGACTATGTTTACCGCCATTTCTTCAATGTCAGAGTGGCCA 635
QY 498 TCTTGTGTTGAGCAACTGTGCGCCAAAGCTTCACATGTTGTCCAACTTGGCGGGCCCTTT 557
DB |||||
DB 636 TCTTGTGTTGAGCAACTGTGCGCCAAAGCTTCACATGTTGTCCAACTTGGCGGGCCCTTT 695
QY 558 GGGATCCATTGCGCACTGTGCTTATGAGAAAGTGGCTAAATTCAGTACTTTTCCCTGTAA 617
DB |||||
DB 696 GGGATCCATTGCGCACTGTGCTTATGAGAAAGTGGCTAAATTCAGTACTTTTCCCTGTAA 755
QY 618 ATATGCGTCTTCTGGATGGAATTAATCTGCGCACACACAGAAAGAGCAGCATGAAGA 677
DB |||||
DB 756 ATATGCGTCTTCTGGATGGAATTAATCTGCGCACACACAGAAAGAGCAGCATGAAGA 815
QY 678 GCTCTGTGAGTTTGGAGCTTATTCATGTCGTCGTCCTGCTTCTGTAATGGAAGG 737
DB |||||
DB 816 GCTCTGTGAGTTTGGAGCTTATTCATGTCGTCGTCCTGCTTCTGTAATGGAAGG 875
QY 738 CTCTCTGGATGCTGTAATGCGCCCATCTGATGCAATCAGCATAGTCCATTACAACTTACA 797
DB |||||
DB 876 CTCTCTGGATGCTGTAATGCGCCCATCTGATGCAATCAGCATAGTCCATTACAACTTACA 935
QY 798 GGGAGAGGATATAGTTTCTTCTGCTACAGCATTAATCTTCTGCTGCTGCTGCTGCTGCT 857
DB |||||
DB 936 GGGAGAGGATATAGTTTCTTCTGCTACAGCATTAATCTTCTGCTGCTGCTGCTGCTGCT 995
QY 858 GATGATGCACTGCTGTTTGGCTTTCACATGCTAGTCTTACAGAAACGAGAAATA 917
DB |||||
DB 996 GATGATGCACTGCTGTTTGGCTTTCACATGCTAGTCTTACAGAAACGAGAAATA 1055
QY 918 CGATGTCACACGAGCTTCTTCCCAATCGTACAGCTGATAGGAACACGCAAGCAAGCTCA 977
DB |||||
DB 1056 CGATGTCACACGAGCTTCTTCCCAATCGTACAGCTGATAGGAACACGCAAGCAAGCTCA 1115
QY 978 AAATTTTGTCTTACCGACTTGAAGTAAATGCTATAGGCGACGATTCATTTGGGAAGCGAC 1037
DB |||||
DB 1116 AAATTTTGTCTTACCGACTTGAAGTAAATGCTATAGGCGACGATTCATTTGGGAAGCGAC 1175
QY 1038 TCTCGATCTTATCATGAGGAATTCACAGCCATTAATGAGGAGCTGCTAGTCTT 1097
DB |||||
DB 1176 TCTCGATCTTATCATGAGGAATTCACAGCCATTAATGAGGAGCTGCTAGTCTT 1235
QY 1098 TGACACGAGCATTCACAGCTTTTTCAGAAATGCAATTTAGGATCAATGTAATAT 1157
DB |||||
DB 1236 TGACACGAGCATTCACAGCTTTTTCAGAAATGCAATTTAGGATCAATGTAATAT 1295
QY 1158 TTCCATGTTGAAATGGCAATCAAAATTTCTGCGCCAGTGTAAATTTTCAAGTTTCA 1217
DB |||||
DB 1296 TTCCATGTTGAAATGGCAATCAAAATTTCTGCGCCAGTGTAAATTTTCAAGTTTCA 1355
QY 1218 CAGAAATAGGACCATCTGCTGCGCACTTAAATCTTTCGTAAGTGGAGC 1274
DB |||||
DB 1356 CAGAAATAGGACCATCTGCTGCGCACTTAAATCTTTCGTAAGTGGAGC 1412

RESULT 14

ADS34363
ID ADS34363 standard; DNA; 1886 BP.

XX AC

ADS34363;

XX DT 02-DEC-2004 (first entry)

XX DE POSH protein associated DNA #117.

XX ds; gene; cytostatic; nontropic; neuroprotective; antiparkinsonian;
KW anticonvulsant; antiviral; neuroleptic; central nervous system;
KW POSH polypeptide; POSH-associated protein; POSH-AP; HERPUD1;
KW Ubiquitin ligase; antiviral agent; anti-apoptotic agent;
KW anti-cancer agent; secretory pathway trafficking inhibitor;

neurological disorder progression disorder; Alzheimer's disease;
Parkinson's disease; Huntington's disease; schizophrenia;
Niemann-Pick's disease.

Homo sapiens.

WO2004078130-A2.

16-SEP-2004.

02-MAR-2004; 2004WO-US006308.

03-MAR-2003; 2003US-0451437P.

05-MAR-2003; 2003US-0452284P.

19-MAR-2003; 2003US-0455760P.

20-MAR-2003; 2003US-0456640P.

03-APR-2003; 2003US-0460526P.

04-APR-2003; 2003US-0460792P.

21-APR-2003; 2003US-046285P.

09-MAY-2003; 2003US-0469462P.

15-MAY-2003; 2003US-0471378P.

20-MAY-2003; 2003US-0472327P.

30-MAY-2003; 2003US-0474706P.

03-JUN-2003; 2003US-0475825P.

17-JUN-2003; 2003US-0475917P.

19-JUN-2003; 2003US-0480215P.

19-JUN-2003; 2003US-0480376P.

08-AUG-2003; 2003US-0493860P.

28-AUG-2003; 2003US-0498634P.

16-SEP-2003; 2003US-0503933P.

10-NOV-2003; 2003WO-US035714.

05-FEB-2004; 2004WO-US003600.

02-MAR-2004; 2004US-0549896P.

(PROT-) PROTEOLOGICS INC.

Taglicht DN, Alroy I, Reiss Y, Yaar L, Ben-Avraham D, Tuvia S;

Greener T;

WPI; 2004-662346/64.

Isolated, purified or recombinant complex, useful for identifying an
antiviral, anti-apoptotic or anti-cancer, comprising POSH polypeptide and
POSH-associated protein (POSH-AP).

Disclosure; SEQ ID NO 127; 374pp; English.

The invention relates to an isolated, purified or recombinant complex (I)
comprising a POSH polypeptide and a POSH-associated protein (POSH-AP) (a)
or HERPUD1 and a ubiquitin ligase (b). Methods using (I), (a) or (b) are
useful for identifying an agent that modulates an activity of a POSH
polypeptide or POSH-AP, for identifying an antiviral agent, an anti-
apoptotic agent, an anti-cancer agent, an agent that inhibits trafficking
of a protein through the secretory pathway, an agent that inhibits the
progression of a neurological disorder, an agent that modulates a POSH
function, an agent that modulates a HERPUD1 function. The methods can be
used for treating a viral infection, for inhibiting an activity of a POSH
-AP in a cell, for treating a POSH-associated disease in a subject. The
POSH-associated disease is viral infection, POSH-associated cancer or
POSH-associated neurological disorder. The methods are useful for
treating or preventing POSH-associated neurological disorder in a subject
e.g. Alzheimer's disease, Parkinson's disease, Huntington's disease,
schizophrenia, Niemann-Pick's disease. This sequence corresponds to a
nucleic acid of the invention.

Sequence 1886 BP; 527 A; 366 C; 373 G; 620 T; 0 U; 0 Other;

QY

322 ATGAGCCGTACAGCTGTACAGCATTTACCTACGGTACCTCGAAGTGTCCACATCCAG 381

QY

|||||

Query Match

74.3%; Score 947; DB 13; Length 1886;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 947; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 3191 GACTGGCAGTCTTTTGGAGTCCAGTCTGTTGACTATGTGTACGCCCATCTTT 3132
QY 481 CAATGTGAGAGTGGCCATCTTGTGTAGCAACTGTCGCCAAAGCTCAGATGTTGTCCA 540
Db 3131 CAATGTGAGAGTGGCCATCTTGTGTAGCAACTGTCGCCAAAGCTCAGATGTTGTCCA 3072
QY 541 ACTTGGCGGGGCGCTTTGGATCCATCTGCAACTGTCGCTATGAGAAAGTGGCTAATCCA 600
Db 3071 ACTTGGCGGGGCGCTTTGGATCCATCTGCAACTGTCGCTATGAGAAAGTGGCTAATCCA 3012
QY 601 GTACTTTTCCCTGTAAATATGCTCTCTGGATGTAATTAATCTGCGCACACAGAA 660
Db 3011 GTACTTTTCCCTGTAAATATGCTCTCTGGATGTAATTAATCTGCGCACACAGAA 2952
QY 661 AAA-GCAGACCAATGAAGA-GCTCTGTAGTGTAGGCTTTATTTCTGCTCGTGGCCCTGGTG 718
Db 2951 AAANGCAGACCAATGAANGCTCTGTAGTGTAGGCTTTATTTCTGCTCGTGGCCCTGGTG 2892
QY 719 CTTCTGTAAATGGCAAGGCTCTCTGGATGCTGTAAATGCGCCCATCTGATGCATCAGCATA 778
Db 2891 CTTCTGTAAATGGCAAGGCTCTCTGGATGCTGTAAATGCGCCCATCTGATGCATCAGCATA 2832
QY 779 AGTCCATTACAACCCCTACAGGAGAGGATATAGTCTTCTGTACAGACATTAATCTTC 838
Db 2831 AGTCCATTACAACCCCTACAGGAGAGGATATAGTCTTCTGTACAGACATTAATCTTC 2772
QY 839 CTGGTCTCTGTACTGGGTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 898
Db 2771 CTGGTCTCTGTACTGGGTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2712
QY 899 TAGAGAAAACAGAAAATACGATGTCACAGCAGTCTTTCGCAATCGTACAGCTGATAG 958
Db 2711 TAGAGAAAACAGAAAATACGATGTCACAGCAGTCTTTCGCAATCGTACAGCTGATAG 2652
QY 959 GAACAGCAAGCAAGCTGAAATTTTCTTACCGACTTCAGCTTAATGCTATAGCGGAC 1018
Db 2651 GAACAGCAAGCAAGCTGAAATTTTCTTACCGACTTCAGCTTAATGCTATAGCGGAC 2592
QY 1019 GATTGACTTGGGAAGCGACTCTCTGATCTATTATGATGAAGAAATGCAACAGCCATTATGA 1078
Db 2591 GATTGACTTGGGAAGCGACTCTCTGATCTATTATGATGAAGAAATGCAACAGCCATTATGA 2532
QY 1079 ATAGCGACTGTCTAGTCTTTCACAGCAGATTCACAGCTTTTTCGCAAAATGCGCAATT 1138
Db 2531 ATAGCGACTGTCTAGTCTTTCACAGCAGATTCACAGCTTTTTCGCAAAATGCGCAATT 2472
QY 1139 TAGGCATCAATGTAATTTTCCATGCTGTGAAATGCAATCAATCAATTTCTGGCCAGT 1198
Db 2471 TAGGCATCAATGTAATTTTCCATGCTGTGAAATGCAATCAATCAATTTCTGGCCAGT 2412
QY 1199 GTTTAAACTTCAGTTTTCACAGAAAATAGGCAACCCATCTGTCGCAACCTAAACTCT 1258
Db 2411 GTTTAAACTTCAGTTTTCACAGAAAATAGGCAACCCATCTGTCGCAACCTAAACTCT 2352
QY 1259 TTTCGGTAGTGAAGC 1274
Db 2351 TTTCGGTAGTGAAGC 2336

RESULT 16

AD34364

ID AD34364 standard; DNA; 2034 BP.

AC AD34364;

XX 02-DEC-2004 (first entry)

DT POSH protein associated DNA #118.

DE ds; gene; cytostatic; neurotropic; neuroprotective; antiparkinsonian;

KW anticonvulsant; antiviral; neuroleptic; central nervous system;

KW POSH polypeptide; POSH-associated protein; POSH-AP; HERPUD1;

XX

KW Ubiquitin ligase; antiviral agent; anti-apoptotic agent;
KW anti-cancer agent; secretory pathway trafficking inhibitor;
KW neurological disorder progression disorder; Alzheimer's disease;
KW Parkinson's disease; Huntington's disease; schizophrenia;
KW Niemann-Pick's disease.
XX Homo sapiens.
OS WO2004078130-A2.
XX 16-SEP-2004.
XX 02-MAR-2004; 2004WO-US006308.
XX 03-MAR-2003; 2003US-0451437P.
XX 05-MAR-2003; 2003US-0452284P.
XX 19-MAR-2003; 2003US-0455760P.
XX 20-MAR-2003; 2003US-0456640P.
XX 03-APR-2003; 2003US-0460526P.
XX 04-APR-2003; 2003US-0460792P.
XX 21-APR-2003; 2003US-0464285P.
XX 09-MAY-2003; 2003US-0469462P.
XX 15-MAY-2003; 2003US-0471378P.
XX 20-MAY-2003; 2003US-0472327P.
XX 30-MAY-2003; 2003US-0474706P.
XX 03-JUN-2003; 2003US-0475825P.
XX 17-JUN-2003; 2003US-0479317P.
XX 19-JUN-2003; 2003US-0480215P.
XX 19-JUN-2003; 2003US-0480376P.
XX 08-AUG-2003; 2003US-0493860P.
XX 28-AUG-2003; 2003US-0498634P.
XX 16-SEP-2003; 2003US-0503931P.
XX 10-NOV-2003; 2003WO-US035712.
XX 05-FEB-2004; 2004WO-US003600.
XX 02-MAR-2004; 2004US-0549896P.
XX (PROT-) PROTEOLOGICS INC.
XX Taglicht DN, Alroy I, Reiss Y, Yaar L, Ben-Avraham D, Tuvia S;
XX Greener T;
XX WPI; 2004-662346/64.
XX Isolated, purified or recombinant complex, useful for identifying an
XX antiviral, anti-apoptotic or anti-cancer, comprising POSH polypeptide and
XX POSH-associated protein (POSH-AP).
XX Disclosure; SEQ ID NO 128; 374pp; English.
XX The invention relates to an isolated, purified or recombinant complex (I)
XX comprising a POSH polypeptide and a POSH-associated protein (POSH-AP) (a)
XX or HERPUD1 and a ubiquitin ligase (b). Methods using (I), (a) or (b) are
XX useful for identifying an agent that modulates an activity of a POSH
XX polypeptide or POSH-AP, for identifying an antiviral agent, an anti-
XX apoptotic agent, an anti-cancer agent, an agent that inhibits trafficking
XX of a protein through the secretory pathway, an agent that inhibits the
XX progression of a neurological disorder, an agent that modulates a POSH
XX function, an agent that modulates a HERPUD1 function. The methods can be
XX used for treating a viral infection, for inhibiting an activity of a POSH
XX -AP in a cell, for treating a POSH-associated disease in a subject. The
XX POSH-associated disease is viral infection, POSH-associated cancer or
XX POSH-associated neurological disorder. The methods are useful for
XX treating or preventing POSH-associated neurological disorder in a subject
XX e.g. Alzheimer's disease, Parkinson's disease, Huntington's disease,
XX schizophrenia, Niemann-Pick's disease. This sequence corresponds to a
XX nucleic acid of the invention.

XX Sequence 2034 BP; 580 A; 378 C; 424 G; 632 T; 0 U; 0 Other;

Query Match 65.8%; Score 838; DB 13; Length 2034;

Best Local Similarity 99.9%; Pred. No. 0;

Matches 958; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

Db 2651 GCTCTCTGGATGCTGTAATGCCCCCATCTGATGCATCAGCATTAAGTCCATTACAAACCCCTAC 2592
QY 797 AGGAGAGATAGATTTTCTTCTGTACAGATTAATCTTCTGGTGTGTGACTGGG 856
Db 2591 AGGAGAGATAGATTTTCTTCTGTACAGATTAATCTTCTGGTGTGTGACTGGG 2532
QY 857 TGATGATGAGCTGCTGTTTGGCTTTCACATTCATGTTAGTC 897
Db 2531 TGATGATGAGCTGCTGTTTGGCTTTCACATTCATGTTAGTC 2491

RESULT 19

AAC98856
ID AAC98856 standard; cDNA; 1535 BP.
XX
AC AAC98856;
XX
DT 09-MAR-2001 (first entry)
XX
DE Human pancreatic cancer antigen nucleotide sequence SEQ ID NO:84.
XX
KW Human; pancreas; pancreatic cancer; pancreatic cancer antigen; detection;
KW diagnosis; identification; cytostatic; neuroprotective; nootropic;
KW immunomodulatory; relaxant; contraceptive; gynaecological;
KW antiinflammatory; cardiac; gene therapy; chromosome mapping;
KW linkage analysis; tissue identification; tissue typing; forensic; neural;
KW immune system; muscular; reproductive; gastrointestinal; pulmonary;
KW cardiovascular; renal; proliferative; ss.
XX
OS Homo sapiens.
XX
PN WO200055320-A1.
XX
PD 21-SEP-2000.
XX
PF 08-MAR-2000; 2000WO-US005989.
XX
PR 12-MAR-1999; 99US-0124270P.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Rosen CA, Ruben SM;
XX
DR WPI: 2000-579444/54.
DR P-PSDB; AAB54091.
XX

New nucleic acid that is a pancreatic cancer antigen for preventing, treating, or ameliorating a medical condition, particular pancreatic cancer, or for use in assays for diagnosing a pathological condition.

Claim 1; Page 554-555; 1379pp; English

AAC98773 to AAC99231 encode the human pancreatic cancer associated proteins, called pancreatic cancer antigens, given in AAB54008 to AAB54466. The human pancreatic cancer antigens have cytostatic, neuroprotective, nootropic, immunomodulatory, relaxant, contraceptive, gynaecological, cardiac and antiinflammatory activities, and can be used in gene therapy. The polynucleotide and proteins can be used for preventing, treating, or ameliorating a medical condition or in assays for diagnosing a pathological condition or a susceptibility to one in a subject. Binding partners to the proteins and the activity of the proteins can be identified. The pancreatic cancer antigens can be used to detect, treat or prevent pancreatic disorders, especially cancer. Agonists and antagonists to the antigens can be screened for. The pancreatic cancer antigen polynucleotides can be used to design nucleic acid hybridisation probes that can be used in chromosome mapping, linkage analysis, tissue identification and/or typing and a variety of forensic and diagnostic methods. The proteins can be used to generate antibodies which are used to purify, detect and target the polypeptides, including both in vivo and in vitro diagnostic and therapeutic methods. The proteins can be used to treat or prevent neural, immune system, muscular, reproductive, gastrointestinal, pulmonary, cardiovascular, renal or

CC proliferative disorders. AAC99232 to AAC99240 and AAB54467 represent CC sequences used in the exemplification of the present invention
XX
SQ Sequence 1535 BP; 459 A; 243 C; 283 G; 544 T; 0 U; 6 Other;
Query Match 27.9%; Score 356; DB 3; Length 1535;
Best Local Similarity 100.0%; Pred. No. 5e-166;
Matches 356; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 919 GATGTCACACGAGCTTCTTCGCAATCGTAGCTGATGAGCAACGCAAGCAAGCTGAA 978
Db 36 GATGTCACACGAGCTTCTTCGCAATCGTAGCTGATGAGCAACGCAAGCAAGCTGAA 95
QY 979 AATTTTGTCTACCGACTTTCGCTAATGCTCATAGCGCAGCAATTCAGTTGGGAGCGACT 1038
Db 96 AATTTTGTCTACCGACTTTCGCTAATGCTCATAGCGCAGCAATTCAGTTGGGAGCGACT 155
QY 1039 CCTGATCTATTTCATGAAGGAATTCGCAACAGCCATATGATAGGAGCTGTCTAGTCTTT 1098
Db 156 CCTGATCTATTTCATGAAGGAATTCGCAACAGCCATATGATAGGAGCTGTCTAGTCTTT 215
QY 1099 GACACGAGCTTTCGCAACAGCTTTTCGCAAGAAATGCAATTCAGGATCAATGTAATATT 1158
Db 216 GACACGAGCTTTCGCAACAGCTTTTCGCAAGAAATGCAATTCAGGATCAATGTAATATT 275
QY 1159 TCCATGCTGTGAAATGCGCAATCAAAACATTTCTGCGCCAGTGTAAAACTTCAGTTTCAC 1218
Db 276 TCCATGCTGTGAAATGCGCAATCAAAACATTTCTGCGCCAGTGTAAAACTTCAGTTTCAC 335
QY 1219 AGAAATTAAGGACCCCATCTGTCTGCCAACCTAAACTCTTCGCTAGGTGGAAGC 1274
Db 336 AGAAATTAAGGACCCCATCTGTCTGCCAACCTAAACTCTTCGCTAGGTGGAAGC 391

RESULT 20

AAB57326/c
ID AAB57326 standard; cDNA; 466 BP.
XX
AC AAB57326;
XX
DT 06-NOV-2001 (first entry)
XX
DE Human polynucleotide SEQ ID NO 7386.
XX
KW Human; cytokine; cell proliferation; cell differentiation; gene therapy;
KW vaccine; peptide therapy; stem cell growth factor; haematopoiesis;
KW tissue growth factor; immunomodulatory; cancer; leukaemia;
KW nervous system disorders; arthritis; inflammation; ss.
XX
OS Homo sapiens.
XX
PN WO200164835-A2.
XX
PD 07-SEP-2001.
XX
PF 26-FEB-2001; 2001WO-US004927.
XX
PR 28-FEB-2000; 2000US-00515126.
PR 18-MAY-2000; 2000US-00577409.
XX
PA (HYSE-) HYSEQ INC.
XX
PI Tang YT, Liu C, Drmanac RT;
XX
DR WPI: 2001-514838/56.
DR P-PSDB; AAO67395.
XX
KW Isolated nucleic acids and polypeptides, useful for preventing diagnosing
PT and treating e.g. leukemia, inflammation and immune disorders.
XX
PS Claim 1; SEQ ID NO 7386; 1399pp + Sequence Listing; English.
XX
CC The invention relates to human polynucleotides (AAB57326-AAB59841) and

CC the encoded proteins (AA000010-AA013910) that exhibit activity elating to
CC cytokine, cell proliferation or cell differentiation or which may induce
CC production of other cytokines in other cell populations. The
CC polynucleotides and polypeptides are useful in gene therapy, vaccines or
CC peptide therapy. The polypeptides have various cytokine-like activities,
CC e.g. stem cell growth factor activity, haematopoiesis regulating
CC activity, tissue growth factor activity, immunomodulatory activity and
CC activin/inhibin activity and may be useful in the diagnosis and/or
CC treatment of cancer, leukaemia, nervous system disorders, arthritis and
CC inflammation. Note: The sequence data for this patent did not form part
CC of the printed specification, but was obtained in electronic format
CC directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 466 BP; 136 A; 86 C; 97 G; 147 T; 0 U; 0 Other;

Query Match 15.9%; Score 203; DB 4; Length 466;
Best Local Similarity 100.0%; Pred. No. 5.1e-90;
Matches 203; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1067 GAGCCATTATGATAGGACTGTCTAGTCTTTGACACCCAGCATTCGACAGTTTTCGAG 1126
DB 294 GAGCCATTATGATAGGACTGTCTAGTCTTTGACACCCAGCATTCGACAGTTTTCGAG 235
QY 1127 ARAATGCAATTAGGCAATCAATGTAATTTCCATGTTGCAATGCAATCAACAT 1186
DB 234 ARAATGCAATTAGGCAATCAATGTAATTTCCATGTTGCAATGCAATCAACAT 175
QY 1187 TTTCTGCGCCAGTGTATAAATCTCAGTTTCACAGAAATAAGGCCACCCATCTGTCGCCA 1246
DB 174 TTTCTGCGCCAGTGTATAAATCTCAGTTTCACAGAAATAAGGCCACCCATCTGTCGCCA 115
QY 1247 ACCTAAATCTTTTCGGTAGGTG 1269
DB 114 ACCTAAATCTTTTCGGTAGGTG 92

RESULT 21
ABV38421/c
ID ABV38421 standard; cDNA; 405 BP.
XX
AC ABV38421;
XX
DT 16-SEP-2002 (first entry)
XX
DE Human prostate expression marker cDNA 38412.
XX
KW Human; prostate cancer; cytostatic; carcinogen; pharmacodynamic marker;
KW pharmacogenomic marker; gene; ss.
XX
OS Homo sapiens.
XX
PN WO200160860-A2.
XX
PD 23-AUG-2001.
XX
PF 20-FEB-2001; 2001WO-US005171.
XX
PR 17-FEB-2000; 2000US-0183319P.
XX
PR 16-MAR-2000; 2000US-0189862P.
XX
PR 25-MAY-2000; 2000US-0207454P.
XX
PR 09-JUN-2000; 2000US-0211314P.
XX
PR 18-JUL-2000; 2000US-0219007P.
XX
PR 13-DEC-2000; 2000US-0255281P.
XX
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
XX
PI Schlegel R, Endege WO, Monahan JE;
XX
DR WPI; 2001-662795/76.
XX

XX Novel isolated nucleic acid molecule associated with cancerous state of
PT prostate cells and correlating with presence of prostate cancer, useful
PT for detecting presence of prostate cancer, stage of prostate cancer.

XX
PS Claim 1; Page 7828; 11750pp; English.
XX
CC The invention relates to an isolated nucleic acid molecule (I) comprising
CC a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the
CC specification or its complement. (I) is useful for: (a) assessing whether
CC a patient is afflicted with prostate cancer; (b) monitoring the efficacy
CC progression of prostate cancer in a patient; (c) assessing the efficacy
CC of a test compound to inhibit prostate cancer in a patient; (d) assessing
CC the efficacy of a therapy for inhibiting prostate cancer in a patient;
CC (e) selecting a competition for inhibiting prostate cancer in a patient;
CC (f) assessing the prostate cell carcinogenic potential of a compound; (g)
CC determining whether prostate cancer has metastasized in a patient; (h)
CC assessing the aggressiveness or indolence of prostate cancer in a patient
CC ; (I) is also useful as a pharmacodynamic or pharmacogenomic marker
XX
SQ Sequence 405 BP; 126 A; 80 C; 96 G; 103 T; 0 U; 0 Other;

Query Match 12.5%; Score 159; DB 5; Length 405;
Best Local Similarity 100.0%; Pred. No. 3.6e-68;
Matches 159; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 177 TTTTAAATCCCTATTATTTCTCTCTTTTCTCAGTAAATTTTGTATGAACTTTAAAG 236
DB 212 TTTTAAATCCCTATTATTTCTCTCTTTTCTCAGTAAATTTTGTATGAACTTTAAAG 153
QY 237 GACTTATGCGCATGTAACATATTATATAAGTAAGTCATGGTTATATTTTCTCTCT 296
DB 152 GACTTATGCGCATGTAAGATTTATATAAGTAAGTCATGGTTATATTTTCTCTCT 93
QY 297 GCCTCTTATGTATTATTATTTTCTCAGAAATGAGCGCTCAGAC 335
DB 92 GCCTCTTATGTATTATTATTTCTCAGAAATGAGCGCTCAGAC 54

RESULT 22
ABV08519/c
ID ABV08519 standard; cDNA; 277 BP.
XX
AC ABV08519;
XX
DT 13-SEP-2002 (first entry)
XX
DE Human prostate expression marker cDNA 8510.
XX
KW Human; prostate cancer; cytostatic; carcinogen; pharmacodynamic marker;
KW pharmacogenomic marker; gene; ss.
XX
OS Homo sapiens.
XX
PN WO200160860-A2.
XX
PD 23-AUG-2001.
XX
PF 20-FEB-2001; 2001WO-US005171.
XX
PR 17-FEB-2000; 2000US-0183319P.
XX
PR 16-MAR-2000; 2000US-0189862P.
XX
PR 25-MAY-2000; 2000US-0207454P.
XX
PR 09-JUN-2000; 2000US-0211314P.
XX
PR 18-JUL-2000; 2000US-0219007P.
XX
PR 13-DEC-2000; 2000US-0255281P.
XX
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
XX
PI Schlegel R, Endege WO, Monahan JE;
XX
DR WPI; 2001-662795/76.
XX

XX Novel isolated nucleic acid molecule associated with cancerous state of
PT prostate cells and correlating with presence of prostate cancer, useful
PT for detecting presence of prostate cancer, stage of prostate cancer.

CC The invention relates to an isolated nucleic acid molecule (I) comprising
CC a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the
CC specification or its complement. (I) is useful for: (a) assessing whether
CC a patient is afflicted with prostate cancer; (b) monitoring the
CC progression of prostate cancer in a patient; (c) assessing the efficacy
CC of a test compound to inhibit prostate cancer in a patient; (d) assessing
CC the efficacy of a therapy for inhibiting prostate cancer in a patient;
CC (e) selecting a composition for inhibiting prostate cancer in a patient;
CC (f) assessing the prostate cell carcinogenic potential of a compound; (g)
CC determining whether prostate cancer has metastasized in a patient; (h)
CC assessing the aggressiveness or indolence of prostate cancer in a patient
CC ; (I) is also useful as a pharmacodynamic or pharmacogenomic marker
XX
SQ Sequence 473 BP; 122 A; 104 C; 124 G; 123 T; 0 U; 0 Other;

Query Match 10.0%; Score 128; DB 5; Length 473;
Best Local Similarity 100.0%; Pred. No. 9,2e-53;
Matches 128; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 969 GCAGCTGAAATTTTGGCTTACCGACTTGGCTGAGCTTGAATGCTATAGCGGAGATTGACTTG 1028
DB 473 GCAAGCTGAAATTTTGGCTTACCGACTTGGCTGAGCTTGAATGCTATAGCGGAGATTGACTTG 414

QY 1029 GGAAGCGACTCTCGATCTATTCATGAGCAATTGCAAGCAGCATTTATGATAGCGACTG 1088
DB 413 GGAAGCGACTCTCGATCTATTCATGAGCAATTGCAAGCAGCATTTATGATAGCGACTG 354

QY 1089 TCTAGTCT 1096
DB 353 TCTAGTCT 346

RESULT 25
ABV13828/c
ID ABV13828 standard; cDNA; 411 BP.
XX
AC ABV13828;
XX
DT 13-SEP-2002 (first entry)
XX
DE Human prostate expression marker cDNA 13819.
XX
KW Human; prostate cancer; cytostatic; carcinogen; pharmacodynamic marker;
KW pharmacogenomic marker; gene; ss.
XX
OS Homo sapiens.
XX
PN WO200160860-A2.
XX
PD 23-AUG-2001.
XX
PF 20-FEB-2001; 2001WO-US005171.
XX
PR 17-FEB-2000; 2000US-0183319P.
PR 16-MAR-2000; 2000US-0189862P.
PR 25-MAY-2000; 2000US-0207454P.
PR 09-JUN-2000; 2000US-0211314P.
PR 18-JUL-2000; 2000US-0219007P.
PR 13-DEC-2000; 2000US-0255281P.
XX
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
XX
PI Schlegel R, Endege WO, Monahan JB;
XX
DR WPI; 2001-662795/76.
XX
PT Novel isolated nucleic acid molecule associated with cancerous state of
PT prostate cells and correlating with presence of prostate cancer, useful
PT for detecting presence of prostate cancer, stage of prostate cancer.
XX
PS Claim 1; Page 2301; 11750pp; English.
XX
CC The invention relates to an isolated nucleic acid molecule (I) comprising

CC a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the
CC specification or its complement. (I) is useful for: (a) assessing whether
CC a patient is afflicted with prostate cancer; (b) monitoring the
CC progression of prostate cancer in a patient; (c) assessing the efficacy
CC of a test compound to inhibit prostate cancer in a patient; (d) assessing
CC the efficacy of a therapy for inhibiting prostate cancer in a patient;
CC (e) selecting a composition for inhibiting prostate cancer in a patient;
CC (f) assessing the prostate cell carcinogenic potential of a compound; (g)
CC determining whether prostate cancer has metastasized in a patient; (h)
CC assessing the aggressiveness or indolence of prostate cancer in a patient
CC ; (I) is also useful as a pharmacodynamic or pharmacogenomic marker
XX
SQ Sequence 411 BP; 153 A; 70 C; 74 G; 114 T; 0 U; 0 Other;

Query Match 9.3%; Score 118; DB 5; Length 411;
Best Local Similarity 100.0%; Pred. No. 8.5e-48;
Matches 118; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1157 TTTCATGTGTTGAATGGCAATCAACATTTTCTGGCCAGTGTTTAAACTTCAGTTTC 1216
DB 364 TTTCATGTGTTGAATGGCAATCAACATTTTCTGGCCAGTGTTTAAACTTCAGTTTC 305

QY 1217 ACAGAAATTAAGSCACCCATCTGTCTGCCAACCTAAACTCTTTCCGTAGGTGGAAGC 1274
DB 304 ACAGAAATTAAGSCACCCATCTGTCTGCCAACCTAAACTCTTTCCGTAGGTGGAAGC 247

RESULT 26
ABV34940/c
ID ABV34940 standard; cDNA; 441 BP.
XX
AC ABV34940;
XX
DT 16-SEP-2002 (first entry)
XX
DE Human prostate expression marker cDNA 34931.
XX
KW Human; prostate cancer; cytostatic; carcinogen; pharmacodynamic marker;
KW pharmacogenomic marker; gene; ss.
XX
OS Homo sapiens.
XX
PN WO200160860-A2.
XX
PD 23-AUG-2001.
XX
PF 20-FEB-2001; 2001WO-US005171.
XX
PR 17-FEB-2000; 2000US-0183319P.
PR 16-MAR-2000; 2000US-0189862P.
PR 25-MAY-2000; 2000US-0207454P.
PR 09-JUN-2000; 2000US-0211314P.
PR 18-JUL-2000; 2000US-0219007P.
PR 13-DEC-2000; 2000US-0255281P.
XX
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
XX
PI Schlegel R, Endege WO, Monahan JB;
XX
DR WPI; 2001-662795/76.
XX
PT Novel isolated nucleic acid molecule associated with cancerous state of
PT prostate cells and correlating with presence of prostate cancer, useful
PT for detecting presence of prostate cancer, stage of prostate cancer.
XX
PS Claim 1; Page 7303; 11750pp; English.
XX
CC The invention relates to an isolated nucleic acid molecule (I) comprising
CC a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the
CC specification or its complement. (I) is useful for: (a) assessing whether
CC a patient is afflicted with prostate cancer; (b) monitoring the
CC progression of prostate cancer in a patient; (c) assessing the efficacy
CC of a test compound to inhibit prostate cancer in a patient; (d) assessing
CC the efficacy of a therapy for inhibiting prostate cancer in a patient;
CC (e) selecting a composition for inhibiting prostate cancer in a patient;
CC (f) assessing the prostate cell carcinogenic potential of a compound; (g)
CC determining whether prostate cancer has metastasized in a patient; (h)
CC assessing the aggressiveness or indolence of prostate cancer in a patient
CC ; (I) is also useful as a pharmacodynamic or pharmacogenomic marker
XX
SQ Sequence 411 BP; 153 A; 70 C; 74 G; 114 T; 0 U; 0 Other;

CC the efficacy of a therapy for inhibiting prostate cancer in a patient;
 CC (e) selecting a composition for inhibiting prostate cancer in a patient;
 CC (f) assessing the prostate cell carcinogenic potential of a compound; (g)
 CC determining whether prostate cancer has metastasized in a patient; (h)
 CC assessing the aggressiveness or indolence of prostate cancer in a patient
 CC ; (i) is also useful as a pharmacodynamic or pharmacogenomic marker
 XX
 SQ Sequence 441 BP; 157 A; 80 C; 86 G; 118 T; 0 U; 0 Other;
 Query Match 9.3%; Score 118; DB 5; Length 441;
 Best Local Similarity 100.0%; Pred. No. 8.5e-48;
 Matches 118; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1157 TTTCCATGTTGAATGCAATCAAACTTTCTGCGCAGTGTAACTTCAAGTTTC 1216
 DB 399 TTTCCATGTTGAATGCAATCAAACTTTCTGCGCAGTGTAACTTCAAGTTTC 340
 QY 1217 ACAGAAATAGGCAACCACTCTGCTGCAACTAACTTTTCGGTAGGTGAAGC 1274
 DB 339 ACAGAAATAGGCAACCACTCTGCTGCAACTAACTTTTCGGTAGGTGAAGC 282
 RESULT 27
 ABV04659/c
 ID ABV04659 standard; cDNA; 438 BP.
 AC ABV04659;
 XX
 DT 13-SEP-2002 (first entry)
 DE Human prostate expression marker cDNA 4650.
 DE Human; prostate cancer; cytostatic; carcinogen; pharmacodynamic marker;
 KW Pharmacogenomic marker; gene; ss.
 KW Homo sapiens.
 OS
 XX
 PN WO200160860-A2.
 XX
 PD 23-AUG-2001.
 XX
 PF 20-FEB-2001; 2001WO-US005171.
 XX
 PR 17-FEB-2000; 2000US-0183319P.
 PR 16-MAR-2000; 2000US-0189862P.
 PR 25-MAY-2000; 2000US-0207454P.
 PR 09-JUN-2000; 2000US-0211314P.
 PR 18-JUL-2000; 2000US-0219007P.
 PR 13-DEC-2000; 2000US-0255281P.
 XX
 PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC
 XX
 PI Schlegel R, Endege WO, Monahan JE;
 XX
 WPI; 2001-662795/76.
 XX
 DR Novel isolated nucleic acid molecule associated with cancerous state of
 PT prostate cells and correlating with presence of prostate cancer, useful
 PT for detecting presence of prostate cancer, stage of prostate cancer.
 XX
 PS Claim 1; Page 805; 11750pp; English.
 XX
 CC The invention relates to an isolated nucleic acid molecule (i) comprising
 CC a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the
 CC specification or its complement. (i) is useful for: (a) assessing whether
 CC a patient is afflicted with prostate cancer; (b) monitoring the efficacy
 CC progression of prostate cancer in a patient; (c) assessing the efficacy
 CC of a test compound to inhibit prostate cancer in a patient; (d) assessing
 CC the efficacy of a therapy for inhibiting prostate cancer in a patient;
 CC (e) selecting a composition for inhibiting prostate cancer in a patient;
 CC (f) assessing the prostate cell carcinogenic potential of a compound; (g)
 CC determining whether prostate cancer has metastasized in a patient; (h)
 CC assessing the aggressiveness or indolence of prostate cancer in a patient

CC ; (i) is also useful as a pharmacodynamic or pharmacogenomic marker
 XX
 SQ Sequence 438 BP; 149 A; 79 C; 85 G; 122 T; 0 U; 3 Other;
 Query Match 6.7%; Score 85; DB 5; Length 438;
 Best Local Similarity 100.0%; Pred. No. 2.1e-31;
 Matches 85; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1190 CTGGCAGTGTAACTTCAAGTTTCAGTTCACAGAAATAGGCAACCACTCTGTCGCAACC 1249
 DB 366 CTGGCAGTGTAACTTCAAGTTTCAGTTCACAGAAATAGGCAACCACTCTGTCGCAACC 307
 QY 1250 TAAACTCTTCGGTAGGTGAAGC 1274
 DB 306 TAAACTCTTCGGTAGGTGAAGC 282
 RESULT 28
 ABI99429
 ID ABI99429 standard; cDNA; 1968 BP.
 AC ABI99429;
 XX
 DT 07-MAR-2002 (first entry)
 DE Mouse ischaemic condition related cDNA sequence SEQ ID NO:354.
 DE Mouse; ischaemia; compressive ischaemia; occlusive ischaemia;
 KW vasospastic ischaemia; ischaemic condition; ischaemic disease; ss.
 XX
 OS Mus musculus.
 XX
 PN WO200188188-A2.
 XX
 PD 22-NOV-2001.
 XX
 PF 18-MAY-2001; 2001WO-JP004192.
 XX
 PR 18-MAY-2000; 2000JP-00145977.
 XX
 PA (UYN-) UNIV NIHON SCHOOL JURIDICAL PERSON.
 XX
 PI Ishikawa K, Asai S, Takahashi Y, Nagata T, Ishii Y;
 XX
 WPI; 2002-034733/04.
 DR P-PSDB; ABB57146.
 XX
 PT Examining the ischemic condition (e.g. occlusive ischemia) by measuring
 PT expression levels of particular genes defined in the specification or by
 PT determining the expression profile of a gene group comprising these
 PT genes.
 XX
 PS Claim 2; Page 956-958; 2690pp; English.
 XX
 CC The present invention describes a method for examining ischaemic
 CC conditions, comprising measuring the expression levels of particular
 CC genes (i) in a test sample or determining the expression profile of a
 CC gene group in the sample comprising genes selected from (i). The method
 CC is useful for examining the ischaemic condition (e.g. compressive
 CC ischaemia, occlusive ischaemia or vasospastic ischaemia) by measuring
 CC expression levels of particular genes (AB199202 to AB199912, encoding the
 CC protein sequences in ABB57020 to ABB57374) or by determining the
 CC expression profile of a gene group comprising these genes. The expression
 CC levels or expression profiles produced by these genes are used as an
 CC indicator when screening for ischaemic condition-improving drugs or
 CC therapeutics for ischaemic diseases. AB199913 and AB199914 represent PCR
 CC primers for a mouse ischaemic condition related sequence, which are used
 CC in the exemplification of the present invention
 XX
 SQ Sequence 1968 BP; 500 A; 397 C; 447 G; 624 T; 0 U; 0 Other;
 Query Match 6.0%; Score 77; DB 6; Length 1968;
 Best Local Similarity 100.0%; Pred. No. 2e-27;

CC 15112 bovine LMFD EST (expressed sequence tag) nucleic acids. Note: The
CC present sequence was not shown in the specification but was obtained in
CC electronic format from the USPTO web site:
CC seqdata.uspto.gov/sequence.html?DocID=20020137139
XX
XX
SQ Sequence 360 BP; 111 A; 75 C; 75 G; 98 T; 0 U; 1 Other;

Query Match 4.9%; Score 62; DB 8; Length 360;
Best Local Similarity 100.0%; Pred. No. 5.6e-20;
Matches 62; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1120 TTTCGAGAAATGCGCAATTAGGCATCAATGTAACTATTTCATGTGTTGAAATGCAAT 1179
Db 211 TTTCGAGAAATGCGCAATTAGGCATCAATGTAACTATTTCATGTGTTGAAATGCAAT 270
QY 1180 CA 1181
Db 271 CA 272

RESULT 30
ABV18678/c
ID ABV18678 standard; cDNA; 426 BP.
AC ABV18678;
XX
XX
DT 13-SEP-2002 (first entry)
XX
XX Human prostate expression marker cDNA 18669.
DE
XX Human; prostate cancer; cytostatic; carcinogen; pharmacodynamic marker;
KW pharmacogenomic marker; gene; ss.
XX
XX Homo sapiens.
XX
XX WO200160860-A2.
XX
XX 23-AUG-2001.
XX
XX 20-FEB-2001; 2001WO-US005171.
XX
XX 17-FEB-2000; 2000US-0183319P.
XX 16-MAR-2000; 2000US-0189862P.
XX 25-MAY-2000; 2000US-0207454P.
XX 09-JUN-2000; 2000US-0211314P.
XX 18-JUL-2000; 2000US-0219007P.
XX 13-DEC-2000; 2000US-0255281P.
XX
XX (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
XX
XX Schlegel R, Endege WO, Monahan JE;
XX WPI; 2001-662795/76.
XX
XX Novel isolated nucleic acid molecule associated with cancerous state of
XX prostate cells and correlating with presence of prostate cancer, useful
XX for detecting presence of prostate cancer, stage of prostate cancer.
XX
XX Claim 1; Page 3073; 11750pp; English
XX
XX The invention relates to an isolated nucleic acid molecule (I) comprising
XX a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the
XX specification or its complement. (I) is useful for: (a) assessing whether
XX a patient is afflicted with prostate cancer; (b) monitoring the
XX progression of prostate cancer in a patient; (c) assessing the efficacy
XX of a test compound to inhibit prostate cancer in a patient; (d) assessing
XX the efficacy of a therapy for inhibiting prostate cancer in a patient;
XX (e) selecting a composition for inhibiting prostate cancer in a patient;
XX (f) assessing the prostate cell carcinogenic potential of a compound; (g)
XX determining whether prostate cancer has metastasized in a patient; (h)
XX assessing the aggressiveness or indolence of prostate cancer in a patient
XX ; (I) is also useful as a pharmacodynamic or pharmacogenomic marker

SQL	Sequence	426 BP; 105 A; 84 C; 87 G; 109 T; 0 U; 41 Other;	PR	05-SEP-2000;	2000US-0229513P;
	Query Match	4.1%; Score 52; DB 5; Length 426;	PR	06-SEP-2000;	2000US-0230437P;
	Best Local Similarity	100.0%; Pred. No. 5.2e-15;	PR	06-SEP-2000;	2000US-0230438P;
	Matches	52; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	PR	08-SEP-2000;	2000US-0231242P;
			PR	08-SEP-2000;	2000US-0231243P;
			PR	08-SEP-2000;	2000US-0231244P;
			PR	08-SEP-2000;	2000US-0231413P;
			PR	08-SEP-2000;	2000US-0231414P;
			PR	08-SEP-2000;	2000US-0232080P;
			PR	08-SEP-2000;	2000US-0232081P;
			PR	12-SEP-2000;	2000US-0231968P;
			PR	14-SEP-2000;	2000US-0232397P;
			PR	14-SEP-2000;	2000US-0232398P;
			PR	14-SEP-2000;	2000US-0232399P;
			PR	14-SEP-2000;	2000US-0232400P;
			PR	14-SEP-2000;	2000US-0232401P;
			PR	14-SEP-2000;	2000US-0233063P;
			PR	14-SEP-2000;	2000US-0233064P;
			PR	14-SEP-2000;	2000US-0233065P;
			PR	21-SEP-2000;	2000US-0234223P;
			PR	21-SEP-2000;	2000US-0234224P;
			PR	25-SEP-2000;	2000US-0234997P;
			PR	25-SEP-2000;	2000US-0234998P;
			PR	26-SEP-2000;	2000US-0235484P;
			PR	27-SEP-2000;	2000US-0235834P;
			PR	27-SEP-2000;	2000US-0235836P;
			PR	29-SEP-2000;	2000US-0236327P;
			PR	29-SEP-2000;	2000US-0236367P;
			PR	29-SEP-2000;	2000US-0236368P;
			PR	29-SEP-2000;	2000US-0236369P;
			PR	29-SEP-2000;	2000US-0236370P;
			PR	02-OCT-2000;	2000US-0236802P;
			PR	02-OCT-2000;	2000US-0237037P;
			PR	02-OCT-2000;	2000US-0237038P;
			PR	02-OCT-2000;	2000US-0237039P;
			PR	02-OCT-2000;	2000US-0237040P;
			PR	13-OCT-2000;	2000US-0239353P;
			PR	13-OCT-2000;	2000US-023937P;
			PR	20-OCT-2000;	2000US-0240960P;
			PR	20-OCT-2000;	2000US-0241221P;
			PR	20-OCT-2000;	2000US-0241785P;
			PR	20-OCT-2000;	2000US-0241786P;
			PR	20-OCT-2000;	2000US-0241787P;
			PR	20-OCT-2000;	2000US-0241808P;
			PR	20-OCT-2000;	2000US-0241825P;
			PR	01-NOV-2000;	2000US-0244617P;
			PR	08-NOV-2000;	2000US-0246474P;
			PR	08-NOV-2000;	2000US-0246475P;
			PR	08-NOV-2000;	2000US-0246476P;
			PR	08-NOV-2000;	2000US-0246477P;
			PR	08-NOV-2000;	2000US-0246478P;
			PR	08-NOV-2000;	2000US-0246523P;
			PR	08-NOV-2000;	2000US-0246524P;
			PR	08-NOV-2000;	2000US-0246525P;
			PR	08-NOV-2000;	2000US-0246526P;
			PR	08-NOV-2000;	2000US-0246527P;
			PR	08-NOV-2000;	2000US-0246528P;
			PR	08-NOV-2000;	2000US-0246532P;
			PR	08-NOV-2000;	2000US-0246609P;
			PR	08-NOV-2000;	2000US-0246610P;
			PR	08-NOV-2000;	2000US-0246611P;
			PR	08-NOV-2000;	2000US-0246613P;
			PR	17-NOV-2000;	2000US-0249207P;
			PR	17-NOV-2000;	2000US-0249208P;
			PR	17-NOV-2000;	2000US-0249209P;
			PR	17-NOV-2000;	2000US-0249210P;
			PR	17-NOV-2000;	2000US-0249211P;
			PR	17-NOV-2000;	2000US-0249212P;
			PR	17-NOV-2000;	2000US-0249213P;
			PR	17-NOV-2000;	2000US-0249214P;
			PR	17-NOV-2000;	2000US-0249215P;
			PR	17-NOV-2000;	2000US-0249216P;

PR 17-NOV-2000; 2000US-0249217P.
PR 17-NOV-2000; 2000US-0249218P.
PR 17-NOV-2000; 2000US-0249244P.
PR 17-NOV-2000; 2000US-0249245P.
PR 17-NOV-2000; 2000US-0249264P.
PR 17-NOV-2000; 2000US-0249265P.
PR 17-NOV-2000; 2000US-0249297P.
PR 17-NOV-2000; 2000US-0249299P.
PR 17-NOV-2000; 2000US-0249300P.
PR 01-DEC-2000; 2000US-0250160P.
PR 01-DEC-2000; 2000US-0250391P.
PR 05-DEC-2000; 2000US-0251030P.
PR 05-DEC-2000; 2000US-0251988P.
PR 05-DEC-2000; 2000US-0256719P.
PR 06-DEC-2000; 2000US-0251479P.
PR 08-DEC-2000; 2000US-0251856P.
PR 08-DEC-2000; 2000US-0251868P.
PR 08-DEC-2000; 2000US-0251869P.
PR 08-DEC-2000; 2000US-0251989P.
PR 08-DEC-2000; 2000US-0251990P.
PR 11-DEC-2000; 2000US-0254097P.
PR 05-JAN-2001; 2001US-0259678P.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
XX Rosen CA, Barash SC, Ruben SM;
PI
XX WPI; 2001-465570/50.
DR P-PSDB; AAM95578.
XX
XX
PT Isolated nucleic acid molecule encoding a reproductive system antigen is
PT used in preventing, treating or ameliorating a medical condition.
XX
XX Claim 1; SEQ ID NO 1549; 1297pp + Sequence Listing; English.
XX
XX The present invention provides the protein and coding sequences of a
CC number of human reproductive system related antigens. These can be used
CC in the prevention and treatment of reproductive system disorders,
CC including cancer. The present sequence is a coding sequence of the
XX invention
XX
SQ Sequence 222 BP; 53 A; 52 C; 64 G; 50 T; 0 U; 3 Other;
Query Match 2.6%; Score 33; DB 4; Length 222;
Best Local Similarity 100.0%; Pred. No. 1.4e-05;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 318 AGAATGAGCCGTCAGACTGCTACAGCATTACC 350
Db 190 AGAATGAGCCGTCAGACTGCTACAGCATTACC 222
RESULT 32
ABL96986
ID ABL96986 standard; cDNA; 222 BP.
XX
XX ABL96986;
XX
DT 21-JUN-2002 (first entry)
XX
DE Human testicular antigen encoding cDNA SEQ ID NO: 654.
XX
XX Human; testicular antigen; testes; cancer; metastasis; immune disorder;
KW reproductive system disorder; urinary system disorder; gene therapy;
KW cardiovascular disorder; respiratory disorder; neurological disorder;
KW gastrointestinal disease; infection; cytostatic; gene; ss.
XX
OS Homo sapiens.
XX
XX WO200155317-A2.
PN
XX
XX
PD 02-AUG-2001.
XX

PF 17-JAN-2001; 2001WO-US001329.
XX
XX 31-JAN-2000; 2000US-0179065P.
PR 04-FEB-2000; 2000US-0180628P.
PR 24-FEB-2000; 2000US-0184664P.
PR 02-MAR-2000; 2000US-0186350P.
PR 16-MAR-2000; 2000US-0189874P.
PR 17-MAR-2000; 2000US-019076P.
PR 18-APR-2000; 2000US-0198123P.
PR 19-MAY-2000; 2000US-0205515P.
PR 07-JUN-2000; 2000US-0209467P.
PR 28-JUN-2000; 2000US-0214886P.
PR 30-JUN-2000; 2000US-0215135P.
PR 07-JUL-2000; 2000US-0216647P.
PR 07-JUL-2000; 2000US-021680P.
PR 11-JUL-2000; 2000US-0217487P.
PR 14-JUL-2000; 2000US-0218290P.
PR 26-JUL-2000; 2000US-0220963P.
PR 26-JUL-2000; 2000US-0220964P.
PR 14-AUG-2000; 2000US-0224518P.
PR 14-AUG-2000; 2000US-0224519P.
PR 14-AUG-2000; 2000US-0225213P.
PR 14-AUG-2000; 2000US-0225214P.
PR 14-AUG-2000; 2000US-0225266P.
PR 14-AUG-2000; 2000US-0225267P.
PR 14-AUG-2000; 2000US-0225268P.
PR 14-AUG-2000; 2000US-0225270P.
PR 14-AUG-2000; 2000US-0225447P.
PR 14-AUG-2000; 2000US-0225757P.
PR 14-AUG-2000; 2000US-0225758P.
PR 14-AUG-2000; 2000US-0225759P.
PR 22-AUG-2000; 2000US-0226279P.
PR 22-AUG-2000; 2000US-0226681P.
PR 22-AUG-2000; 2000US-0226868P.
PR 22-AUG-2000; 2000US-0227182P.
PR 23-AUG-2000; 2000US-0227009P.
PR 30-AUG-2000; 2000US-0228924P.
PR 01-SEP-2000; 2000US-0229287P.
PR 01-SEP-2000; 2000US-0229343P.
PR 01-SEP-2000; 2000US-0229344P.
PR 01-SEP-2000; 2000US-0229345P.
PR 05-SEP-2000; 2000US-0229509P.
PR 05-SEP-2000; 2000US-0229513P.
PR 06-SEP-2000; 2000US-0230437P.
PR 06-SEP-2000; 2000US-0230438P.
PR 08-SEP-2000; 2000US-0231242P.
PR 08-SEP-2000; 2000US-0231243P.
PR 08-SEP-2000; 2000US-0231244P.
PR 08-SEP-2000; 2000US-0231413P.
PR 08-SEP-2000; 2000US-0231414P.
PR 08-SEP-2000; 2000US-0232080P.
PR 08-SEP-2000; 2000US-0232081P.
PR 12-SEP-2000; 2000US-0231968P.
PR 14-SEP-2000; 2000US-0232397P.
PR 14-SEP-2000; 2000US-0232398P.
PR 14-SEP-2000; 2000US-0232399P.
PR 14-SEP-2000; 2000US-0232400P.
PR 14-SEP-2000; 2000US-0232401P.
PR 14-SEP-2000; 2000US-0233063P.
PR 14-SEP-2000; 2000US-0233064P.
PR 14-SEP-2000; 2000US-0233065P.
PR 21-SEP-2000; 2000US-0234223P.
PR 21-SEP-2000; 2000US-0234274P.
PR 25-SEP-2000; 2000US-0234997P.
PR 25-SEP-2000; 2000US-0234998P.
PR 26-SEP-2000; 2000US-0235484P.
PR 27-SEP-2000; 2000US-0235834P.
PR 27-SEP-2000; 2000US-0235836P.
PR 29-SEP-2000; 2000US-0236327P.
PR 29-SEP-2000; 2000US-0236367P.
PR 29-SEP-2000; 2000US-0236368P.
PR 29-SEP-2000; 2000US-0236369P.

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PT 29-SEP-2000; 2000US-0236370P.
XX 02-OCT-2000; 2000US-0236802P.
PS 02-OCT-2000; 2000US-0237037P.
XX 02-OCT-2000; 2000US-0237038P.
CC 02-OCT-2000; 2000US-0237039P.
CC 02-OCT-2000; 2000US-0237040P.
CC 02-OCT-2000; 2000US-0239935P.
CC 13-OCT-2000; 2000US-0239937P.
CC 13-OCT-2000; 2000US-0240960P.
CC 20-OCT-2000; 2000US-0241221P.
CC 20-OCT-2000; 2000US-0241785P.
CC 20-OCT-2000; 2000US-0241786P.
XX 20-OCT-2000; 2000US-0241787P.
XX 20-OCT-2000; 2000US-0241808P.
XX 20-OCT-2000; 2000US-0241809P.
XX 20-OCT-2000; 2000US-0241826P.
XX 01-NOV-2000; 2000US-0244617P.
XX 08-NOV-2000; 2000US-0246474P.
XX 08-NOV-2000; 2000US-0246475P.
XX 08-NOV-2000; 2000US-0246476P.
XX 08-NOV-2000; 2000US-0246477P.
XX 08-NOV-2000; 2000US-0246478P.
XX 08-NOV-2000; 2000US-0246523P.
XX 08-NOV-2000; 2000US-0246524P.
XX 08-NOV-2000; 2000US-0246525P.
XX 08-NOV-2000; 2000US-0246526P.
XX 08-NOV-2000; 2000US-0246527P.
XX 08-NOV-2000; 2000US-0246528P.
XX 08-NOV-2000; 2000US-0246532P.
XX 08-NOV-2000; 2000US-0246609P.
XX 08-NOV-2000; 2000US-0246610P.
XX 08-NOV-2000; 2000US-0246611P.
XX 08-NOV-2000; 2000US-0246613P.
XX 17-NOV-2000; 2000US-0249207P.
XX 17-NOV-2000; 2000US-0249208P.
XX 17-NOV-2000; 2000US-0249209P.
XX 17-NOV-2000; 2000US-0249210P.
XX 17-NOV-2000; 2000US-0249211P.
XX 17-NOV-2000; 2000US-0249212P.
XX 17-NOV-2000; 2000US-0249213P.
XX 17-NOV-2000; 2000US-0249214P.
XX 17-NOV-2000; 2000US-0249215P.
XX 17-NOV-2000; 2000US-0249216P.
XX 17-NOV-2000; 2000US-0249217P.
XX 17-NOV-2000; 2000US-0249218P.
XX 17-NOV-2000; 2000US-0249244P.
XX 17-NOV-2000; 2000US-0249245P.
XX 17-NOV-2000; 2000US-0249264P.
XX 17-NOV-2000; 2000US-0249265P.
XX 17-NOV-2000; 2000US-0249297P.
XX 17-NOV-2000; 2000US-0249299P.
XX 17-NOV-2000; 2000US-0249300P.
XX 01-DEC-2000; 2000US-0250160P.
XX 01-DEC-2000; 2000US-0250391P.
XX 05-DEC-2000; 2000US-0251030P.
XX 05-DEC-2000; 2000US-0251988P.
XX 05-DEC-2000; 2000US-0256719P.
XX 06-DEC-2000; 2000US-0251479P.
XX 08-DEC-2000; 2000US-0251856P.
XX 08-DEC-2000; 2000US-0251869P.
XX 08-DEC-2000; 2000US-0251989P.
XX 08-DEC-2000; 2000US-0251990P.
XX 11-DEC-2000; 2000US-0254037P.
XX 05-JAN-2001; 2001US-0259678P.
(HUMA-) HUMAN GENOME SCI INC.
XX PA
XX PI Rosen CA, Barash SC, Ruben SM;
XX XX
DR WPI; 2001-483232/52.
XX XX
PT Nucleic acids encoding 973 human testicular antigen polypeptides, useful

for preventing, diagnosing and/or treating testicular cancer.
Claim 1; SEQ ID NO 654; 766pp; English.
The present invention provides the protein and coding sequences of 973 human testicular antigens, and fragments of their genomic sequences. The sequences can be used in the treatment of cardiovascular, urinary system, reproductive system, immune, respiratory, neurological and gastrointestinal disorders, infections, and particularly cancer, especially testicular cancers. The present sequence is a cDNA of the invention
SQ Sequence 222 BP; 53 A; 52 C; 64 G; 50 T; 0 U; 3 Other;
Query Match 2.6%; Score 33; DB 4; Length 222;
Best Local Similarity 100.0%; Pred. No. 1.4e-05;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 318 AGAATGAGCGCTCAGACTGCTACAGCATTACC 350
DB 190 AGAATGAGCGCTCAGACTGCTACAGCATTACC 222
RESULT 33
ABI99430
ID ABI99430 standard; cDNA; 2198 BP.
XX AC ABI99430;
XX DT 07-MAR-2002 (first entry)
XX DE Mouse ischaemic condition related cDNA sequence SEQ ID NO:356.
XX KW Mouse; ischaemia; compressive ischaemia; occlusive ischaemia;
XX KW vasospastic ischaemia; ischaemic condition; ischaemic disease; ss.
XX OS Mus musculus.
XX PN WO200188188-A2.
XX PD 22-NOV-2001.
XX PF 18-MAY-2001; 2001WO-JP004192.
XX PR 18-MAY-2000; 2000JP-00145977.
XX PA (UYNI-) UNIV NIHON SCHOOL JURIDICAL PERSON.
XX PI Ishikawa K, Asai S, Takahashi Y, Nagata T, Ishii Y;
XX PT WPI; 2002-034733/04.
XX PT P-PSDB; ABB57147.
XX PS Examining the ischemic condition (e.g. occlusive ischemia) by measuring expression levels of particular genes defined in the specification or by determining the expression profile of a gene group comprising these genes.
XX PS Claim 2; Page 960-963; 2690pp; English.
XX CC The present invention describes a method for examining ischaemic conditions, comprising measuring the expression levels of particular genes (I) in a test sample or determining the expression profile of a gene group in the sample comprising genes selected from (I). The method is useful for examining the ischaemic condition (e.g. compressive ischaemia, occlusive ischaemia or vasospastic ischaemia) by measuring expression levels of particular genes (ABI99202 to ABI9912, encoding the protein sequences in ABB57020 to ABB57374) or by determining the expression profile of a gene group comprising these genes. The expression levels or expression profiles produced by these genes are used as an indicator when screening for ischaemic condition-improving drugs or therapeutics for ischaemic diseases. ABI9913 and ABI9914 represent primers for a mouse ischaemic condition related sequence, which are used


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RESULT 36
ADF54668
ID ADF54668 standard; DNA; 21 BP.
XX AC ADF54668;
XX DT 12-FEB-2004 (first entry)
XX DE Human SIAH1 reverse transcriptase PCR primer #1.
XX KW ss; reverse transcriptase; RT-PCR; primer; cell proliferation;
XX KW paternally expressed gene 10; PEG10; cell death; cancer; liver cancer;
XX KW hepatoma; hepatic carcinoma; apoptosis; SIAH1; human.
XX OS Homo sapiens.
XX PN JP2003093066-A.
XX PD 02-APR-2003.
XX PF 21-SEP-2001; 2001JP-00290248.
XX PR 21-SEP-2001; 2001JP-00290248.
XX PA (UITY) UNIV TOKYO.
XX PA (ONKO-) ONKO THERAPY SCI KK.
XX DR WPI; 2003-572666/54.
XX PT Promoting or suppressing cell proliferation by increasing or decreasing
XX PT paternally expressed gene 10 (PEG10) protein levels.
XX PS Example 3; SEQ ID NO 5; 25pp; Japanese.
XX CC The invention relates to a method of promoting or suppressing cell
XX CC proliferation by increasing or decreasing paternally expressed gene 10
XX CC (PEG10) protein levels, and suppressing or promoting cell death by
XX CC increasing or decreasing PEG10 protein levels in the cell. The method is
XX CC useful for promoting or suppressing cell proliferation or cell death.
XX CC Preferably, the method is useful for promoting or suppressing
XX CC proliferation or death of cancer cell, preferably liver cancer cell e.g.,
XX CC hepatoma cell. A pharmaceutical composition is useful for treating or
XX CC preventing cell proliferative diseases. The diagnosing method and the
XX CC diagnostic reagent are useful for diagnosing hepatic carcinoma,
XX CC preferably hepatoma. The present sequence is used in the exemplification
XX CC of the invention.
XX SQ Sequence 21 BP; 6 A; 5 C; 5 G; 5 T; 0 U; 0 Other;
XX
XX Query Match 1.6%; Score 21; DB 10; Length 21;
XX Best Local Similarity 100.0%; Pred. No. 13;
XX Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 412 TCCACAATGACTTGGCGACT 432
DB 1 TCCACAATGACTTGGCGACT 21
XX
RESULT 37
ADF54669/c
ID ADF54669 standard; DNA; 21 BP.
XX AC ADF54669;
XX DT 12-FEB-2004 (first entry)
XX DE Human SIAH1 reverse transcriptase PCR primer #2.
XX KW ss; reverse transcriptase; RT-PCR; primer; cell proliferation;
XX KW paternally expressed gene 10; PEG10; cell death; cancer; liver cancer;
XX KW hepatoma; hepatic carcinoma; apoptosis; SIAH1; human.
XX OS Homo sapiens.
XX PN JP2003093066-A.
XX PD 02-APR-2003.
XX PF 21-SEP-2001; 2001JP-00290248.
XX PR 21-SEP-2001; 2001JP-00290248.
XX PA (UITY) UNIV TOKYO.
XX PA (ONKO-) ONKO THERAPY SCI KK.
XX DR WPI; 2003-572666/54.
XX PT Promoting or suppressing cell proliferation by increasing or decreasing
XX PT paternally expressed gene 10 (PEG10) protein levels.
XX PS Example 3; SEQ ID NO 5; 25pp; Japanese.
XX CC The invention relates to a method of promoting or suppressing cell
XX CC proliferation by increasing or decreasing paternally expressed gene 10
XX CC (PEG10) protein levels, and suppressing or promoting cell death by
XX CC increasing or decreasing PEG10 protein levels in the cell. The method is
XX CC useful for promoting or suppressing cell proliferation or cell death.
XX CC Preferably, the method is useful for promoting or suppressing
XX CC proliferation or death of cancer cell, preferably liver cancer cell e.g.,
XX CC hepatoma cell. A pharmaceutical composition is useful for treating or
XX CC preventing cell proliferative diseases. The diagnosing method and the
XX CC diagnostic reagent are useful for diagnosing hepatic carcinoma,
XX CC preferably hepatoma. The present sequence is used in the exemplification
XX CC of the invention.
XX SQ Sequence 21 BP; 6 A; 5 C; 5 G; 5 T; 0 U; 0 Other;
XX
XX Query Match 1.6%; Score 21; DB 10; Length 21;
XX Best Local Similarity 100.0%; Pred. No. 13;
XX Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 412 TCCACAATGACTTGGCGACT 432
DB 1 TCCACAATGACTTGGCGACT 21
XX
RESULT 38
ACH28397
ID ACH28397 standard; cDNA; 442 BP.
XX AC ACH28397;
XX DT 13-OCT-2003 (first entry)
XX DE Human adult ovary cDNA #6777.
XX KW Human; ss; sequencing by hybridisation; SBH; expressed sequence tag; EST;
XX KW genome mapping; biodiversity; genetic disorder.
XX OS Homo sapiens.
XX PN US2003073623-A1.
XX PD 17-APR-2003.
XX PF 30-JUL-2001; 2001US-00918995.
XX PR 30-JUL-2001; 2001US-00918995.
XX PA (DRMA/) DRMANAC R T.
XX PA (LABA/) LABAT I.
XX PA (STAC/) STACHE-CRAIN B.
XX PA (DICK/) DICKSON M C.
XX PA (JONE/) JONES L W.
```

XX Drmanac RT, Labat I, Stache-Crain B, Dickson MC, Jones LW;
XX WPI; 2003-615964/58.
XX
XX New polynucleotide sequences obtained from various cDNA libraries, useful
XX as hybridization probes, as oligomers for PCR, for chromosome and gene
XX mapping, in the recombinant production of protein, or in generating
XX antisense DNA or RNA.
XX
XX Claim 1; SEQ ID NO 15609; 44pp; English.
XX
XX The invention relates to an isolated polynucleotide comprising any one of
XX 38043 cDNA sequences, appearing as ACH12789-ACH50831, whose sequence was
XX determined by the technique of SBH (sequencing by hybridisation). Also
XX included is a purified polypeptide comprising a sequence corresponding to
XX a reading frame of the novel polynucleotide. The nucleic acid sequences
XX are useful in diagnostics as expressed sequence tags (EST) for
XX identifying expressed genes or for physical mapping of the human genome,
XX in forensics, in assessing biodiversity, or in identifying mutations
XX responsible for genetic disorders and other traits. The nucleotide
XX sequences are also useful as hybridisation probes, as oligomers for PCR,
XX for chromosome and gene mapping, in the recombinant production of
XX protein, or in generating antisense DNA or RNA. The purified polypeptide
XX is useful for generating antibodies specific for it. The present sequence
XX is one of the 38043 isolated cDNA/EST sequences. Note: The sequence data
XX obtained in electronic format directly from USPTO at
XX seqdata.uspto.gov/sequence.html?DocID=20030073623
XX
SQ Sequence 442 BP; 149 A; 58 C; 92 G; 142 T; 0 U; 1 Other;
Query Match 1.6%; Score 21; DB 9; Length 442;
Best Local Similarity 100.0%; Pred. No. 13;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 165 TTTTAAATATCTTTTAAAT 185
DB 307 TTTTAAATATCTTTTAAAT 327
RESULT 39
ACH28129
ID ACH28129 standard; cDNA; 477 BP.
XX
XX ACH28129;
XX
XX 13-OCT-2003 (first entry)
XX
XX Human adult ovary cDNA #6509.
XX
XX Human; ss; sequencing by hybridisation; SBH; expressed sequence tag; EST;
XX genome mapping; biodiversity; genetic disorder.
XX
XX Homo sapiens.
XX
XX US2003073623-A1.
XX
XX 17-APR-2003.
XX
XX 30-JUL-2001; 2001US-00918995.
XX
XX 30-JUL-2001; 2001US-00918995.
XX
XX (DRNA/) DRMANAC R T.
XX (LABA/) LABAT I.
XX (STAC/) STACHE-CRAIN B.
XX (DICK/) DICKSON M C.
XX (JONE/) JONES L W.
XX
XX Drmanac RT, Labat I, Stache-Crain B, Dickson MC, Jones LW;
XX WPI; 2003-615964/58.
XX

XX New polynucleotide sequences obtained from various cDNA libraries, useful
XX as hybridization probes, as oligomers for PCR, for chromosome and gene
XX mapping, in the recombinant production of protein, or in generating
XX antisense DNA or RNA.
XX
XX Claim 1; SEQ ID NO 15341; 44pp; English.
XX
XX The invention relates to an isolated polynucleotide comprising any one of
XX 38043 cDNA sequences, appearing as ACH12789-ACH50831, whose sequence was
XX determined by the technique of SBH (sequencing by hybridisation). Also
XX included is a purified polypeptide comprising a sequence corresponding to
XX a reading frame of the novel polynucleotide. The nucleic acid sequences
XX are useful in diagnostics as expressed sequence tags (EST) for
XX identifying expressed genes or for physical mapping of the human genome,
XX in forensics, in assessing biodiversity, or in identifying mutations
XX responsible for genetic disorders and other traits. The nucleotide
XX sequences are also useful as hybridisation probes, as oligomers for PCR,
XX for chromosome and gene mapping, in the recombinant production of
XX protein, or in generating antisense DNA or RNA. The purified polypeptide
XX is useful for generating antibodies specific for it. The present sequence
XX is one of the 38043 isolated cDNA/EST sequences. Note: The sequence data
XX obtained in electronic format directly from USPTO at
XX seqdata.uspto.gov/sequence.html?DocID=20030073623
XX
SQ Sequence 477 BP; 155 A; 70 C; 98 G; 152 T; 0 U; 2 Other;
Query Match 1.6%; Score 21; DB 9; Length 477;
Best Local Similarity 100.0%; Pred. No. 13;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 165 TTTTAAATATCTTTTAAAT 185
DB 355 TTTTAAATATCTTTTAAAT 375
RESULT 40
ADL14958
ID ADL14958 standard; DNA; 1094 BP.
XX
XX ADL14958;
XX
XX 06-MAY-2004 (first entry)
XX
XX Human glaucoma-related optineurin (OPTN) exon 12.
XX
XX Human; glaucoma; optineurin; OPTN; diagnosis; ds.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
XX primer_bind complement(354..380)
XX /tag= a
XX exon /note= "Primer SF12"
XX 501..594
XX /tag= b
XX /number= 12
XX primer_bind 800..820
XX /tag= c
XX /note= "Primer SR12"
XX
XX EP1388590-A2.
XX
XX 11-FEB-2004.
XX
XX 29-JUL-2003; 2003EP-00447201.
XX
XX 02-AUG-2002; 2002JP-00226612.
XX
XX (SYSM-) SYSMEX CORP.
XX
XX Kouchi Y, Maeago A, Takahata T;
XX

XX WPI; 2004-146134/15.
 XX DR
 XX Gene assay for predicting future onset of glaucoma, particularly primary
 PT open angle glaucoma or normal ocular tension glaucoma, comprises
 PT detecting a mutation of at least one base of the optineurin gene.
 XX
 XX Example 1; SEQ ID NO 10; 31pp; English.
 XX
 CC The present sequence comprises exon 12 of the glaucoma-associated gene,
 CC OPTN (optineurin) ADL14949. The invention relates to a gene assay method
 CC for predicting future onset of primary open angle glaucoma and/or normal
 CC ocular tension glaucoma. This involves detecting a mutation in the OPTN
 CC gene coding sequence, specifically a substitution of G for A at position
 CC 619 and/or a substitution of A for G at position 898 of the OPTN coding
 CC sequence. The mutation(s) is detected using a nucleic acid amplification
 CC method using primers specific for the different exons of the coding
 CC sequence, including primers SF12 ADL14979 and SR12 ADL14980 for exon 12.
 XX
 XX Sequence 1094 BP; 316 A; 200 C; 242 G; 336 T; 0 U; 0 Other;
 SQ
 Query Match 1.6%; Score 21; DB 12; Length 1094;
 Best Local Similarity 100.0%; Pred. No. 13;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 165 TTTTAAATATCTTTTAAAT 185
 DB 478 TTTTAAATATCTTTTAAAT 498
 RESULT 41
 ID ADL14957
 AC ADL14957 standard; DNA; 1150 BP.
 AC ADL14957;
 XX
 DT 06-MAY-2004 (first entry)
 XX
 DE Human glaucoma-related optineurin (OPTN) exon 11.
 XX
 KW Human; glaucoma; optineurin; OPTN; diagnosis; ds.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT primer_bind /*tag= a
 FT complement (325..344)
 FT /note= "Primer SF11"
 FT exon 501..650
 FT /*tag= b
 FT /number= 11
 FT primer_bind 834..853
 FT /*tag= c
 FT /note= "Primer SR11"
 XX
 XX EPI388590-A2.
 XX
 PD 11-FEB-2004.
 XX
 XX 29-JUL-2003; 2003EP-00447201.
 XX
 XX 02-AUG-2002; 2002JP-00226612.
 XX
 XX (SYSM-) SYSMEX CORP.
 XX
 XX Kouchi Y, Masago A, Takahata T;
 XX
 XX WPI; 2004-146134/15.
 XX
 XX Gene assay for predicting future onset of glaucoma, particularly primary
 PT open angle glaucoma or normal ocular tension glaucoma, comprises
 PT detecting a mutation of at least one base of the optineurin gene.
 XX

PS Example 1; SEQ ID NO 9; 31pp; English.
 XX
 CC The present sequence comprises exon 11 of the glaucoma-associated gene,
 CC OPTN (optineurin) ADL14949. The invention relates to a gene assay method
 CC for predicting future onset of primary open angle glaucoma and/or normal
 CC ocular tension glaucoma. This involves detecting a mutation in the OPTN
 CC gene coding sequence, specifically a substitution of G for A at position
 CC 619 and/or a substitution of A for G at position 898 of the OPTN coding
 CC sequence. The mutation(s) is detected using a nucleic acid amplification
 CC method using primers specific for the different exons of the coding
 CC sequence, including primers SF11 ADL14977 and SR11 ADL14977 for exon 11.
 XX
 XX Sequence 1150 BP; 381 A; 172 C; 229 G; 368 T; 0 U; 0 Other;
 SQ
 Query Match 1.6%; Score 21; DB 12; Length 1150;
 Best Local Similarity 100.0%; Pred. No. 13;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 165 TTTTAAATATCTTTTAAAT 185
 DB 1006 TTTTAAATATCTTTTAAAT 1026
 RESULT 42
 ID ADE13891
 AC ADE13891 standard; DNA; 46951 BP.
 AC ADE13891;
 XX
 DT 29-JAN-2004 (first entry)
 XX
 DE Human optineurin gene.
 XX
 KW Human; optineurin; ds; gene; ophthalmological;
 KW single nucleotide polymorphism; SNP; glaucoma;
 KW progressive ocular hypertensive disorder; glaucoma related disorder.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT variation replace(391,G)
 FT /*tag= a
 FT /standard_name= "Single nucleotide polymorphism"
 FT variation replace(691,G)
 FT /*tag= b
 FT /standard_name= "Single nucleotide polymorphism"
 FT variation replace(709,G)
 FT /*tag= c
 FT /standard_name= "Single nucleotide polymorphism"
 FT variation replace(887,A)
 FT /*tag= d
 FT /standard_name= "Single nucleotide polymorphism"
 FT variation replace(894,T)
 FT /*tag= e
 FT /standard_name= "Single nucleotide polymorphism"
 FT variation replace(987,C)
 FT /*tag= f
 FT /standard_name= "Single nucleotide polymorphism"
 FT variation replace(1112,C)
 FT /*tag= g
 FT /standard_name= "Single nucleotide polymorphism"
 FT variation replace(1505,CC)
 FT /*tag= h
 FT /standard_name= "Single nucleotide polymorphism"
 FT variation replace(1606,A)
 FT /*tag= i
 FT /standard_name= "Single nucleotide polymorphism"
 FT variation replace(2405,T)
 FT /*tag= j
 FT /standard_name= "Single nucleotide polymorphism"
 FT variation replace(2606,G)
 FT /*tag= k
 FT /standard_name= "Single nucleotide polymorphism"
 FT

FT variation replace(3313,A)
FT /tag= 1
FT /standard name= "Single nucleotide polymorphism"
FT variation replace(3555,TT)
FT /tag= m
FT /standard name= "Single nucleotide polymorphism"
FT variation replace(3625,G)
FT /tag= n
FT /standard name= "Single nucleotide polymorphism"
FT variation replace(3629,C)
FT /tag= o
FT /standard name= "Single nucleotide polymorphism"
FT variation replace(3882,TT)
FT /tag= p
FT /standard name= "Single nucleotide polymorphism"
FT variation replace(3988,T)
FT /tag= q
FT /standard name= "Single nucleotide polymorphism"
FT variation replace(4452,A)
FT /tag= r
FT /standard name= "Single nucleotide polymorphism"
XX US2003190617-A1.
XX
XX
XX 09-OCT-2003.
XX
XX 06-MAR-2002; 2002US-00091281.
XX
XX 06-MAR-2002; 2002US-00091281.
XX
XX (SIEE/) SI E.
XX (RAYM/) RAYMOND V.
XX (MORI/) MORISSETTE J.
XX
XX Raymond V, Morissette J, Si E;
XX WPI; 2003-864168/80.
XX
XX New nucleic acid sequences of the optineurin gene are useful to detect
XX polymorphisms particularly single nucleotide polymorphisms in the
XX optineurin promoter to diagnose, prognose and treat glaucoma and related
XX disorders.
XX
XX Disclosure; SEQ ID NO 2; 159pp; English.
XX
XX The invention relates to an isolated nucleic acid (N1) comprising at
XX least 20 but not more than 1500 consecutive nucleotides of the optineurin
XX promoter appearing as ADB1390. Also included are the optineurin promoter
XX operably linked to a heterologous nucleic acid, a nucleic acid capable of
XX detecting a single nucleotide polymorphism (SNP) in the optineurin
XX promoter, a host cell comprising the promoter operably linked to a
XX heterologous sequence, diagnosing or prognosing glaucoma in a sample
XX obtained from a cell or bodily fluid (comprising detecting a polymorphism
XX in a promoter region of the optineurin gene, associated with a glaucoma
XX phenotype), detecting a SNP sequence variation in a sample containing
XX DNA, detecting the presence of an optineurin promoter sequence variation
XX in a sample containing DNA, determining the presence or increased
XX susceptibility to glaucoma or to a progressive ocular hypertensive
XX disorder resulting in loss of visual field in a patient (or the severity
XX or progression of glaucoma in a patient, comprising providing
XX amplification reaction primers that direct amplification of a selected
XX nucleic acid region containing the variation within the optineurin
XX promoter and amplifying the DNA) and detecting a polymorphism (comprising
XX obtaining a sample containing human genomic DNA, providing a nucleic acid
XX capable of detecting a SNP located within an optineurin promoter, and
XX detecting the polymorphism). The invention is used to diagnose and
XX prognose glaucoma and also to treat glaucoma related disorders. The
XX present sequence is the optineurin gene.
XX
XX Sequence 46951 BP; 12703 A; 10108 C; 10051 G; 14089 T; 0 U; 0 Other;
SQ

Query Match 1.6%; Score 21; DB 10; Length 46951;
Best Local Similarity 100.0%; Pred. No. 13;

Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 165 TTTTAAATATCTTTTAAAT 185
Db 30767 TTTTAAATATCTTTTAAAT 30787
RESULT 43
AAC67288
ID AAC67288 standard; DNA; 28 BP.
XX AAC67288;
XX AC
XX DT 09-APR-2001 (first entry)
XX DE Human Siah-1alpha PCR primer SEQ ID NO: 42.
XX KW Human; protein degradation; siah-mediated degradation protein; SMDP;
KW SCP-complex protein; SCP; siah-1alpha; Siah-1 interacting protein; SIP;
KW Skp1-associated F-box protein; SAF-1; SAF-2; SAD; cancer; cell division;
KW Skp1-associated destruction-box protein; inflammatory disease;
KW PCR primer; ss.
XX OS Homo sapiens.
XX PN WO200077207-A2.
XX PD 21-DEC-2000.
XX PF 09-JUN-2000; 2000WO-US015873.
XX PR 11-JUN-1999; 99US-00330517.
XX PA (BURN-) BURNHAM INST.
XX PI Reed JC, Matsuzawa S;
XX DR WPI; 2001-071273/08.
XX Siah-Mediated Degradation Protein, useful for drug screening, for
XX therapeutic applications and for functional genomics.
XX Example 2; Page 58; 121pp; English.
XX The present invention provides the protein and coding sequences of
XX several siah-mediated degradation proteins and SCP-complex proteins.
XX These are designated Siah-1alpha, Siah-1 interacting protein (SIP), which
XX encodes two proteins due to alternative splicing (SIP-L and SIP-S), Skp1-
XX associated F-box protein-alpha and beta and -2 (SAF-1alpha, SAF-1beta
XX and SAF-2) and Skp1-associated destruction-box protein (SAD). The
XX proteins and their coding sequences are useful in the diagnosis and
XX treatment of cancers, disorders where too little cell division occurs
XX such as bone marrow aplasia, immunodeficiencies and inflammatory
XX diseases including sepsis, fibrosis, arthritis and graft versus host
XX disease
XX Sequence 28 BP; 9 A; 4 C; 8 G; 7 T; 0 U; 0 Other;
SQ
Query Match 1.6%; Score 20; DB 4; Length 28;
Best Local Similarity 100.0%; Pred. No. 41;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 236 GGACTTATGGCATGTAAACA 255
Db 9 GGACTTATGGCATGTAAACA 28
RESULT 44
ACA55799
ID ACA55799 standard; cDNA; 257 BP.
XX ACA55799;
XX

DT 06-JUN-2003 (first entry)
 XX Human signalling pathway polynucleotide probe SEQ ID NO 397.
 DE Human; probe; ss; array element; Parkinson's disease;
 XX signalling pathway polynucleotide; cancer; adenocarcinoma; leukaemia;
 KW immunopathy; AIDS; asthma; neuropathy; Alzheimer's disease; microarray.
 KW
 XX Homo sapiens.
 OS
 XX US6500938-B1.
 PN
 XX 31-DEC-2002.
 PD
 XX 30-JAN-1998; 98US-00016434.
 PF
 XX 30-JAN-1998; 98US-00016434.
 PR
 XX (INCY-) INCYTE GENOMICS INC.
 PA
 XX Au-Young J, Seilhamer JJ;
 PI
 XX WPI; 2003-352189/33.
 DR
 XX Combination of polynucleotide probes, useful as array elements in a
 PT microarray for monitoring the expression of a number of target
 PT polynucleotides.
 PT
 XX Claim 1; SEQ ID NO 397; 65pp; English.
 PS
 CC The invention relates to a combination which, comprises a number of
 CC polynucleotide probes comprising a sequence selected from one of the 1490
 CC sequences mentioned in the specification. The combination is useful as an
 CC array element in a microarray for monitoring the expression of a number
 CC of target polynucleotides. The microarray is particularly useful in the
 CC diagnosis and treatment of cancer and immunopathology and neuropathology.
 CC The microarray is useful in diagnostics and treatment regimens, drug
 CC discovery and development, toxicological and carcinogenicity studies,
 CC forensics and pharmacogenomics. The microarray is also useful for
 CC monitoring progression of diseases and for developing sophisticated
 CC profiles for the effects of currently available therapeutic drugs. The
 CC combination is also useful for purifying a subpopulation of mRNAs, cDNAs
 CC and genomic fragments and in research and diagnostic applications. The
 CC array can detect changes in expression in a large number of genes coding
 CC for different signalling pathway populations which can be used to diagnose
 CC various diseases including cancer e.g. adenocarcinoma and leukaemia.
 CC immunopathies e.g. AIDS and asthma, neuropathies e.g. Alzheimer's disease
 CC and Parkinson's disease. The present sequence represents a polynucleotide
 CC probe of the invention. Note: The sequence data for this patent did not
 CC form part of the printed specification but was obtained in electronic
 CC format directly from USPTO at
 CC seqdata.uspto.gov/sequence.html?docID=06500938B1
 CC
 XX Sequence 257 BP; 59 A; 75 C; 63 G; 60 T; 0 U; 0 Other;
 SQ
 Query Match 1.6%; Score 20; DB 10; Length 257;
 Best Local Similarity 100.0%; Pred. No. 41;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 850 GACTGGGTGATGATGCAGTC 869
 Db 222 GACTGGGTGATGATGCAGTC 241
 RESULT 45
 ADI55595
 ID ADI55595 standard; DNA; 257 BP.
 XX
 AC ADI55595;
 XX
 XX 22-APR-2004 (first entry)
 DT
 XX Human polynucleotide probe #397.
 DE

XX Human; probe; ss; receptor-like polypeptide; transducing polypeptide;
 KW effector-like polypeptide; cancer; immunopathology; neuropathology;
 KW drug development; toxicology; carcinogenicity;
 KW signalling pathway polypeptide; adrenal gland; bladder; bone;
 KW bone marrow; brain; breast; cervix; tumour; immunopathology; AIDS;
 KW diabetes; pancreatitis; osteoporosis; ulcerative colitis; neuropathology;
 KW dementia; amnesia; epilepsy; Alzheimer's disease; depression.
 XX
 OS Homo sapiens.
 XX US2004010136-A1.
 PN
 XX 15-JAN-2004.
 PD
 XX 26-NOV-2002; 2002US-00305720.
 PF
 XX 30-JAN-1998; 98US-00016434.
 PR
 XX (INCY-) INCYTE GENOMICS INC.
 PA
 XX Au-Young J, Seilhamer JJ;
 PI
 XX WPI; 2004-090520/09.
 DR
 XX New composition comprising polynucleotide probes, useful as array
 PT elements in a microarray for monitoring the expression of target
 PT polynucleotides or purifying a subpopulation of mRNAs, cDNA, or genomic
 PT fragments.
 PT
 XX Claim 6; SEQ ID NO 397; 73pp; English.
 PS
 CC The invention relates to a composition of polynucleotide probes
 CC comprising first polynucleotide probes comprising at least a portion of a
 CC gene encoding a receptor-like polypeptide, second polynucleotide probes
 CC comprising at least a portion of a gene encoding a transducing
 CC polypeptide and third polynucleotide probes comprising at least a portion
 CC of a gene encoding an effector-like polypeptide. The probes of the
 CC composition are useful as array elements in a microarray for monitoring
 CC the expression of target polynucleotides. The microarray is useful in the
 CC diagnosis and treatment of cancer, an immunopathology or a
 CC neuropathology. It can also be used for drug discovery and development,
 CC toxicological and carcinogenicity studies, forensics or pharmacogenomics.
 CC Microarrays can also be used for monitoring the progression of diseases
 CC that may be associated with the altered expression of signalling pathway
 CC polypeptides. The composition can also be used to purify a subpopulation
 CC of mRNAs, cDNAs, or genomic fragments in a sample. The expression profile
 CC is also useful for the diagnosis and treatment of cancer, e.g. cancers of
 CC the adrenal gland, bladder, bone, bone marrow, brain, breast or cervix,
 CC an immunopathology, e.g. AIDS, diabetes, pancreatitis, osteoporosis or
 CC ulcerative colitis, or a neuropathology, e.g. dementia, amnesia,
 CC epilepsy, Alzheimer's disease or depression. This sequence represents a
 CC human polynucleotide probe of the invention. Note: The sequence data for
 CC this patent did not form part of the printed specification but was
 CC obtained in electronic format directly from USPTO at
 CC seqdata.uspto.gov/sequence.html.
 CC
 XX Sequence 257 BP; 59 A; 75 C; 63 G; 60 T; 0 U; 0 Other;
 SQ
 Query Match 1.6%; Score 20; DB 12; Length 257;
 Best Local Similarity 100.0%; Pred. No. 41;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 850 GACTGGGTGATGATGCAGTC 869
 Db 222 GACTGGGTGATGATGCAGTC 241
 RESULT 46
 ABL08593
 ID ABL08593 standard; cDNA; 834 BP.
 XX
 AC ABL08593;

XX DT 26-MAR-2002 (first entry)
 XX DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 20261.
 XX PA Drosophila; developmental biology; cell signalling; insecticide;
 KW pharmacological; gene; ss.
 XX OS Drosophila melanogaster.
 XX PN WO200171042-A2.
 XX PD 27-SEP-2001.
 XX PF 23-MAR-2001; 2001WO-US009231.
 XX PR 23-MAR-2000; 2000US-0191637P.
 XX PR 11-JUL-2000; 2000US-00614150.
 XX PA (PEKE) PE CORP NY.
 XX PI Venter JC, Adams M, Li PWD, Myers EW;
 XX DR WPI; 2001-656860/75.
 XX DR P-PSDB; ABB64490.
 XX PT New isolated nucleic acid detection reagent for detecting 1000 or more
 PT genes from Drosophila and for elucidating cell signalling and cell-cell
 PT interactions.
 XX PS Claim 1; SEQ ID NO 20261; 21pp + Sequence Listing; English.
 XX CC The invention relates to an isolated nucleic acid detection reagent
 CC capable of detecting 1000 or more genes from Drosophila. The invention is
 CC useful in developmental biology and in elucidating cell signalling and
 CC cell-cell interactions in higher eukaryotes for the development of
 CC insecticides, therapeutics and pharmaceutical drugs. The invention
 CC discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA
 CC sequences (ABL01840-ABL16175) and the encoded proteins (ABB57737-
 CC ABB72072). The sequence data for this patent did not form part of the
 CC printed specification, but was obtained in electronic format directly
 CC from WIPO at ftp.wipo.int/pub/published_pct_sequences
 XX SQ Sequence 834 BP; 255 A; 180 C; 165 G; 234 T; 0 U; 0 Other;
 Query Match 1.6%; Score 20; DB 4; Length 834;
 Best Local Similarity 100.0%; Pred. No. 41;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 247 ATGTAACATTATTATATAA 266
 Db 49 ATGTAACATTATTATATAA 68
 RESULT 47
 ADR25256
 ID ADR25256 standard; DNA; 975 BP.
 XX AC ADR25256;
 XX DT 21-OCT-2004 (first entry)
 XX DE Breast cancer prognosis marker #1117.
 XX KW ds; breast cancer; prognosis; gene expression; diagnosis.
 XX OS Homo sapiens.
 XX PN WO2004065545-A2.
 XX PD 05-AUG-2004.
 XX PF 15-JAN-2004; 2004WO-US001100.

XX PR 15-JAN-2003; 2003US-00342887.
 XX PA (ROSE-) ROSETTA INPHARMATICS LLC.
 XX PI (NECA-) NETHERLANDS CANCER INST.
 XX PI Van't Veer LJ, He Y;
 XX DR WPI; 2004-593473/57.
 XX PT Classifying a breast cancer patient according to prognosis comprises
 PT determining the similarity between the level of expression of each of
 PT five genes in a cell sample taken from patient, to control levels.
 XX PS Disclosure; SEQ ID NO 1117; 226pp; English.
 XX CC The invention relates to a method of classifying a breast cancer patient
 CC according to prognosis by determining the similarity between the level of
 CC expression of each of five genes for which markers are listed in the
 CC specification, in a cell sample taken from the breast cancer patient, to
 CC control levels of expression for each respective five genes to obtain a
 CC patient similarity value. The methods are useful for classifying a breast
 CC cancer patient according to prognosis. Kits and computer program products
 CC are useful for data analysis using the diagnostic, prognostic and
 CC statistical methods of the invention. This sequence corresponds to a
 CC marker used in the method of the invention.
 XX SQ Sequence 975 BP; 188 A; 316 C; 271 G; 200 T; 0 U; 0 Other;
 Query Match 1.6%; Score 20; DB 13; Length 975;
 Best Local Similarity 100.0%; Pred. No. 41;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 850 GACTGGTGATGATGCAGTC 869
 Db 649 GACTGGTGATGATGCAGTC 668
 RESULT 48
 ACC50292
 ID ACC50292 standard; cDNA; 2240 BP.
 XX AC ACC50292;
 XX DT 12-JUN-2003 (first entry)
 XX DE Breast cancer associated cDNA sequence SEQ ID NO:424.
 XX KW Human; breast cancer; cytostatic; gene therapy; gene; ss.
 XX OS Homo sapiens.
 XX PN WO2003004989-A2.
 XX PD 16-JAN-2003.
 XX PF 21-JUN-2002; 2002WO-US019669.
 XX PR 21-JUN-2001; 2001US-0299887P.
 XX PR 27-JUN-2001; 2001US-0301572P.
 XX PR 18-JUL-2001; 2001US-0306501P.
 XX PR 25-SEP-2001; 2001US-0325002P.
 XX PR 05-MAR-2002; 2002US-0362585P.
 XX PR 14-MAY-2002; 2002US-0380391P.
 XX PA (MILL-) MILLENIUM PHARM INC.
 XX PI Lillie J, Gannavarapu M, Glatt K, Hoersh S, Kamatkar S;
 PI Mertens M, Monahan JE, Myer V, Wang Y, Xu Y, Zhao X, Meyers RE;
 PI Bast RC, Hortobagyi GN, Fuztai L, Meric F, Sahin A, Mills GB;
 XX WPI; 2003-210381/20.
 XX DR P-PSDB; ABR47593.

XX Breast cancer diagnosis or treatment by comparing the level of expression
PT of a marker in a patient sample with that in the control non-breast
PT cancer sample.
XX
XX Claim 1; SEQ ID NO 424; 128pp; English.
XX
XX The present invention describes a method for assessing whether a patient
CC is afflicted with breast cancer. The method comprises comparing the level
CC of expression of a marker (gene/polypeptide see ACC50076 to ACC50334 and
CC ABR47386 to ABR47632) in a patient sample and the normal level of
CC expression of the marker in a control non-breast cancer sample, where a
CC significant increase in the level of expression of the marker in the
CC patient sample and the normal level is an indication that the patient is
CC afflicted with breast cancer. The breast cancer associated sequences from
CC the present invention have cytostatic activities and can be used in gene
CC therapy. The method is useful for diagnosing and treating breast cancer.
CC N.B. The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 2240 BP; 429 A; 676 C; 637 G; 498 T; 0 U; 0 Other;
SQ
Query Match 1.6%; Score 20; DB 8; Length 2240;
Best Local Similarity 100.0%; Pred. No. 41;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 850 GACTGGGTGATGATGCAGTC 869
DB 1175 GACTGGGTGATGATGCAGTC 1194
RESULT 49
ADP13401
ID ADP13401 standard; DNA; 2240 BP.
XX
XX ADP13401;
XX
XX 26-AUG-2004 (first entry)
XX
XX Renal cell carcinoma differentially expressed gene #137.
XX
XX ds; diagnosis; non-blood disease; solid tumor; gene expression;
KW peripheral blood mononuclear cell; renal cell carcinoma; prostate cancer;
KW head/neck cancer; differential expression.
XX
XX Homo sapiens.
XX
XX WO2004048933-A2.
XX
XX 10-JUN-2004.
XX
XX 21-NOV-2003; 2003WO-US037481.
XX
XX 21-NOV-2003; 2002US-0427982P.
PR 03-APR-2003; 2003US-0459782P.
XX
XX (AMEP) WYETH.
PA (TWIN/) TWINE N C.
PA (BURC/) BURCZYNSKI M E.
PA (TREF/) TREFICCHIO W L.
PA (DORN/) DORNER A.
PA (STOV/) STOVER J A.
PA (SLON/) SLONI D K.
XX
XX Twine NC, Burczynski ME, Trepicchio WL, Dornier A, Stover JA;
PI Sloni DK;
XX
XX WPI; 2004-460799/43.
XX
XX Diagnosing non-blood disease such as solid tumor, involves comparing
PT differential expression profile of specific genes in peripheral blood
PT sample of subject with reference expression profile of specific genes.

XX Disclosure; SEQ ID NO 137; 350pp; English.
XX
XX The invention relate to a method of diagnosing (M1) non-blood disease
CC such as solid tumor by providing peripheral blood sample of human having
CC non-blood disease, and comparing an expression profile of specific genes
CC in the peripheral blood sample to reference expression profile of the
CC genes, where each of the genes is differentially expressed in peripheral
CC blood mononuclear cells (PBMCs) of patients having the disease as
CC compared to PBMCs of normal humans. The method is useful for diagnosing
CC non-blood disease such as solid tumor. The solid tumor is chosen from
CC renal cell carcinoma (RCC), prostate cancer and head/neck cancer. The
CC peripheral blood sample comprises enriched PBMCs. The peripheral blood
CC sample is a whole blood sample (Claimed). (M1) is useful for identifying
CC genes that are differentially expressed in peripheral blood samples
CC isolated at different stages of progression, development or treatment of
CC RCC and/or other solid tumors. This sequence corresponds to a gene that
CC is differentially expressed and detected by the method of the invention.
CC (Note: this sequence is not given as part of the printed specification
CC but was obtained from WIPO in electronic format at
CC ftp.wipo.int/pub/published_pct_sequences).
XX
XX Sequence 2240 BP; 429 A; 676 C; 637 G; 498 T; 0 U; 0 Other;
SQ
Query Match 1.6%; Score 20; DB 12; Length 2240;
Best Local Similarity 100.0%; Pred. No. 41;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 850 GACTGGGTGATGATGCAGTC 869
DB 1175 GACTGGGTGATGATGCAGTC 1194
RESULT 50
ADP14122
ID ADP14122 standard; DNA; 2240 BP.
XX
XX ADP14122;
XX
XX 21-OCT-2004 (first entry)
XX
XX Human NF-kappaB pathway-associated gene SeqID123.
XX
XX NF-kappaB pathway; antiinflammatory; cytostatic; hepatotropic; virucide;
KW antiarthritic; antirheumatic; gastrointestinal-Gen; antiasthmatic;
KW antiarteriosclerotic; immunomodulator; cerebroprotective; vasotropic;
KW immunosuppressive; vulnery; gene therapy; immune disorder;
KW inflammatory disorder; NF-kappaB regulation; cancer; aberrant apoptosis;
KW hepatic disorder; Hodgkin's lymphoma; haematopoietic tumour;
KW hyper-igm syndrome; hypohidrotic ectodermal dysplasia;
KW X-linked anhidrotic ectodermal dysplasia; immunodeficiency;
KW viral infection; HIV-1; HTLV-1; hepatitis B; hepatitis C; EBV; influenza;
KW viral replication; host cell survival; evasion of immune response;
KW rheumatoid arthritis; inflammatory bowel disease; colitis; asthma;
KW atherosclerosis; cachexia; euthyroid sick syndrome; stroke; EAE;
KW autoimmune disorder; hyper immune activity;
KW aberrant acute phase response; hypercongenital condition;
KW necrotic lesion; wound; organ transplant rejection;
KW aberrant signal transduction; proliferating disorder; cancer;
KW HIV propagation; gene; ds; human.
XX
XX Homo sapiens.
XX
XX WO2004065577-A2.
XX
XX 05-AUG-2004.
XX
XX 13-JAN-2004; 2004WO-US000798.
XX
XX 14-JAN-2003; 2003US-0440068P.
PR 12-MAY-2003; 2003US-0469757P.
XX
XX (BRIM) BRISTOL-MYERS SQUIBB CO.
PA

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OM nucleic - nucleic search, using sw model

Run on: April 25, 2005, 00:27:47 ; Search time 4597 Seconds
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10549.027 Million cell updates/sec

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Scoring table: OLIGO NUC
Gapop 60.0 , Gapext 60.0

Searched: 34239544 seqs, 19032134700 residues

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- 2: gb_est2:*
- 3: gb_hc:*
- 4: gb_est3:*
- 5: gb_est4:*
- 6: gb_est5:*
- 7: gb_est6:*
- 8: gb_gss1:*
- 9: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1062	83.4	1221	7	U70056 U70056 Soar
2	958	75.2	1360	3	CR607323 full-length
3	958	75.2	1857	3	CR614925 full-length
4	894	70.2	1287	3	CR598465 full-length
5	849	66.6	849	9	AY402255 Homo sapi
6	685	53.8	1576	5	CR593197 full-length
7	666	52.3	714	5	BQ447177 UI-H-EUL
8	666	52.3	769	9	BQ447177 UI-H-EUL
9	645	50.6	849	9	AY402256 Pan trogl
10	642	50.4	812	1	AU119916
11	637	50.0	859	5	EX366404
12	633	49.7	693	5	BU662334
13	624	49.0	824	4	BG619351
14	622	48.8	622	7	CV030563
15	615	48.3	649	2	BF446537
16	611	48.0	779	1	AI936347
17	590	46.3	735	4	BI560892
18	561	44.0	778	1	AI971258
19	525	41.2	980	6	CD251717
20	502	39.4	586	7	CK8322873
21	499	39.2	734	1	AU138740
22	498	39.1	852	5	EX463976
23	497	39.0	969	5	EX390856
24	494	38.8	637	1	AI681134

98	274	21.5	325	7	F10277	F10277 HSC3CG052 n	171	77	6.0	544	7	CF896796	CF896796 A0215F10-
99	274	21.5	795	4	BG496349	BG496349 602541037	172	77	6.0	545	5	BX529126	BX529126 BX529126
100	272	21.4	323	1	AI351910	AI351910 qg22b09.x	173	77	6.0	560	7	CF896134	CF896134 A0206G11-
101	265	20.8	443	6	C16944	C16944 C16944 Clon	174	77	6.0	591	4	BG083073	BG083073 H3084C01-
102	265	20.8	968	5	BX355840	BX355840 BX355840	175	77	6.0	615	7	CF898807	CF898807 A0244G07-
103	258	20.3	399	1	AA829262	AA829262 qg07a02.s	176	77	6.0	659	2	AW231069	AW231069 uo70d10.y
104	256	20.1	386	1	AA258606	AA258606 zrf6c05.s	177	77	6.0	904	4	BI561883	BI561883 G03255752
105	254	19.9	317	1	AA966352	AA966352 crf9508.s	178	77	6.0	953	6	CA980024	CA980024 AGENCOURT
106	254	19.9	437	1	AV654246	AV654246 AV654246	179	76	6.0	831	4	BG163936	BG163936 602343115
107	252	19.8	450	1	AI167464	AI167464 ox68a08.s	180	75	5.9	849	9	AY402257	AY402257 Mus muscu
108	247	19.4	277	1	AI783762	AI783762 tu45d11.x	181	74	5.8	341	4	BG899050	BG899050 HOA23-1-D
109	246	19.4	409	1	AA455093	AA455093 aa04f04.s	182	73	5.7	493	7	N80959	N80959 zai2b08.r1
110	246	19.3	434	7	R17298	R17298 ygl2b11.r1	183	71	5.6	685	6	CD469824	CD469824 LeukoS2.5
111	246	19.3	492	1	AA923663	AA923663 ch08e09.s	184	68	5.3	334	2	BE674633	BE674633 7e03b12.x
112	240	18.8	469	1	AI952715	AI952715 wq48a12.x	185	65	5.1	836	6	CB961599	CB961599 AGENCOURT
113	237	18.6	359	2	BF928182	BF928182 CM4-NT021	186	63	4.9	241	4	BG997395	BG997395 RC4-HT103
114	238	18.3	412	7	N36671	N36671 yx91e10.r1	187	62	4.9	462	2	AW657049	AW657049 109555 MA
115	238	17.9	477	6	CB161851	CB161851 K-EST0221	188	59	4.6	654	7	CO679805	CO679805 DG11-1060
116	213	16.7	419	2	BF827041	BF827041 RC3-HN002	189	59	4.6	997	4	BG436508	BG436508 602509182
117	212	16.6	380	7	T84679	T84679 yd49g11.r1	190	57	4.5	271	1	AA242857	AA242857 zrf64e03.r
118	210	16.5	338	2	BF807952	BF807952 RC3-CI004	191	53	4.2	456	6	CB740493	CB740493 AMGNNUC.M
119	206	16.2	986	5	BX337711	BX337711 BX337711	192	53	4.2	462	6	CB736105	CB736105 AMGNNUC.N
120	205	16.1	490	7	T74315	T74315 yc84d05.r1	193	53	4.2	685	7	CK839809	CK839809 UI-R-B01-
121	205	16.1	723	1	AI953523	AI953523 wq29g12.x	194	52	4.1	319	1	AI538784	AI538784 tp54e06.x
122	204	16.0	640	2	AW750277	AW750277 PMO-BT058	195	52	4.1	190	2	BF769925	BF769925 RC3-IT001
123	204	16.0	844	7	CF593353	CF593353 AGENCOURT	196	50	3.9	582	1	AI239983	AI239983 qh33e03.x
124	200	15.7	517	7	T89028	T89028 yc84d05.s1	197	49	3.8	548	1	AA930482	AA930482 vz44f12.r
125	199	15.6	334	5	BUS21256	BUS21256 AGENCOURT	198	48	3.8	299	9	CG514737	CG514737 OST68637
126	192	15.1	411	2	BF808607	BF808607 CM1-CI013	199	47	3.7	431	9	CG504911	CG504911 OST33626
127	189	14.8	419	2	AW581174	AW581174 CM2-LT005	200	47	3.7	431	9	CG510424	CG510424 OST62125
128	185	14.5	607	2	AW593893	AW593893 hg28f02.x	201	47	3.7	443	9	CG662362	CG662362 OST445714
129	184	14.4	418	7	N31049	N31049 vx63a01.r1	202	47	3.7	446	9	CG542510	CG542510 OST137120
130	173	13.6	340	2	AW770577	AW770577 rl86h04.x	203	47	3.7	482	9	CG542510	CG542510 OST137120
131	168	13.2	678	7	CN360509	CN360509 170004706	204	47	3.7	507	9	CG553351	CG553351 OST18612
132	161	12.6	229	6	AW003281	AW003281 wq64h09.x	205	47	3.7	510	9	CG583428	CG583428 OST225535
133	161	12.6	426	1	C18219	C18219 C18219 Huma	206	47	3.7	553	9	CG577085	CG577085 OST12499
134	159	12.5	181	7	T90930	T90930 yd49g11.s1	207	47	3.7	669	9	CG580439	CG580439 OST19796
135	157	12.3	981	7	CF593834	CF593834 AGENCOURT	208	47	3.7	669	9	CG580439	CG580439 UI-M-EV0-
136	156	12.2	661	4	BG434523	BG434523 602506567	209	47	3.7	1048	5	BUS20275	BUS20275 AGENCOURT
137	155	12.2	300	1	AU099135	AU099135 AU099135	210	47	3.7	1194	5	BQ939487	BQ939487 AGENCOURT
138	153	12.0	174	1	AI886230	AI886230 wm08c12.x	211	47	3.7	1194	5	BQ939487	BQ939487 PMO-ET020
139	153	12.0	281	7	R28432	R28432 yhs0f04.r1	212	47	3.7	1194	5	BQ939487	BQ939487 PMO-ET020
140	150	11.8	1042	7	CK232523	CK232523 ILLUMIGEN	213	46	3.6	125	7	CV359633	CV359633 qd55e08.x
141	146	11.5	479	2	BF895068	BF895068 RC1-MT013	214	46	3.6	277	1	AI191563	AI191563 qd55e08.x
142	139	10.9	893	4	BG392014	BG392014 602409968	215	45	3.5	513	6	CA561517	CA561517 K0288B10-
143	138	10.8	369	2	BF858347	BF858347 RC5-F019	216	45	3.5	779	7	CF723667	CF723667 UI-M-GZ0-
144	134	10.5	557	2	AW196873	AW196873 xdi4907.x	217	45	3.5	100	9	CG585108	CG585108 OST232186
145	134	10.4	290	7	H83742	H83742 yv84d01.r1	218	44	3.5	541	9	CG537764	CG537764 OST127034
146	132	10.4	397	2	BF107171	BF107171 601824241	219	44	3.5	845	7	CV116728	CV116728 AGENCOURT
147	129	10.1	180	7	TL1012	TL1012 hbc420 Huma	220	44	3.4	390	6	CV116728	CV116728 AGENCOURT
148	128	10.1	250	7	TL2004	TL2004 A805F Heart	221	43	3.4	789	7	CV116728	CV116728 AGENCOURT
149	123	9.7	445	1	AA224095	AA224095 zrl4310.x	222	43	3.4	789	7	CV116728	CV116728 AGENCOURT
150	121	9.5	343	1	AA216263	AA216263 hp0817.be	223	41	3.2	172	1	AA411301	AA411301 zv24q05.r
151	119	9.3	376	1	AI150855	AI150855 qb68f07.x	224	41	3.2	342	6	CB693591	CB693591 AMGNNUC.S
152	118	9.3	484	1	AI696629	AI696629 tx68f12.x	225	41	3.2	486	1	AI650868	AI650868 wb25c10.x
153	116	9.1	319	1	AA987413	AA987413 qg93a12.s	226	41	3.2	498	1	AA267965	AA267965 va04c05.f
154	112	8.8	468	2	BF855131	BF855131 RC3-FN020	227	40	3.1	621	7	CG777231	CG777231 PMO-CT064
155	109	8.6	248	7	TL1029	TL1029 hbc472 Huma	228	39	3.1	347	2	BF759823	BF759823 PMO-CT064
156	109	8.6	415	1	AI379061	AI379061 tc59a04.x	229	39	3.1	697	2	AW390258	AW390258 CM4-ST018
157	108	8.5	223	7	TL2005	TL2005 A805R Heart	230	38	3.0	296	9	CG481565	CG481565 OST14104
158	107	8.4	877	4	BI762319	BI762319 603049461	231	38	3.0	313	8	AZ424720	AZ424720 IM0204024
159	102	8.0	467	2	BF894509	BF894509 RC1-MT013	232	38	3.0	419	9	CG667617	CG667617 OST461562
160	99	7.8	319	7	FL2666	FL2666 HSC3CG051 n	233	38	3.0	427	6	CB795032	CB795032 AMGNNUC.N
161	96	7.5	440	2	BF080907	BF080907 233671 WA	234	38	3.0	464	9	CG525680	CG525680 ut98f11.y
162	96	7.5	442	2	BF080901	BF080901 233665 MA	235	38	3.0	464	9	CG525680	CG525680 ut98f11.y
163	94	7.4	809	5	BU746475	BU746475 CH3#004.D	236	38	3.0	472	2	BF016262	BF016262 yv39e06.y
164	90	7.1	452	5	BQ373377	BQ373377 RCS-F019	237	38	3.0	478	1	AA789533	AA789533 yw61a04.r
165	88	6.9	707	8	AZ960755	AZ960755 2M0228K22	238	38	3.0	517	4	BG100014	BG100014 ux31a12.y
166	88	6.9	812	1	BI752339	BI752339 603028066	239	38	3.0	520	1	AA638338	AA638338 V198605.r
167	85	6.7	151	4	BI752339	BI752339 aal6g04.r	240	38	3.0	536	9	CG575071	CG575071 OST208518
168	79	6.2	442	4	BG899783	BG899783 HOA32-1-G	241	38	3.0	541	1	AA413470	AA413470 vc54b09.s
169	78	6.1	847	2	BF242479	BF242479 6018f6047	242	38	3.0	542	9	CG563878	CG563878 OST187511
170	77	6.0	450	2	AW988034	AW988034 uf91c05.y	243	38	3.0	553	7	CN696374	CN696374 E0378D05-

244	38	3.0	583	4	BM537526	BM537526 ha83d12.9	317	30	2.4	524	1	AA445471	AA445471 v557c10.r
245	38	3.0	596	1	AA080210	mm34h08.r	318	30	2.4	525	6	CA558835	CA558835 K0250B10-
246	38	3.0	656	1	AA170429	ms69e09.r	319	30	2.4	527	1	AA437881	AA437881 vQ20h11.s
247	38	3.0	673	2	W08942	ma60h11.r1	320	30	2.4	544	2	BF780988	BF780988 602106617
248	38	3.0	830	2	BF180760	601804878	321	30	2.4	551	1	AA656873	AA656873 v551a10.s
249	38	3.0	925	1	AI558189	vk25e06.y	322	30	2.4	558	9	AY407963	AY407963 Mub muscu
250	37	2.9	126	9	CG589118	OST240899	C 323	30	2.4	567	1	AI1178202	AI1178202 EST221867
251	36	2.8	447	6	CB746687	AMGNNUC.N	324	30	2.4	609	1	AA691043	AA691043 v770f02.s
252	36	2.8	680	1	AA123337	mp94D06.r	325	30	2.4	622	7	CKG18835	CKG18835 mk17b01.y
253	35	2.7	488	1	AA874637	vx81e09.r	326	30	2.4	631	1	AA546965	AA546965 vk68c08.s
254	35	2.7	542	6	CD739545	4027780.1	327	30	2.4	636	1	AA545567	AA545567 v190f02.s
255	35	2.7	700	7	CO422558	GGEZHT100	328	30	2.4	649	4	BG083831	BG083831 H3092E12-
256	35	2.7	716	5	BU260826	603504644	329	30	2.4	655	7	CF893001	CF893001 A0117E10-
257	35	2.7	717	5	BU261233	603504646	330	30	2.4	733	4	BI086691	BI086691 6028S0020
258	35	2.7	798	7	CF286310	AGENCOURT	331	30	2.4	745	7	CV103474	CV103474 AGENCOURT
259	35	2.7	819	5	BU120136	603143976	332	30	2.4	810	5	BU939197	BU939197 AGENCOURT
260	35	2.7	930	5	BU112879	603130680	333	30	2.4	831	1	AA794664	AA794664 v74d11.s
261	35	2.7	938	5	BU113489	603129844	334	30	2.4	841	6	CA464705	CA464705 AGENCOURT
262	34	2.7	435	7	CN999973	UNC-Bend	335	30	2.4	900	2	BF233917	BF233917 6020Z4592
263	34	2.7	456	1	AI810587	tu01e11.x	336	30	2.4	990	6	BY761918	BY761918 BY761918
264	33	2.6	357	6	CB813016	AMGNNUC.N	C 337	29	2.3	228	1	AA693211	AA693211 v758a10.s
265	33	2.6	486	2	AW139558	UT-H-B11-	338	29	2.3	522	6	CD731259	CD731259 4040903.1
266	33	2.6	586	1	AA543593	vk25e06.r	339	29	2.3	529	6	CD218223	CD218223 p9r1n.pk0
267	32	2.5	324	1	AA022923	2e72b01.s	340	29	2.3	626	5	EX278548	EX278548 BX278548
268	32	2.5	395	6	CB845436	W2FN-1082	341	29	2.3	627	5	EX278547	EX278547 BX278547
269	32	2.5	474	1	AL780569	AL780569	342	29	2.3	664	6	CB017049	CB017049 p9n1c.pk0
270	32	2.5	583	5	BP216594	BP216594	343	29	2.3	705	1	AA623698	AA623698 vg68h06.s
271	32	2.5	587	1	AL886426	AL886426	344	29	2.3	723	1	AJ393052	AJ393052 v793052
272	32	2.5	591	1	AL797779	AL797779	345	29	2.3	887	1	AA823764	AA823764 v769h10.s
273	32	2.5	604	1	AL637099	AL637099	346	28	2.2	616	6	CD218793	CD218793 p9r1n.pk0
274	32	2.5	614	1	AL895119	AL895119	C 347	28	2.2	928	5	EX340271	EX340271 BX340271
275	32	2.5	615	1	AL846086	AL846086	348	27	2.1	104	2	BE073058	BE073058 MR1-BT054
276	32	2.5	629	1	AL865163	AL865163	349	27	2.1	1142	5	BQ917904	BQ917904 AGENCOURT
277	32	2.5	641	5	BQ391117	NISC.mq16	350	26	2.0	163	1	AI261995	AI261995 GK39a02.x
278	32	2.5	644	1	AL854577	AL854577	C 351	26	2.0	419	5	BU757040	BU757040 UT-1-CFO-
279	32	2.5	644	1	AL882016	AL882016	352	26	2.0	545	4	BA866975	BA866975 dc97a07.y
280	32	2.5	650	1	AL594221	AL594221	353	26	2.0	549	1	AJ657791	AJ657791 AJ657791
281	32	2.5	658	1	AL639501	AL639501	354	26	2.0	568	5	EX675789	EX675789 BX675789
282	32	2.5	666	1	AL656230	AL656230	355	26	2.0	568	5	EX675788	EX675788 BX675788
283	32	2.5	682	1	AL963066	AL963066	356	26	2.0	609	7	CN161210	CN161210 95040 MA
284	32	2.5	691	7	CN079427	EC2BBA16C	C 357	26	2.0	609	7	CN162617	CN162617 952016 MA
285	32	2.5	712	7	CN079426	EC2BBA16C	358	26	2.0	626	5	BQ383804	BQ383804 NISC.mn03
286	32	2.5	777	5	EX698940	EX698940	359	26	2.0	641	2	AW644620	AW644620 cm43C02.w
287	32	2.5	792	7	CR449542	CR449542	360	26	2.0	676	7	CF181241	CF181241 818050 MA
288	32	2.5	811	5	EX776731	EX776731	361	26	2.0	734	5	BP694865	BP694865 BP694865
289	32	2.5	813	5	EX783981	EX783981	362	26	2.0	849	5	BU912024	BU912024 AGENCOURT
290	32	2.5	837	5	EX715858	EX715858	363	26	2.0	895	6	CA787895	CA787895 AGENCOURT
291	32	2.5	842	7	CF217265	AGENCOURT	364	26	2.0	912	2	BF300230	BF300230 6020Z2135
292	32	2.5	853	5	EX776490	EX776490	C 365	25	2.0	631	6	CB456165	CB456165 713387 MA
293	32	2.5	882	5	EX757871	EX757871	366	25	2.0	714	1	AA620169	AA620169 v063402.r
294	32	2.5	884	7	CR584650	CR584650	C 367	25	2.0	953	5	EX357982	EX357982 BX357982
295	32	2.5	885	5	EX770482	EX770482	368	24	1.9	196	5	BQ353712	BQ353712 QV2-HT054
296	32	2.5	902	5	EX715857	EX715857	369	24	1.8	129	9	CG498875	CG498875 OST42381
297	32	2.5	903	5	EX770276	EX770276	370	23	1.8	187	7	H89968	H89968 yv95d09.r1
298	32	2.5	928	5	EX757123	EX757123	371	23	1.8	219	1	AA691092	AA691092 v768a12.s
299	31	2.4	160	7	R57837	F6059 Fetal	372	23	1.8	343	7	R86519	R86519 RABEST213T
300	30	2.4	361	5	BY366879	BY366879	C 373	23	1.8	570	7	CF359801	CF359801 821074 MA
301	30	2.4	399	5	BY156312	BY156312	C 374	23	1.8	712	5	BX330041	BX330041 BX330041
302	30	2.4	409	1	AI894021	mg47e07.y	375	23	1.8	715	9	CE332921	CE332921 t1gr-g88-
303	30	2.4	409	6	CB804680	AMGNNUC.S	376	23	1.8	1480	9	AG280278	AG280278 Mub muscu
304	30	2.4	421	2	BB790376	BB790376	377	23	1.8	422	6	CB173403	CB173403 OR 2007F0
305	30	2.4	425	1	AI385747	mg47e07.x	378	22	1.7	487	2	BF148826	BF148826 uv35d09.x
306	30	2.4	428	1	AA690274	vr81c11.s	379	22	1.7	487	2	BF148826	BF148826 uv35d09.x
307	30	2.4	433	2	BB710533	BB710533	380	22	1.7	600	6	CB173235	CB173235 OR 2010G1
308	30	2.4	440	1	AA239209	mx89e01.r	381	22	1.7	614	6	CD006535	CD006535 vVB087C07
309	30	2.4	440	6	BY548414	BY548414	C 382	22	1.7	659	6	CD712380	CD712380 vVB007A03
310	30	2.4	450	1	AA473951	vc97h10.s	383	22	1.7	677	1	AL646814	AL646814 AL646814
311	30	2.4	455	1	AA672370	vk91c12.s	C 384	22	1.7	700	9	CE236242	CE236242 t1gr-g88-
312	30	2.4	457	1	AI552193	vf57c10.y	385	22	1.7	701	6	CD005005	CD005005 vVB045C09
313	30	2.4	475	5	BQ780239	UT-R-PF0-	386	22	1.7	712	6	CB001431	CB001431 vVB004A07
314	30	2.4	485	1	AA003340	mg47e07.r	387	22	1.7	727	6	CB001607	CB001607 vVB007A03
315	30	2.4	489	1	AA666901	vr85h10.s	C 388	22	1.7	788	8	CC170969	CC170969 1169c10.s
316	30	2.4	495	1	AI154931	ud77e08.r	389	22	1.7	806	8	CC170970	CC170970 1169c10.s

C 390	21	1.6	253	7	CN896149	CN896149	010528AAZ	463	20	1.6	449	7	C0320287	C0320287	CK283622.
C 391	21	1.6	277	7	CN898304	CN898304	010702AAZ	C 464	20	1.6	451	6	CA433304	CA433304	UI-H-COO-
C 392	21	1.6	296	1	AL719998	AL719998	AL719998	465	20	1.6	455	8	R29412	R29412	E1-H-COO-
C 393	21	1.6	297	1	AI629298	AI629298	fc05d01.y	466	20	1.6	463	8	BH739859	BH739859	GF0909.b
C 394	21	1.6	297	1	AL719999	AL719999	AL719999	467	20	1.6	464	5	BQ386188	BQ386188	NISC-mm16
C 395	21	1.6	314	1	AI626604	AI626604	fc05d01.x	468	20	1.6	469	7	CO277527	CO277527	EK125410.
C 396	21	1.6	404	4	BJ649567	BJ649567	BJ649567	469	20	1.6	471	8	BH739433	BH739433	GF14912.b
C 397	21	1.6	411	7	CN777592	CN777592	taf65f105.	C 470	20	1.6	475	6	CA867172	CA867172	ir58d02.x
C 398	21	1.6	456	7	CN868758	CN868758	001117AAO	471	20	1.6	477	1	AV651911	AV651911	AV651911
C 399	21	1.6	457	7	CN557537	CN557537	tae51a12.	C 472	20	1.6	477	6	CD313575	CD313575	STPpu621.
C 400	21	1.6	472	7	CN771954	CN771954	ba004	C 473	20	1.6	479	6	CA672386	CA672386	wlsu2.pko
C 401	21	1.6	499	9	CL536953	CL536953	OB_Ba004	C 474	20	1.6	482	7	CN567479	CN567479	tag10a12.
C 402	21	1.6	500	7	CN558651	CN558651	ta07ae12	C 475	20	1.6	485	2	AM334384	AM334384	S34B5.AGS
C 403	21	1.6	518	7	CN868173	CN868173	010412AAO	C 476	20	1.6	485	7	CO322803	CO322803	EK188946.
C 404	21	1.6	523	4	BJ645886	BJ645886	BJ645886	C 477	20	1.6	484	7	CO417570	CO417570	Mdftt3031
C 405	21	1.6	523	8	BZ111876	BZ111876	CH230-219	C 478	20	1.6	494	7	CO417570	CO417570	Mdftt3034
C 406	21	1.6	541	8	AZ043204	AZ043204	RPCI-23-3	C 479	20	1.6	496	4	BI073348	BI073348	kt29912.y
C 407	21	1.6	544	7	CK578590	CK578590	IST_W15_1	C 480	20	1.6	505	2	AM083462	AM083462	xc02d08.x
C 408	21	1.6	550	7	CK578526	CK578526	IST_W15_1	C 481	20	1.6	507	4	BI703367	BI703367	rsf5d12.y
C 409	21	1.6	568	1	AL727256	AL727256	AL727256	C 482	20	1.6	507	9	CL333865	CL333865	RPCI44_25
C 410	21	1.6	570	6	CB394503	CB394503	OSTR138H1	C 483	20	1.6	508	5	BM346628	BM346628	BM346628
C 411	21	1.6	578	7	CK578606	CK578606	IST_W15_1	C 484	20	1.6	510	6	CB437394	CB437394	684853.MA
C 412	21	1.6	579	9	CRO55443	CRO55443	Forward's	C 485	20	1.6	515	2	AW302339	AW302339	xw02d07.x
C 413	21	1.6	600	7	CK581282	CK581282	IST_W15_3	C 486	20	1.6	518	4	BI500452	BI500452	rs7h02.y
C 414	21	1.6	609	8	AZ527192	AZ527192	265PbD12	C 487	20	1.6	521	4	BM229987	BM229987	K0288B10-
C 415	21	1.6	614	1	AL723384	AL723384	AL723384	C 488	20	1.6	525	7	CK970500	CK970500	4086192.B
C 416	21	1.6	640	1	AL727196	AL727196	IST_W15_1	C 489	20	1.6	526	7	CV523595	CV523595	Md1v4013d
C 417	21	1.6	645	7	CK576798	CK576798	IST_W15_1	C 490	20	1.6	530	9	CG879456	CG879456	ZMMBBb050
C 418	21	1.6	672	9	AG091935	AG091935	Pan trogl	C 491	20	1.6	533	7	CR552932	CR552932	CR552932
C 419	21	1.6	672	9	AG091935	AG091935	Pan trogl	C 492	20	1.6	534	4	BJ676087	BJ676087	BJ676087
C 420	21	1.6	684	7	CK580797	CK580797	IST_W15_1	C 493	20	1.6	534	4	BM129781	BM129781	1f23a12.y
C 421	21	1.6	694	7	CK576794	CK576794	IST_W15_1	C 494	20	1.6	534	4	BM129781	BM129781	1f23a12.y
C 422	21	1.6	696	1	AL723384	AL723384	AL723384	C 495	20	1.6	534	4	BM129781	BM129781	1f23a12.y
C 423	21	1.6	723	1	AL722498	AL722498	AL722498	C 496	20	1.6	534	4	BM129781	BM129781	1f23a12.y
C 424	21	1.6	728	7	CK576772	CK576772	IST_W15_1	C 497	20	1.6	534	4	BM129781	BM129781	1f23a12.y
C 425	21	1.6	735	8	BH794719	BH794719	ME_MBA000	C 498	20	1.6	534	4	BM129781	BM129781	1f23a12.y
C 426	21	1.6	738	7	CN220754	CN220754	RJA069C01	C 499	20	1.6	534	4	BM129781	BM129781	1f23a12.y
C 427	21	1.6	739	8	CK576785	CK576785	IST_W15_1	C 500	20	1.6	534	4	BM129781	BM129781	1f23a12.y
C 428	21	1.6	758	8	AQ869090	AQ869090	nbe0033N	C 501	20	1.6	534	4	BM129781	BM129781	1f23a12.y
C 429	21	1.6	763	7	CV480939	CV480939	AGENCOURT	C 502	20	1.6	534	4	BM129781	BM129781	1f23a12.y
C 430	21	1.6	767	7	CK576777	CK576777	IST_W15_1	C 503	20	1.6	534	4	BM129781	BM129781	1f23a12.y
C 431	21	1.6	767	7	CK576777	CK576777	IST_W15_1	C 504	20	1.6	534	4	BM129781	BM129781	1f23a12.y
C 432	21	1.6	817	8	BZ194558	BZ194558	CH230-269	C 505	20	1.6	534	4	BM129781	BM129781	1f23a12.y
C 433	21	1.6	947	8	CL369332	CL369332	PUHIO52TD	C 506	20	1.6	534	4	BM129781	BM129781	1f23a12.y
C 434	21	1.6	956	7	CF224782	CF224782	AGENCOURT	C 507	20	1.6	534	4	BM129781	BM129781	1f23a12.y
C 435	21	1.6	1059	2	BF274699	BF274699	GN_BD002	C 508	20	1.6	534	4	BM129781	BM129781	1f23a12.y
C 436	21	1.6	1117	8	CC205976	CC205976	CH261-129	C 509	20	1.6	534	4	BM129781	BM129781	1f23a12.y
C 437	21	1.6	1217	8	BZ695549	BZ695549	SP_Ba006	C 510	20	1.6	534	4	BM129781	BM129781	1f23a12.y
C 438	21	1.6	2210	7	CO635628	CO635628	Contt19258	C 511	20	1.6	534	4	BM129781	BM129781	1f23a12.y
C 439	20	1.6	102	8	BZ689002	BZ689002	PUCB064TD	C 512	20	1.6	534	4	BM129781	BM129781	1f23a12.y
C 440	20	1.6	105	2	BE682417	BE682417	180450.MA	C 513	20	1.6	534	4	BM129781	BM129781	1f23a12.y
C 441	20	1.6	241	9	CE267892	CE267892	tigr-g88-	C 514	20	1.6	534	4	BM129781	BM129781	1f23a12.y
C 442	20	1.6	272	8	AQ105319	AQ105319	HS_3020.B	C 515	20	1.6	534	4	BM129781	BM129781	1f23a12.y
C 443	20	1.6	322	7	CO871617	CO871617	EST00431	C 516	20	1.6	534	4	BM129781	BM129781	1f23a12.y
C 444	20	1.6	322	8	BM253116	BM253116	512475.MA	C 517	20	1.6	534	4	BM129781	BM129781	1f23a12.y
C 445	20	1.6	328	4	CL281886	CL281886	ZMMBBb062	C 518	20	1.6	534	4	BM129781	BM129781	1f23a12.y
C 446	20	1.6	342	9	CL740445	CL740445	OR_BBa007	C 519	20	1.6	534	4	BM129781	BM129781	1f23a12.y
C 447	20	1.6	377	9	CL417464	CL417464	ZMMBBb042	C 520	20	1.6	534	4	BM129781	BM129781	1f23a12.y
C 448	20	1.6	379	1	AL846166	AL846166	AL846166	C 521	20	1.6	534	4	BM129781	BM129781	1f23a12.y
C 449	20	1.6	383	1	AI441145	AI441145	8459D01.y	C 522	20	1.6	534	4	BM129781	BM129781	1f23a12.y
C 450	20	1.6	387	1	AI120098	AI120098	uc27405.f	C 523	20	1.6	534	4	BM129781	BM129781	1f23a12.y
C 451	20	1.6	389	4	BI742805	BI742805	Kx35C05.y	C 524	20	1.6	534	4	BM129781	BM129781	1f23a12.y
C 452	20	1.6	391	8	AQ471785	AQ471785	CITBI-El-	C 525	20	1.6	534	4	BM129781	BM129781	1f23a12.y
C 453	20	1.6	391	4	BI670780	BI670780	PfEST0a0	C 526	20	1.6	534	4	BM129781	BM129781	1f23a12.y
C 454	20	1.6	407	7	D54183	D54183	HUM131D02B	C 527	20	1.6	534	4	BM129781	BM129781	1f23a12.y
C 455	20	1.6	416	8	AZ620109	AZ620109	IM0452M09	C 528	20	1.6	534	4	BM129781	BM129781	1f23a12.y
C 456	20	1.6	425	2	BE447898	BE447898	ut41906.y	C 529	20	1.6	534	4	BM129781	BM129781	1f23a12.y
C 457	20	1.6	430	4	BJ654519	BJ654519	BJ654519	C 530	20	1.6	534	4	BM129781	BM129781	1f23a12.y
C 458	20	1.6	432	6	CB428465	CB428465	604172.MA	C 531	20	1.6	534	4	BM129781	BM129781	1f23a12.y
C 459	20	1.6	435	6	CB428465	CB428465	604172.MA	C 532	20	1.6	534	4	BM129781	BM129781	1f23a12.y
C 460	20	1.6	437	7	CK846802	CK846802	969351.MA	C 533	20	1.6	534	4	BM129781	BM129781	1f23a12.y
C 461	20	1.6	445	4	BM254474	BM254474	515914.MA	C 534	20	1.6	534	4	BM129781	BM129781	1f23a12.y
C 462	20	1.6	449	6	CB156923	CB156923	K-EST0215	C 535	20	1.6	534	4	BM129781	BM129781	1f23a12.y

C 536	20	1.6	618	9	AG230190	Lotus cor	609	20	1.6	806	7	CR417945	CR417945
C 537	20	1.6	622	1	AL674749	AL674749	C 610	20	1.6	809	9	CG304555	CG304555
C 538	20	1.6	625	1	AV841171	AV841171	611	20	1.6	818	7	CR582937	CR582937
C 539	20	1.6	632	4	BM790493	K-EST0070	C 612	20	1.6	825	8	BZ255361	BZ255361
540	20	1.6	641	4	BI168259	R508857.5	613	20	1.6	836	9	CC826591	CC826591
541	20	1.6	642	5	BM346293	BM346293	614	20	1.6	846	9	CC485382	CC485382
542	20	1.6	647	2	BE581998	K57809.Y	615	20	1.6	847	5	BQ220310	BQ220310
543	20	1.6	647	4	BJ697375	BJ697375	C 616	20	1.6	847	5	CG654797	CG654797
544	20	1.6	648	5	BW255679	BW255679	C 617	20	1.6	848	9	CL9392701	CL9392701
545	20	1.6	649	8	AZ615790	1M0445L13	618	20	1.6	856	9	CL839696	CL839696
C 546	20	1.6	650	9	CE033761	tigr-gss-	C 619	20	1.6	858	9	CG694501	CG694501
547	20	1.6	657	2	BE580308	K39f10.Y	C 620	20	1.6	859	2	BF272342	BF272342
548	20	1.6	658	9	CC619652	CGWC192TH	C 621	20	1.6	868	5	EX736384	EX736384
549	20	1.6	659	5	BW329467	BW329467	C 622	20	1.6	873	9	CL250563	CL250563
C 550	20	1.6	659	9	CG871446	CG871446	C 623	20	1.6	874	9	CG433160	CG433160
551	20	1.6	664	8	BZ955499	CH240.961	C 624	20	1.6	877	9	CG739325	CG739325
552	20	1.6	666	7	CK023635	AGENCOURT	C 625	20	1.6	882	9	CG032248	CG032248
553	20	1.6	676	8	AZ574928	334PVD02	C 626	20	1.6	885	5	BU164429	BU164429
C 554	20	1.6	676	8	CC834134	ZMMBB018	C 627	20	1.6	886	9	CG235556	CG235556
C 555	20	1.6	680	5	BW186062	BW186062	C 628	20	1.6	889	9	CG032249	CG032249
556	20	1.6	680	7	CR435389	CR435389	C 629	20	1.6	890	5	EX760425	EX760425
557	20	1.6	682	4	BJ689168	BJ689168	630	20	1.6	893	4	BG255319	BG255319
558	20	1.6	689	4	BM551946	AGENCOURT	C 631	20	1.6	902	9	CG874395	CG874395
559	20	1.6	692	4	BI909621	603066646	C 632	20	1.6	914	5	EX772276	EX772276
C 560	20	1.6	693	1	AV866684	AV866684	C 633	20	1.6	915	9	CG331038	CG331038
561	20	1.6	700	9	CG917869	ZMMBB038	634	20	1.6	928	9	CL991827	CL991827
562	20	1.6	706	9	CC832038	ZMMBB018	635	20	1.6	931	9	CL317081	CL317081
563	20	1.6	707	1	AA697948	HL03517.5	C 636	20	1.6	939	9	CL447543	CL447543
564	20	1.6	708	9	CR330078	CR330078	637	20	1.6	952	9	CG90405	CG90405
565	20	1.6	709	9	CC877682	ZMMBB021	C 638	20	1.6	953	9	CL457197	CL457197
566	20	1.6	710	8	BZ396230	EINAY14TR	639	20	1.6	954	8	CC196243	CC196243
567	20	1.6	713	9	AG556257	Mus muscu	640	20	1.6	957	9	CG420847	CG420847
C 568	20	1.6	714	6	CD781337	EST652698	C 641	20	1.6	960	9	CL400568	CL400568
569	20	1.6	718	5	BW383540	BW383540	C 642	20	1.6	972	9	CG013746	CG013746
C 570	20	1.6	718	7	CN925108	CN925108	C 643	20	1.6	981	9	CG908751	CG908751
571	20	1.6	721	7	CN925584	000512AEN	C 644	20	1.6	990	9	CL260337	CL260337
C 572	20	1.6	721	9	CE448504	tigr-gss-	645	20	1.6	992	8	CC314927	CC314927
C 573	20	1.6	727	9	CE409035	tigr-gss-	C 646	20	1.6	993	9	CG900859	CG900859
C 574	20	1.6	730	5	BW417324	BW417324	C 647	20	1.6	995	9	CC973749	CC973749
C 575	20	1.6	730	9	CL155719	104.342.1	C 648	20	1.6	996	9	CL235504	CL235504
C 576	20	1.6	732	9	CC824172	ZMMBB016	649	20	1.6	1002	5	BX355762	BX355762
C 577	20	1.6	734	5	BW395908	BW395908	C 650	20	1.6	1008	9	CG876520	CG876520
C 578	20	1.6	735	5	CG798015	CG798015	C 651	20	1.6	1012	8	BZ746420	BZ746420
C 579	20	1.6	736	5	BP714500	BP714500	C 652	20	1.6	1012	8	CL292438	CL292438
580	20	1.6	736	7	CK978640	4110250.B	C 653	20	1.6	1016	3	CR683141	CR683141
581	20	1.6	738	9	CC750658	ZMMBB013	654	20	1.6	1016	5	BX370682	BX370682
C 582	20	1.6	739	8	BH327596	CH230-174	C 655	20	1.6	1032	9	CL446232	CL446232
C 583	20	1.6	739	9	CL287086	ZMMBB063	C 656	20	1.6	1058	9	CL082094	CL082094
C 584	20	1.6	741	5	EX696845	EX696845	657	20	1.6	1078	9	CNS06890	CNS06890
585	20	1.6	742	9	CC828120	ZMMBB017	C 658	20	1.6	1083	9	AL561412	AL561412
C 586	20	1.6	747	5	BW330540	BW330540	659	20	1.6	1130	1	AL561412	AL561412
C 587	20	1.6	748	5	BW400395	BW400395	660	20	1.6	1133	9	CG878461	CG878461
C 588	20	1.6	753	5	BW272269	BW272269	661	20	1.6	1171	9	CL648737	CL648737
589	20	1.6	755	9	CL237651	ZMMBB057	662	20	1.6	1241	9	CL647711	CL647711
C 590	20	1.6	760	8	CC338732	OGIAS17TV	663	20	1.6	1323	4	BG430724	BG430724
C 591	20	1.6	761	9	CL381974	RPCI44.32	664	20	1.6	2243	3	CR610024	CR610024
592	20	1.6	766	6	CD559436	AGENCOURT	665	19	1.5	137	5	BP509566	BP509566
593	20	1.6	767	5	BU144068	603229376	666	19	1.5	169	7	CK907022	CK907022
C 594	20	1.6	767	7	CF217266	AGENCOURT	C 667	19	1.5	175	8	AZ034720	AZ034720
C 595	20	1.6	773	5	BW129504	BW129504	C 668	19	1.5	189	7	CNS73991	CNS73991
C 596	20	1.6	773	5	BW387717	BW387717	C 669	19	1.5	190	4	BI814537	BI814537
C 597	20	1.6	774	5	BW079214	BW079214	C 670	19	1.5	200	4	BM446610	BM446610
C 598	20	1.6	774	5	BW397735	BW397735	671	19	1.5	241	1	AV143692	AV143692
599	20	1.6	776	8	BZ969506	PUIF109TB	C 672	19	1.5	241	4	BG734977	BG734977
C 600	20	1.6	778	5	BW010130	BW010130	673	19	1.5	243	7	CV246887	CV246887
601	20	1.6	781	9	CG883553	ZMMBB049	674	19	1.5	253	9	CE033070	CE033070
C 602	20	1.6	785	4	BG217318	RST37023	675	19	1.5	277	6	CA302129	CA302129
C 603	20	1.6	786	5	BW079936	BW079936	676	19	1.5	301	9	CE516406	CE516406
C 604	20	1.6	789	8	BZ396217	EINAY14TF	677	19	1.5	316	2	BB222262	BB222262
C 605	20	1.6	789	9	CG397286	ZMMBB001	678	19	1.5	316	9	CE785938	CE785938
C 606	20	1.6	792	5	BW142580	BW142580	C 679	19	1.5	323	9	CE641681	CE641681
C 607	20	1.6	795	8	BZ452886	BONSX80TR	C 680	19	1.5	333	6	CD011850	CD011850
608	20	1.6	803	5	BU251348	603403612	C 681	19	1.5	346	2	AW363358	AW363358

682	19	1.5	349	4	BJ378821	BJ378821	C	755	19	1.5	521	7	CN741425
C 683	19	1.5	360	7	D37065	CELK040B7F		756	19	1.5	521	8	AZ728536
C 684	19	1.5	360	9	D37065	tigr-gss-		757	19	1.5	525	4	BG565051
C 685	19	1.5	362	4	BE250570	BJ318349		758	19	1.5	526	6	CB720030
C 686	19	1.5	362	8	BM582883	BOHCIC22TF		759	19	1.5	527	1	AU261975
C 687	19	1.5	365	4	BM161546	EST564069		760	19	1.5	527	8	AQ776195
C 688	19	1.5	370	6	AD417046	Gm ck7548		761	19	1.5	528	8	AZ074619
C 689	19	1.5	371	8	AZ953328	2M0218G05		762	19	1.5	529	5	BX563688
C 690	19	1.5	374	2	BF549676	UI-R-A0-a		763	19	1.5	529	9	CL587099
C 691	19	1.5	376	1	AI551625	VE38A04.Y		764	19	1.5	536	9	AG201375
C 692	19	1.5	387	5	BY024850	BY024850		765	19	1.5	536	9	CEI13387
C 693	19	1.5	388	1	AI781852	EST262731		766	19	1.5	540	7	CNI16152
C 694	19	1.5	388	7	CV128874	Mdfrt3090		767	19	1.5	540	7	CEI13387
C 695	19	1.5	388	7	CV129655	Mdfrt3086		768	19	1.5	548	9	EXR95863
C 696	19	1.5	388	4	BI815980	PFEStocaa3		769	19	1.5	548	9	CR105821
C 697	19	1.5	390	4	BI815980	CK778830		770	19	1.5	551	4	BJ341865
C 698	19	1.5	393	7	CK778830	966003 MA		771	19	1.5	551	4	BF1514156
C 699	19	1.5	395	9	AG253558	Lotus cor		772	19	1.5	552	6	CB110335
C 700	19	1.5	398	5	BU497167	PFEStoab5		773	19	1.5	555	8	AQ490052
C 701	19	1.5	398	1	AI814774	wk65f05.x		774	19	1.5	556	9	CC842873
C 702	19	1.5	402	5	BU495641	PFEStocab7		775	19	1.5	558	1	AJ500616
C 703	19	1.5	402	7	CK340612	CK340612		776	19	1.5	563	4	BI815498
C 704	19	1.5	403	8	AZ599537	IM0414O22		777	19	1.5	565	2	BP353126
C 705	19	1.5	406	1	AA706466	AA706466		778	19	1.5	568	6	CB094370
C 706	19	1.5	416	5	BP671122	BP671122		779	19	1.5	568	4	BT101369
C 707	19	1.5	417	7	CV187916	aa001-14m		780	19	1.5	568	9	BE225595
C 708	19	1.5	425	8	BH251978	BH251978		781	19	1.5	569	5	BU297731
C 709	19	1.5	428	1	AI243632	qR88a08.x		782	19	1.5	570	4	BI928878
C 710	19	1.5	430	7	CE546295	lae70f09.		783	19	1.5	572	4	CE571666
C 711	19	1.5	430	9	CE549393	tigr-gss-		784	19	1.5	575	2	BE052275
C 712	19	1.5	431	1	AV792057	AV792057		785	19	1.5	577	9	CK961504
C 713	19	1.5	431	8	B91032	CIT-HSP-216		786	19	1.5	578	7	CK582894
C 714	19	1.5	438	7	CO578881	ta157h10.		787	19	1.5	581	2	AW038487
C 715	19	1.5	439	8	CC126872	NDL_57H4.		788	19	1.5	581	2	CE177344
C 716	19	1.5	440	1	AA423286	AA423286		789	19	1.5	582	5	BU084029
C 717	19	1.5	442	7	CN060443	7943_1001		790	19	1.5	582	6	CS586610
C 718	19	1.5	443	2	BE053529	GA_Ea002		791	19	1.5	585	4	BJ381494
C 719	19	1.5	445	2	BP425626	BP425626		792	19	1.5	585	7	CN058999
C 720	19	1.5	446	5	BF594481	BP594481		793	19	1.5	587	9	CNS01G4H
C 721	19	1.5	446	6	BY565273	BY565273		794	19	1.5	588	4	AZ367177
C 722	19	1.5	446	6	BY566080	BY566080		795	19	1.5	590	8	AZ367177
C 723	19	1.5	446	6	CA066555	SCBQAD101		796	19	1.5	591	6	CD289847
C 724	19	1.5	447	4	BG047021	sa375905.		797	19	1.5	591	6	CG693521
C 725	19	1.5	448	1	AV794422	AV794422		798	19	1.5	592	8	BH076622
C 726	19	1.5	453	2	BF762153	IL2-CS004		799	19	1.5	594	2	BF254940
C 727	19	1.5	454	8	AT785997	AZ785997		800	19	1.5	595	6	CD057324
C 728	19	1.5	455	8	AQ122710	HS_3080_A		801	19	1.5	597	4	BJ807631
C 729	19	1.5	456	8	BH256207	BH256207		802	19	1.5	597	7	CF512979
C 730	19	1.5	458	1	AU269983	RDH5BAM00		803	19	1.5	599	1	CA200606
C 731	19	1.5	458	9	CE134648	tigr-gss-		804	19	1.5	600	6	CA200606
C 732	19	1.5	459	5	BY233914	BY233914		805	19	1.5	601	6	CA200677
C 733	19	1.5	465	4	BI678446	SW2202 SW		806	19	1.5	603	9	CR535956
C 734	19	1.5	466	1	AV596132	AV596132		807	19	1.5	603	9	CR721247
C 735	19	1.5	466	5	BM119809	BM119809		808	19	1.5	606	7	CK582881
C 736	19	1.5	466	8	AZ286837	AZ286837		809	19	1.5	606	9	CR081307
C 737	19	1.5	480	7	CF933061	CF-06-R-		810	19	1.5	607	9	CG693523
C 738	19	1.5	481	8	AQ391069	CITB1-E01		811	19	1.5	609	5	BP118292
C 739	19	1.5	484	7	CF383971	lab99f05.		812	19	1.5	611	1	AJ614435
C 740	19	1.5	486	5	BU494793	PFEStoab6		813	19	1.5	613	5	BQ408781
C 741	19	1.5	487	8	AQ980966	AQ980966		814	19	1.5	614	8	AZ522417
C 742	19	1.5	489	1	AJ675437	AJ675437		815	19	1.5	616	2	BE823750
C 743	19	1.5	489	1	AJ675437	AJ675437		816	19	1.5	618	6	BY718723
C 744	19	1.5	492	6	CD554572	CD554572		817	19	1.5	618	6	BY718723
C 745	19	1.5	492	8	AZ659892	AZ659892		818	19	1.5	619	8	CN052350
C 746	19	1.5	498	8	AZ721107	RPIC1-24-1		819	19	1.5	619	9	RI125901
C 747	19	1.5	500	5	BP185299	BP185299		820	19	1.5	623	5	BH125901
C 748	19	1.5	500	7	CV002138	aa001-7ms		821	19	1.5	624	6	CA201077
C 749	19	1.5	503	9	CC854450	CC854450		822	19	1.5	626	9	CO881215
C 750	19	1.5	511	7	CK300087	UL-R-EJ1-		823	19	1.5	626	9	CC766855
C 751	19	1.5	513	8	CN928628	00601AEP		824	19	1.5	628	9	CG165807
C 752	19	1.5	513	8	AZ128584	OSUNBB009		825	19	1.5	631	8	AG2252982
C 753	19	1.5	516	1	AI883431	fc64b02.Y		826	19	1.5	631	8	BI928878
C 754	19	1.5	519	8	AZ598154	IM0412K18		827	19	1.5	631	8	BH741680

C 828	19	1.5	632	5	BP230894	RP230894	BP230894	901	19	1.5	733	9	AG572013	Mus muscu
C 829	19	1.5	632	5	CE507450	CE507450	tigr-gss-	C 902	19	1.5	734	8	AQ864496	nbeb0023K
C 830	19	1.5	633	5	BM342314	BM342314	BM342314	C 903	19	1.5	735	8	AZ188722	SP_1012_B
C 831	19	1.5	634	5	BP764942	BP764942	BP764942	C 904	19	1.5	735	9	AG485568	Mus muscu
C 832	19	1.5	636	2	BB636230	BB636230	BB636230	C 905	19	1.5	736	9	AG331773	Mus muscu
C 833	19	1.5	637	1	AL635202	AL635202	Danio rer	C 906	19	1.5	739	9	BX236453	Danio rer
C 834	19	1.5	639	1	DR461117	DR461117	DR461117	C 907	19	1.5	742	5	BU396304	603802918
C 835	19	1.5	641	4	BG415790	BG415790	HVSMERK000	C 908	19	1.5	742	5	AG588331	Mus muscu
C 836	19	1.5	641	4	BI506169	BI506169	BI506169	C 909	19	1.5	746	5	BU306571	603737374
C 837	19	1.5	648	8	BZ917568	BZ917568	CH240_103	C 910	19	1.5	746	5	BU306571	603737374
C 838	19	1.5	650	1	AU002854	AU002854	AU002854	C 911	19	1.5	749	8	CC131455	NDL_34P22
C 839	19	1.5	651	5	BM019379	BM019379	BM019379	C 912	19	1.5	749	9	AG518532	Mus muscu
C 840	19	1.5	652	6	CB483584	CB483584	ccuwtb10	C 913	19	1.5	750	4	BJ406285	BJ406285
C 841	19	1.5	653	9	AG083223	AG083223	Pan trogl	C 914	19	1.5	752	9	EX171036	Danio rer
C 842	19	1.5	654	2	BF277981	BF277981	GA_EB003	C 915	19	1.5	754	9	EX183271	Danio rer
C 843	19	1.5	656	4	BM162351	BM162351	EST564874	C 916	19	1.5	755	8	CC112133	NDL_19K23
C 844	19	1.5	657	5	BQ412882	BQ412882	GA_Ed006	C 917	19	1.5	758	4	BJ345724	BJ345724
C 845	19	1.5	657	8	BH348838	BH348838	CH230-160	C 918	19	1.5	758	5	BU906516	AGENCOURT
C 846	19	1.5	658	5	BQ412866	BQ412866	GA_Ed006	C 919	19	1.5	761	9	CL150835	104_332_1
C 847	19	1.5	659	9	DR34C55	DR34C55	DR34C55	C 920	19	1.5	762	6	CE680351	tigr-gss-
C 848	19	1.5	659	9	CE377017	CE377017	tigr-gss-	C 921	19	1.5	763	7	CN509572	AGENCOURT
C 849	19	1.5	660	8	AZ562230	AZ562230	RPCI-23-2	C 922	19	1.5	763	7	CD644301	AGENCOURT
C 850	19	1.5	662	1	AI909661	AI909661	PM-BT219-	C 923	19	1.5	765	6	CD644301	AGENCOURT
C 851	19	1.5	662	1	AJ818080	AJ818080	AJ818080	C 924	19	1.5	765	4	BZ396349	ETNAL59TR
C 852	19	1.5	662	8	AZ652198	AZ652198	IM0525M18	C 925	19	1.5	767	9	AG609250	Mus muscu
C 853	19	1.5	665	6	CD609517	CD609517	55145813H	C 926	19	1.5	767	9	CR318387	Medicago
C 854	19	1.5	669	7	CO983049	CO983049	GM89017B1	C 927	19	1.5	767	9	CL547461	OB_Ba008
C 855	19	1.5	669	7	CE585211	CE585211	tigr-gss-	C 928	19	1.5	769	8	BZ144708	CH230-413
C 856	19	1.5	670	5	BQ404007	BQ404007	GA_Ed006	C 929	19	1.5	770	4	BG849590	1024025H1
C 857	19	1.5	675	9	CE269062	CE269062	tigr-gss-	C 930	19	1.5	771	8	BH072553	RPCI-24-3
C 858	19	1.5	676	7	CK289059	CK289059	EST5751781	C 931	19	1.5	771	9	CC869360	NDL_131M1
C 859	19	1.5	679	9	CL550022	CL550022	OB_Ba008	C 932	19	1.5	773	9	CG976667	CH240_166
C 860	19	1.5	681	7	CF444220	CF444220	EST680565	C 933	19	1.5	775	5	CG837480	ZMMBCC021
C 861	19	1.5	681	9	CE201152	CE201152	tigr-gss-	C 934	19	1.5	776	5	BW410198	BW410198
C 862	19	1.5	682	9	CE691334	CE691334	tigr-gss-	C 935	19	1.5	777	9	AG475380	Mus muscu
C 863	19	1.5	684	9	DR491215	DR491215	Danio rer	C 936	19	1.5	779	9	CC499079	CH240_336
C 864	19	1.5	685	6	CD766287	CD766287	AGENCOURT	C 937	19	1.5	781	2	BF865675	963061E03
C 865	19	1.5	685	8	BH996448	BH996448	oeif2b09.	C 938	19	1.5	781	5	BU415446	603670313
C 866	19	1.5	685	9	CL576507	CL576507	OB_Ba002	C 939	19	1.5	783	5	BW119829	BW119829
C 867	19	1.5	689	4	BI398124	BI398124	UMN45G07	C 940	19	1.5	783	9	AG184454	Pan trogl
C 868	19	1.5	689	6	CB449496	CB449496	703699_MA	C 941	19	1.5	791	8	CC077961	CSU-K33r.
C 869	19	1.5	689	8	BH929953	BH929953	odh98G03.	C 942	19	1.5	792	9	EX174849	Danio rer
C 870	19	1.5	694	4	BI209829	BI209829	EST527869	C 943	19	1.5	798	8	CL934151	OA_Aba004
C 871	19	1.5	697	9	AG281231	AG281231	Mus muscu	C 944	19	1.5	802	8	BH536532	BOGVU7TF
C 872	19	1.5	697	9	AG284032	AG284032	Mus muscu	C 945	19	1.5	802	8	CL802528	OR_CBa001
C 873	19	1.5	698	9	CL540326	CL540326	OB_Ba006	C 946	19	1.5	803	9	AG503031	Mus muscu
C 874	19	1.5	700	4	BJ431510	BJ431510	BJ431510	C 947	19	1.5	805	4	BM400637	5009-0-76
C 875	19	1.5	700	9	CE147772	CE147772	tigr-gss-	C 948	19	1.5	806	9	CL839503	OR_CBa006
C 876	19	1.5	702	1	AJ797247	AJ797247	tigr-gss-	C 949	19	1.5	810	7	CN506882	AGENCOURT
C 877	19	1.5	702	6	CD609514	CD609514	55145721J	C 950	19	1.5	813	7	CK142399	AGENCOURT
C 878	19	1.5	702	8	CC087939	CC087939	CSU-K33r.	C 951	19	1.5	813	8	BZ397994	ETNAO80TF
C 879	19	1.5	704	8	CC089296	CC089296	CSU-K33r.	C 952	19	1.5	827	8	BZ573255	mh2_3021
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C 881	19	1.5	707	8	AZ248478	AZ248478	RPCI-23-5	C 954	19	1.5	832	8	CC139459	NDL_49J24
C 882	19	1.5	707	9	AG302078	AG302078	Mus muscu	C 955	19	1.5	836	8	BZ805988	PUGAU57TB
C 883	19	1.5	708	6	CD609516	CD609516	55145805J	C 956	19	1.5	836	8	CC131397	NDL_40I20
C 884	19	1.5	709	4	BI866821	BI866821	ZF637-1-0	C 957	19	1.5	839	8	CC003761	PUDEP27TD
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C 893	19	1.5	720	9	CE512798	CE512798	tigr-gss-	C 966	19	1.5	858	1	AJ816213	AJ816213
C 894	19	1.5	725	9	CC854389	CC854389	NDL_124M1	C 967	19	1.5	859	4	BG718310	602696305
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C 898	19	1.5	732	9	CR331959	CR331959	Medicago	C 971	19	1.5	872	7	CF514711	CABUQ0005
C 899	19	1.5	733	8	BH940605	BH940605	ode70b10.	C 972	19	1.5	873	9	CG255739	CGWBU527H
C 900	19	1.5	733	8	CC069675	CC069675	CSU-K33r.	C 973	19	1.5	873	8	BZ803137	PUFPAV29TD

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978 1.5 881 8 BH163824
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c 980 1.5 884 9 CG907568
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c 982 1.5 892 8 AZ545568
983 1.5 894 8 BH134549
984 1.5 898 5 BQ433334
985 1.5 898 9 CG819589
986 1.5 900 8 AZ550542
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988 1.5 902 8 AZ680689
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994 1.5 922 8 BH139744
995 1.5 923 4 BM358301
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997 1.5 924 9 CG157918
998 1.5 927 8 AZ686627
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ALIGNMENTS

RESULT 1
LOCUS U70056 1221 bp mRNA linear EST 27-OCT-1999
DEFINITION U70056 Soares infant brain INIB Homo sapiens cDNA clone 25050, mRNA
sequence.
U70056
U70056.1 GI:2731404
EST.
Homo sapiens (human)
Homo sapiens
Mammalia; Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1221)
Volorio, S., Simon, G., Repetto, M., Cucciarini, M., Banfi, S.,
Borsani, G., Ballabio, A. and Zollo, M.
Sequencing analysis of forty-eight human image cDNA clones similar
to drosophila mutant protein
DNA Seq. 9 (5-6), 307-315 (1998)
99452388
10524757
Contact: Zollo, Massimo
Telethon Institute of Genetics and Medicine
Via Olgettina 58, Milan, MI 20132, Italy
Email: zollo@tigem.it.

FEATURES
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/mol_type="mRNA"
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I - oligo(dT) primer [5],
AACTGGAGAATTCGGCGCGGAGGAATTTTTTTTTTTT 3';
double-stranded cDNA was ligated to Hind III adaptors
(Pharmacia), digested with Not I and directionally cloned

into the Not I and Hind III sites of the Lafmid BA vector.
Library went through one round of normalization. Library
constructed by Bento Soares and M.Fatima Bonaldo."

ORIGIN
Query Match 83.4%; Score 1062; DB 7; Length 1221;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1062; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 213 AAATTTTCTATGAACATTTTAAAGGACATTATGGCATGTAAACATTTATTAATAAGTAAGT 272
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121 GACTGCTACAGCATTTACCTACGGGTACCTCGAAGTGTCCACCATCCAGAGGGTGCCTGTC 180
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1113 ACAGCTTTTTCGAGAAAATGCGAAATTTAGGCATCAATGTAATTTCCATGTTGTTGAAA 1172
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was normalized. Library was constructed by Life Technologies, a division of Invitrogen

FEATURES
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/mol_type="mRNA"
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Matches 958; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 677 AGCTCTGTGAGTTAGGCTTATCTGTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 736
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CR598465 1287 bp mRNA linear HTC 21-JUL-2004
full-length cDNA clone CS0DI004YF12 of Placenta Cot 25-normalized
of Homo sapiens (human).
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CR598465.1 GI:50479272
HTC; CDSLT_cDNA
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1287)
Li W.B., Gruber C., Jessup J. and Polayes, D.
Full-length cDNA libraries and normalization
Unpublished
JOURNAL
REMARK
Contact : Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
Faraday Avenue
2 (bases 1 to 1287)
Genoscope.
Direct Submission
Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :
BP 191/91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fr)
- Web : www.genoscope.cns.fr)
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen.
Location/Qualifiers
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Query Match 70.2%; Score 894; DB 3; Length 1287;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 894; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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AY402255 849 bp DNA linear GSS 15-DEC-2003
Homo sapiens SIAH1 gene, VIRTUAL TRANSCRIPT, partial sequence,
genomic survey sequence.
ACCESSION AY402255
VERSION AY402255.1 GI:39758241
KEYWORDS GSS.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 849)
Clark, A.G., Gnanowaki, S., Nielson, R., Thomas, P., Kejarawal, A.,
Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B.,
Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J.,
Adams, M.D. and Cargill, M.
Inferring nonneutral evolution from human-chimp-mouse orthologous
gene trios
Science 302 (5652), 1950-1963 (2003)
14671302 {
2 (bases 1 to 849)
Clark, A.G., Gnanowski, S., Nielson, R., Thomas, P., Kejarawal, A.,
Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B.,
Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J.,
Adams, M.D. and Cargill, M.
Direct Submission
Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
Rockville, MD 20850, USA
This sequence was made by sequencing genomic exons and ordering
them based on alignment
LOCATION/Qualifiers
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Matches 849; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 661 TTTTGTCTTACCGACTTGAGCTAAATGGTCTATAGCGCAAGCTTCACTTGGGAAGCGACTCT 720
Qy 1042 CGATCTATTCATGAAGGAATTCGCAACAGCCATTTATGAATAGCGAGTGTCTAGTCTTTGAC 1101
Db 721 CGATCTATTCATGAAGGAATTCGCAACAGCCATTTATGAATAGCGAGTGTCTAGTCTTTGAC 780
Qy 1102 ACCAGCATTCACAGCTTTTTCAGAAAAATGCAATTTAGGCATCAATGTAATCTATTTCC 1161
Db 781 ACCAGCATTCACAGCTTTTTCAGAAAAATGCAATTTAGGCATCAATGTAATCTATTTCC 840
Qy 1162 ATGTGTTGA 1170
Db 841 ATGTGTTGA 849
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```
RESULT 6
CR593197      1576 bp      mRNA      linear      HTC 21-JUL-2004
LOCUS      full-length cDNA clone CS0D1011Y112 of Placenta Cot 25-normalized
DEFINITION      of Homo sapiens (human).
ACCESSION      CR593197
VERSION      HTG; CnSLT cDNA.
KEYWORDS      Homo sapiens (human)
SOURCE      Homo sapiens
ORGANISM      Homo sapiens
REFERENCE      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS      Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
TITLE      1 (bases 1 to 1576)
JOURNAL      Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
REMARK      Full-length cDNA libraries and normalization
Contact : Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/Invitrogen Corporation 1600
Paraday Avenue
2 (bases 1 to 1576)
Genoscope.
Direct Submission
Submitted (20-JUL-2004) Genoscope, Centre National de Sequencage :
BP 191 91006 EVRY Cedex - FRANCE [E-mail : seqref@genoscope.cns.fr
- Web : www.genoscope.cns.fr]
COMMENT      1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen.
FEATURES
Location/Qualifiers
1..1576
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0D1011Y112"
/tissue_type="Placenta Cot 25-normalized"
/plasmid="pCMVSPORT 6"
ORIGIN
Query Match      53.8%; Score 685; DB 3; Length 1576;
Best Local Similarity 100.0%; Pred. NO. 0;
Matches 685; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY      590      TGCGTAATTCAGTACTTTTCCCTGTAAATATGCGTCTTCGATGTGAAATGAATCTGCG 649
DB      1      TGCGTAATTCAGTACTTTTCCCTGTAAATATGCGTCTTCGATGTGAAATGAATCTGCG 60
QY      650      CACACACAGAAAAGCAGACCATGAGAGCTCTGTGAGTTTGGGCTTATTCCTGTCCT 709
DB      61      CACACACAGAAAAGCAGACCATGAGAGCTCTGTGAGTTTGGGCTTATTCCTGTCCT 120
QY      710      GCCTGGTCTCTGTAATGCGAAGCTCTCTGATGCTGTATGCCCCATCTGATGC 769
DB      121      GCCTGGTCTCTGTAATGCGAAGCTCTCTGATGCTGTATGCCCCATCTGATGC 180
QY      770      ATCAGCATAGTCCATTACACCCCTACAGGAGGATAGTTTCTTCTGTACAGACA 829
DB      181      ATCAGCATAGTCCATTACACCCCTACAGGAGGATAGTTTCTTCTGTACAGACA 240
QY      830      TTAATCTTCTGCTGCTGTGATGCGGTGATGATGAGTCCCTGTTTGGCTTTCATCA 889
DB      241      TTAATCTTCTGCTGCTGTGATGCGGTGATGATGAGTCCCTGTTTGGCTTTCATCA 300
QY      890      TGTAGTCTTAGAAGAACAGGAAATAGATGGTCCACGAGGTTCTTCGCAATCGTAC 949
DB      301      TGTAGTCTTAGAAGAACAGGAAATAGATGGTCCACGAGGTTCTTCGCAATCGTAC 360
QY      950      AGCTGATAGGAACACGACGAGCTGAAATTTTCTTACCGACTTGAGCTAAATGGTC 1009
DB      361      AGCTGATAGGAACACGACGAGCTGAAATTTTCTTACCGACTTGAGCTAAATGGTC 420
QY      1010      ATAGGCGCAGTATGACTTGGGAAGCGACTCCTCGATCTATTATGAAAGGAATGCAACAG 1069
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Db      421      ATAGCGCAGGATTCAGTTTGGGAAGCGACTCCTCGATCTATTTCATGAGGAATTCGAACAG 480
QY      1070      CCATTATGAATAGGACGCTGTCTAGTCTTTGACACGACCATTCGACAGCTTTTTCGAGAAA 1129
DB      481      CCATTATGAATAGGACGCTGTCTAGTCTTTGACACGACCATTCGACAGCTTTTTCGAGAAA 540
QY      1130      ATGGCAATTTAGGCAATCAATGTAATCTATTTCCATGTGTGAAATGGCAATCAAAATTTT 1189
DB      541      ATGGCAATTTAGGCAATCAATGTAATCTATTTCCATGTGTGAAATGGCAATCAAAATTTT 600
QY      1190      CTGGCCAGTGTTTAAACTTCAGTTTCACGAAATAAGGACCCCATCTGCTGCAACACC 1249
DB      601      CTGGCCAGTGTTTAAACTTCAGTTTCACGAAATAAGGACCCCATCTGCTGCAACACC 660
QY      1250      TAAAACTCTTTTCGGTAGTGGAGGC 1274
DB      661      TAAAACTCTTTTCGGTAGTGGAGGC 685

RESULT 7
BQ447177      714 bp      mRNA      linear      EST 29-MAY-2002
LOCUS      UI-H-EUI-Bad-i-20-0-UI.s1 NCI-CGAP_Ctl Homo sapiens cDNA clone
DEFINITION      UI-H-EUI-Bad-i-20-0-UI 3', mRNA sequence.
ACCESSION      BQ447177
VERSION      BQ447177.1 GI:21250289
KEYWORDS      EST.
SOURCE      Homo sapiens (human)
ORGANISM      Homo sapiens
REFERENCE      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS      Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
TITLE      1 (bases 1 to 714)
JOURNAL      NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
COMMENT      National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
Contact: Robert Straubeberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue procurement: Dr. Jose Mercuende
cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Clone distribution information can be obtained
from Dr. M. Bento Soares, bento-soares@iowa.edu
The following repetitive elements were found in this cDNA
sequence: 1-53, >POLY A#Simple_repeat (matched complement)
Seq primer: M13 FORWARD
POLY A=Yes.
Location/Qualifiers
1..714
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="UI-H-EUI-Bad-i-20-0-UI"
/tissue_type="Osteoarthritic Cartilage"
/lab_host="DH10B (Life Technologies)"
/clone_lib="NCI CGAP Ctl"
/note="Organ: Knee; Vector: pUT3-Pac (Pharmacia) with a
modified polylinker; Site 1: EcoR I; Site 2: Not I;
NCI CGAP Ctl is a normalized cDNA library containing the
following tissue(s): Osteoarthritic Cartilage The library
was constructed according to Bonaldo, Lennon and Soares,
Genome Research, 6:791-806, 1996. First strand cDNA
synthesis was primed with an oligo-dT primer containing a
Not I site. Double stranded cDNA was ligated to an EcoR I
adaptor, digested with Not I, and cloned directionally
into pUT3-Pac vector. The oligonucleotide used to prime
the synthesis of first-strand cDNA contains a library tag
sequence that is located between the Not I site and the
(dT)18 tail. The sequence tag for this library is
TGATCAGCT.
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TAG_TISSUE=osteoarthritic cartilage
TAG_LIB=UI-H-EU1
TAG_SEQ=TGATCACGCT"

ORIGIN	Query Match	52.3%	Score 666;	DB 5;	Length 714;
	Best Local Similarity	100.0%;	Pred. No. 0;		
	Matches 666;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
Qy	174	ATCTTTTAAATCCTATTTTCTTCCTCTCAGTAAATTTTGTATGAAACTTTAA	233		
Db	22	ATCTTTTAAATCCTATTTTCTTCCTCTCAGTAAATTTTGTATGAAACTTTAA	81		
Qy	234	AAGGACTTATGCGCATGTAAACATTTATTAAGTAAGTCATGTTATTAATTTTCT	293		
Db	82	AAGGACTTATGCGCATGTAAACATTTATTAAGTAAGTCATGTTATTAATTTTCT	141		
Qy	294	CTGCGCTCCTTATGTAATTTATTTTCAGAAATGAGCGCTCAGACTGCTACAGCATTTACCTAC	353		
Db	142	CTGCGCTCCTTATGTAATTTATTTTCAGAAATGAGCGCTCAGACTGCTACAGCATTTACCTAC	201		
Qy	354	CGGTACCTCGAAGTGTCCACCATCCAGAGGGTGCTGCCCTGACTGGCAACTGCATC	413		
Db	202	CGGTACCTCGAAGTGTCCACCATCCAGAGGGTGCTGCCCTGACTGGCAACTGCATC	261		
Qy	414	CAACAATGACTTGGCGAGTCTTTTGTAGTGTCCAGTCTGCTTTTGACTATGTGTACCGCC	473		
Db	262	CAACAATGACTTGGCGAGTCTTTTGTAGTGTCCAGTCTGCTTTTGACTATGTGTACCGCC	321		
Qy	474	CATTCTTCAATGTCAGAGTGGCCATCTGTTTGTAGCAACTGTGCGCCCAAGCTCACATG	533		
Db	322	CATTCTTCAATGTCAGAGTGGCCATCTGTTTGTAGCAACTGTGCGCCCAAGCTCACATG	381		
Qy	534	TTGTCCAACTTGGCGGGCCCTTTGGGATCCATTCGCAACTTGGCTATGAGAAAGTGGC	593		
Db	382	TTGTCCAACTTGGCGGGCCCTTTGGGATCCATTCGCAACTTGGCTATGAGAAAGTGGC	441		
Qy	594	TAATTACGACTTTTCCCTGTAAATATGGTCTTCTGGATGTGAAATACTCTGCCACA	653		
Db	442	TAATTACGACTTTTCCCTGTAAATATGGTCTTCTGGATGTGAAATACTCTGCCACA	501		
Qy	654	CACAGAAAAAGCAGACCATGAAGAGCTCTGTGAGTATTAGGCCCTATTTCCTCGTGGCC	713		
Db	502	CACAGAAAAAGCAGACCATGAAGAGCTCTGTGAGTATTAGGCCCTATTTCCTCGTGGCC	561		
Qy	714	TGGTGTCTTCTGTAAATGGCAAGGCTCTCTGGATGCTGTAATGCCCATCTGATCATCA	773		
Db	562	TGGTGTCTTCTGTAAATGGCAAGGCTCTCTGGATGCTGTAATGCCCATCTGATCATCA	621		
Qy	774	GCATAAGTCATTACAAACCTTACAGGAGAGGATATAGTTTTTCTTGCTACAGACATTAA	833		
Db	622	GCATAAGTCATTACAAACCTTACAGGAGAGGATATAGTTTTTCTTGCTACAGACATTAA	681		
Qy	834	TCCTCC 839			
Db	682	TCCTCC 687			

RESULT 8
BY007202/4

BX097203 769 bp mRNA linear EST:04-FEB-2003
 BX097203 Soares retina N2b4HR Homo sapiens cDNA clone
 IMAGE380736, mRNA sequence.

BX097203
BX097203 1 GT:27843130

EST.

Homo sapiens (human)
Homo sapiens

Eukaryota; Metazoa;
Mammalia; Eutheria;

1 (bases 1 to 769)

Radelof, U., Schneide

TITLE Human Unigeneset - RZPD3
JOURNAL Unpublished (2003)
COMMENT Contact: Ina Rofls

Contact: Ina Rolfs
RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH
Im Neuenheimer Feld 580, D-69120 Heidelberg, Germany
RZPDLIB: IWAGp998N01881.
RZPDLIB: I.M.A.G.E. CDNA Clone Collection;
Human UnigeneSet - RZPD3 (RZPDLIB No.972)
[http://www.rzpd.de/Clonecards/cgi-
bin/showLib.pl.cgi?responseLibNo=372](http://www.rzpd.de/Clonecards/cgi-bin/showLib.pl.cgi?responseLibNo=372) Contact: Ina Rolfs
Deutsches Ressourcenzentrum fuer Genomforschung GmbH
Heubenerweg 6, D-14059 Berlin, Germany
Tel: +49 30 32639 101
Fax: +49 30 32639 111
www.rzpd.de
This clone is available royalty-free from RZPD;
Contact RZPD (clone@rzpd.de) for further information. Seq primer:
M13 primer sequences: ~~TTTCCACGCTTAAACCTTATGAC~~

FEATURES

```

I. .769
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IWAGp998N01881 ; IMAGE:380736"
/sex="male"
/tissue_type="retina"
/dev_host="55 year old"
/lab_notes="DH10B (ampicillin resistant)"
/clone_lib="Soares retina N2b4b"
/notes="Organ: eye; Vector: pTRC3D (Phar
modified polylinker; Site 1: Not I; Site 2:
strand cDNA was primed with a Not I - o
TGTTACAACTCTGAAGTGGAGCGCCGCGCTTTT
double-stranded cDNA was size selected,
adapters (Pharmacia), digested with Not
the Not I and Eco RI sites of a modified
(Pharmacia). The retinas were obtained
Caucasian and total cellular poly(A)
hrs after their removal. The retina RNA
provided by Roderick R. McInnes M.D. Ph.D.
University of Toronto. Library construc
Soares and M.Fatima Bonaldo. "

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ORIGIN

Query Match	52.3%;	Score 666;	DB 5;	Length 769
Best Local Similarity	100.0%;	Pred. No. 0;		
Matches 666;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
609	CCCTGTTAAATATGGCTCTTCGGATGTGAATAACTTCGCCACACACAGAAATAGCAGA	668		
686	CCCTGTTAAATATGGCTCTTCGGATGTGAATAACTTCGCCACACACAGAAATAGCAGA	627		
669	CCATGAAGAGCTCTGTGAGTTTGTAGGCTTTATTCCTGTCGGTGCCCTGCTTCCTCTTAA	728		
626	CCATGAAGAGCTCTGTGAGTTTGTAGGCTTTATTCCTGTCGGTGCCCTGCTTCCTGTAA	567		
729	ATGGCAAGGCTCTCGGATGCTGTAAATGCCCATCTGATGCATCAGCATAAATCCATTAC	788		
566	ATGGCAAGGCTCTCGGATGCTGTAAATGCCCATCTGATGCATCAGCATAAATCCATTAC	507		
789	AACCCCTACAGGAGAGGATATAGTTTTTCTTGCTACAGACATTAATCTTCTGGTGCTGT	848		
506	AACCCCTACAGGAGAGGATATAGTTTTTCTTGCTACAGACATTAATCTTCTGGTGCTGT	447		
849	TGACTGGGTGATGATGCAGTCCTGTTTTGGCTTTCACTTTCATGTTAGTCTTTAGAGAAACA	908		
446	TGACTGGGTGATGATGCAGTCCTGTTTTGGCTTTCACTTTCATGTTAGTCTTTAGAGAAACA	387		
909	GGAAAAATACGATGGTCAACGAGAGTTCTTTGGCAATCGTACAGCTGATAGGAACACGCCAA	968		
386	GGAAAAATACGATGGTCAACGAGAGTTCTTTGGCAATCGTACAGCTGATAGGAACACGCCAA	327		
969	GCAAGCTGNAATTTTGGCTTACCGACTTGAGCTTAAATGGTTCATAGGGACGATTGACTTG	1028		

TITLE HRI-human cDNA project
JOURNAL Unpublished (2000)
COMMENT Contact: Takao Isogai
Genomics Laboratory
Helix Research Institute
1530-3 Yana, Kisarazu, Chiba 292-0812, Japan
Tel: 81-438-52-3975
Fax: 81-438-52-3986
Email: genomics@hri.co.jp
HRI human cDNA project; 5'- & 3'-end one pass sequencing: Helix
Research Institute; cDNA library construction: Department of
Virology, Institute of Medical Science, University of Tokyo, and
Helix Research Institute.

FEATURES

source Location/Qualifiers
1. 812
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="HEMBA1006927"
/tissue_type="whole embryo, mainly head"
/dev_stage="embryo, 10 weeks"
/clone_lib="HEMBA1"
/note="Vector3, pME18SFL3"

ORIGIN

Query Match 50.4%; Score: 642; DB 1; Length 812;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 642; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 633 ATGTGAAATTAATCTGCCACACAGAAAAGGACCAATGAGAGCTCTGTGAGTTTAA 692
DB 800 ATGTGAAATTAATCTGCCACACAGAAAAGGACCAATGAGAGCTCTGTGAGTTTAA 741
QY 693 GCCTTATTCCTGTCGCGCCCTGCTCTCTGTAATGCGAAGGCTCTCTGATGCTCT 752
DB 740 GCCTTATTCCTGTCGCGCCCTGCTCTCTGTAATGCGAAGGCTCTCTGATGCTCT 681
QY 753 AATGCCCATCTGATGATCAGCATAAGTCCATTACACGCTACAGGGAGAGATATAGT 812
DB 680 AATGCCCATCTGATGATCAGCATAAGTCCATTACACGCTACAGGGAGAGATATAGT 621
QY 813 TTTTCTGTACAGACATTAATCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 872
DB 620 TTTTCTGTACAGACATTAATCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 561
QY 873 TTTTGGCTTTCACTTCATGTTAGTCTTTAGAGAAACAGGAAAATACGATGGTCACAGCA 932
DB 560 TTTTGGCTTTCACTTCATGTTAGTCTTTAGAGAAACAGGAAAATACGATGGTCACAGCA 501
QY 933 GTTCTTGGCAATCGTACAGCTGATAGGAACACGCAAGCAAGCTGAAATTTTGTTCACG 992
DB 500 GTTCTTGGCAATCGTACAGCTGATAGGAACACGCAAGCAAGCTGAAATTTTGTTCACG 441
QY 993 ACTTGAGCTTAATGTCATAGGAGCAGTATGCTGGGAGGAGCTGCTGCATCTATTCA 1052
DB 440 ACTTGAGCTTAATGTCATAGGAGCAGTATGCTGGGAGGAGCTGCTGCATCTATTCA 381
QY 1053 TGAAGGAATTCACACAGCATTATTAATAGCGACTGCTGCTGCTGCTGCTGCTGCTGCTG 1112
DB 380 TGAAGGAATTCACACAGCATTATTAATAGCGACTGCTGCTGCTGCTGCTGCTGCTGCTG 321
QY 1113 ACAGCTTTTTCAGAAAAATGGCAATTTAGGCAATCAATGTAATTTTCAATGTTGAAA 1172
DB 320 ACAGCTTTTTCAGAAAAATGGCAATTTAGGCAATCAATGTAATTTTCAATGTTGAAA 261
QY 1173 TGGCAATCAAAATTTTTCGGCAGTGTAAAACTTCAGTTTTCAGAAAAATAGGCAC 1232
DB 260 TGGCAATCAAAATTTTTCGGCAGTGTAAAACTTCAGTTTTCAGAAAAATAGGCAC 201
QY 1233 CCATCTGTGCGCAACCTTAATCTTTTCGGTAGTGGAGC 1274
DB 200 CCATCTGTGCGCAACCTTAATCTTTTCGGTAGTGGAGC 159

RESULT 11

BX366404
LOCUS BX366404 Homo sapiens NEUROBLASTOMA COT 25-NORMALIZED Homo sapiens
DEFINITION CDNA clone CSODC023YH14 5-PRIME, mRNA sequence.
ACCESSION BX366404
VERSION BX366404.2 GI:46572835
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 859)
AUTHORS Li, W. B., Grubel, C., Jessee, J. and Polayes, D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished (2000)
COMMENT On May 8, 2003 this sequence version replaced gi:30447532.
Contact: Genoscope
Genoscope - Centre National de Sequencage
2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
Email: seqref@genoscope.cns.fr, Web: www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo (dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen. This sequence belongs to sequence cluster
8104.r

For more information about this cluster, see

http://www.genoscope.cns.fr/cdnap?e=CSODC023DD07QP2&c=8104.r.

FEATURES

source Location/Qualifiers
1. 859
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CSODC023YH14"
/tissue_type="NEUROBLASTOMA COT 25-NORMALIZED"
/clone_lib="Homo sapiens NEUROBLASTOMA COT 25-NORMALIZED"
/note="1st strand cDNA was primed with a NotI-oligo (dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and EcoR sites of the pCMVSPORT 6 vector. Library was
normalized." sites of the pCMVSPORT 6 vector. Library was normalized."

ORIGIN

Query Match 50.0%; Score 637; DB 5; Length 859;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 687; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 317 CAGAAATGAGCGCTCAGACTGCTACAGCAATTAACCTACCGGTACCTCGAAGTGTCCACCAT 376
DB 1 CAGAAATGAGCGCTCAGACTGCTACAGCAATTAACCTACCGGTACCTCGAAGTGTCCACCAT 60
QY 377 CCCAGAGGTGCTCCCTGACTGCGACACACTGCATCCCAATGACTTGGCGAGTCTTT 436
DB 61 CCCAGAGGTGCTCCCTGACTGCGACACACTGCATCCCAATGACTTGGCGAGTCTTT 120
QY 437 TTGAGTGTCCAGTCTGCTTTGACTATGTTTACCGCCCATCTTCAATGTCAGAGTGGCC 496
DB 121 TTGAGTGTCCAGTCTGCTTTGACTATGTTTACCGCCCATCTTCAATGTCAGAGTGGCC 180
QY 497 ATCTGTTTGTAGCAACTGTGCCCAAGCTCACATGTTGTCCAACTTGC CGGGGCCCTT 556
DB 181 ATCTGTTTGTAGCAACTGTGCCCAAGCTCACATGTTGTCCAACTTGC CGGGGCCCTT 240
QY 557 TGGGATTCATTCGCAACTTGGCTATGGAGAAAGTGGCTAAATTCAGTACTTTTCCCTGTA 616
DB 241 TGGGATTCATTCGCAACTTGGCTATGGAGAAAGTGGCTAAATTCAGTACTTTTCCCTGTA 300
QY 617 AATATGCGTCTTCTGGATGTGAATAACTCTGCCACACACAGAAAAGCAGACCATGAG 676
DB 301 AATATGCGTCTTCTGGATGTGAATAACTCTGCCACACACAGAAAAGCAGACCATGAG 360
QY 677 AGCTCTGTGAGTTTAGGCTTATTCTCTGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 736

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|||||
361 AGCTCTGTGAGTTAGGCTTATCTGTGCGCTGCTTCTCTGTAATGGCAAG 420
QY 737 GCTCTCTGATGCTGTAATGCCATCTGATGATCAGCATAGTCCATTACAACTTAC 796
Db 421 GCTCTCTGATGCTGTAATGCCATCTGATGATCAGCATAGTCCATTACAACTTAC 480
QY 797 AGGGAGAGGATAGTATTTCTTCTGCTACAGCAATTAATCTTCTGCTGCTGTTGACTGG 856
Db 481 AGGGAGAGGATAGTATTTCTTCTGCTACAGCAATTAATCTTCTGCTGCTGTTGACTGG 540
QY 857 TGATGATGAGCTGCTGTTTCTGCTTCTGCTTCTGCTTCTGCTTCTGCTTCTGCTTCT 916
Db 541 TGATGATGAGCTGCTGTTTCTGCTTCTGCTTCTGCTTCTGCTTCTGCTTCTGCTTCT 600
QY 917 AGGATGCTCACAGAGCTTCTTCTGCTTCTGCTTCTGCTTCTGCTTCTGCTTCTGCTTCT 976
Db 601 AGGATGCTCACAGAGCTTCTTCTGCTTCTGCTTCTGCTTCTGCTTCTGCTTCTGCTTCT 660
QY 977 AAAATTTTGTCTTACCGACTTGTAGCTAAA 1004
Db 661 AAAATTTTGTCTTACCGACTTGTAGCTAAA 688

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RESULT 12
BU662334
LOCUS
DEFINITION
  BU662334
  sapiens cDNA clone cl84612 5', mRNA sequence.
ACCESSION
  BU662334
  GI:23374518
VERSION
  EST.
KEYWORDS
  Homo sapiens (human)
SOURCE
  Homo sapiens
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
  1 (bases 1 to 693)
AUTHORS
  Gubin,A.N., Lee,Y.T., Bouffard,G.G. and Miller,J.L.
  Gene Expression in Human Erythroid Precursor Cells
  Unpublished (2002)
  Contact: Jeffery L. Miller
  Laboratory of Chemical Biology
  National Institute of Diabetes and Digestive and Kidney Diseases
  Building 10, Room 9B17, National Institutes of Health, Bethesda, MD
  20892, USA
  Tel: 301 402 2373
  Fax: 301 435 5148
  Email: jlm@nih.gov
  The 'cl' library was constructed by Alexander Gubin, Ph.D. in the
  Laboratory of Chemical Biology, NIDDK, NIH. DNA Sequencing and/or
  analyses by National Institutes of Health Intramural Sequencing
  Center (NISC). More information available at:
  http://hembase.nidk.nih.gov
  Plate: 84 row: e column: 12
  Seq primer: 5' lambda-Triplex2 Sequencing Primer.
  Location/Qualifiers
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      /organism="Homo sapiens"
      /mol_type="mRNA"
      /db_xref="taxon:9606"
      /clone="cl84612"
      /sex="unknown"
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      /cell_type="Erythroid Precursor Cells"
      /cell_line="Primary Culture of Peripheral Blood
      Mononuclear Cells"
      /dev_stage="Precursor erythroblasts; GPA++"
      /lab_host="DH5alpha"
      /clone_lib="Hembase; Erythroid Precursor Cells (LCB:cl
      library)"
      /note="Organ: blood; Vector: pTriplex2; Site_1: SfiI;
      Site_2: SfiI; A complementary DNA (cDNA) library from
      human erythroid precursor cells was constructed using

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FEATURES

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Source
Query Match 49.7%; Score 633; DB 5; Length 693;
Best Local Similarity 99.9%; Pred.No. 0;
Matches 683; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 95 GGAACATTTTGAAGAGAGAGCTTATCCAGTGTACAGATCCTAATAAAGTGCAATTCAGT 154
Db 10 GGAACATTTTGAAGAGAGAGCTTATCCAGTGTACAGATCCTAATAAAGTGCAATTCAGT 69
QY 155 GTAATTTTATTTTAAATATCTTTTAAATCTTTTAAATCTTTTCTCTCTCTCTCTCTCT 214
Db 70 GTAATTTTATTTTAAATATCTTTTAAATCTTTTAAATCTTTTCTCTCTCTCTCTCTCT 129
QY 215 ATTTTGTATGAACCTTAAAGAGAGCTTATGCATGTAAACATTTATTAAGAGTAAAGTCA 274
Db 130 ATTTTGTATGAACCTTAAAGAGAGCTTATGCATGTAAACATTTATTAAGAGTAAAGTCA 189
QY 275 TGGTTATATTTATTTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 334
Db 190 TGGTTATATTTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 249
QY 335 CTGTACAGCATTTACCTACCGTACCTGAGTGTCCACCATCCAGAGGGTCTCTGCCC 394
Db 250 CTGTACAGCATTTACCTACCGTACCTGAGTGTCCACCATCCAGAGGGTCTCTGCCC 309
QY 395 TGACTGGCAGCAACTGCATCCCAATGACTTGGCGAGTCTTTTTCAGTGTCCAGTCTGCT 454
Db 310 TGACTGGCAGCAACTGCATCCCAATGACTTGGCGAGTCTTTTTCAGTGTCCAGTCTGCT 369
QY 455 TTGACTATGTGTATACCGCCCAATTTCTCAATGTACAGTGGCCATCTTGTGTAGCAAT 514
Db 370 TTGACTATGTGTATACCGCCCAATTTCTCAATGTACAGTGGCCATCTTGTGTAGCAAT 429
QY 515 GTGCGCCAAAGCTCACATGTTGTCCAACTTCCGGGGCCCTTTGGGATCCATTCCCACT 574
Db 430 GTGCGCCAAAGCTCACATGTTGTCCAACTTCCGGGGCCCTTTGGGATCCATTCCCACT 489
QY 575 TGGCTATGGAGAAAGTGGCTAATTCAGTACTTTTCCCTGTAAATATGCTCTTCTGGAT 634
Db 490 TGGCTATGGAGAAAGTGGCTAATTCAGTACTTTTCCCTGTAAATATGCTCTTCTGGAT 549
QY 635 GTGAATAAATCTGTCCACACACAGAAAAAGCAGACCATGAGAGCTGTGTAGTTAGGC 694
Db 550 GTGAATAAATCTGTCCACACACAGAAAAAGCAGACCATGAGAGCTGTGTAGTTAGGC 609
QY 695 CTTATTTCTGTCCGGGCTGTGTCTTCTGTAAATGGCAAGCTCTCTGGATGCTGTAA 754
Db 610 CTTATTTCTGTCCGGGCTGTGTCTTCTGTAAATGGCAAGCTCTCTGGATGCTGTAA 669
QY 755 TGCCCCCATCTGATGATCAGCAT 778
Db 670 TGCCCCCATCTGATGATCAGCAT 693

```

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RESULT 13
BG619351
LOCUS
DEFINITION

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```

BG619351
602619484F1 NIH_MGC_79 Homo Sapiens cDNA clone IMAGE:4733228 5'
mRNA sequence.
EST 18-APR-2001

```

SMART PCR (polymerase chain reaction) cDNA Library Construction Kit (Clontech, Palo Alto, CA) according to the manufacturer's directions, but with slight modifications. Briefly, reverse transcription was performed in the presence of 1 umol/L peptide nucleic acid (PNA) oligos (N-terminal)-biotin-GTC-CAC-CCG-AAG-CTT-G- (C-terminal) and (N-terminal)-biotin-C(T/C)T-GAA-GTT-CTC-AGG-A- (C-terminal). Synthesized cDNA was digested with SfiI and size-selected on a 1% agarose gel (>800bp). Large-scale sequencing of the library was performed by the NIH Intramural Sequencing Center (NISC; <http://www.nisc.nih.gov/>).

Db 541 AATTGCAACAGCCATTATGAATGGGAGCTGTCTAGTCTTTTGACACAGCAGTTGCACAGCT 600

Qy 1119 TTTTGCAGAAATGG 1133

Db 601 TTTTGCAGAAATGG 615

RESULT 16

AI936347

LOCUS

DEFINITION

similar to TR:043269 O43269 HSAHL.1., mRNA sequence.

ACCESSION

AI936347

VERSION

EST.

KEYWORDS

EST.

SOURCE

Homo sapiens (human)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

1 (bases 1 to 779)

AUTHORS

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

TITLE

National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index

JOURNAL

Unpublished (1997)

COMMENT

Contact: Robert Strausberg, Ph.D.

Email: cgabbs-remail.nih.gov

Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R. Emmert-Buck, M.D., Ph.D.

CDNA Library Preparation: M. Bento Soares, Ph.D.

CDNA Library Arrayed by: Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center

Clone Distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: www-bio.llnl.gov/bbrp/image/image.html

Insert Length: 1411

Seq primer: -40UP from Gibco

High quality sequence stop: 444

Location/Qualifiers

1. .779

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="IMAGE:2461725"

/lab_host="DH10B"

/clone_lib="NCI CGAP Kid1"

/note="Organ: Kidney; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site: 1: Not 1; Site 2: Eco RI; Plasmid DNA from the normalized library NCI CGAP Kid3 was prepared, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from a pool of 5,000 clones made from the same library (cloneID# 1322376-1323911, 1456007-1456775, and 1500552-1502853). Subtraction by Bento Soares and M. Fatima Bonaldo."

ORIGIN

Query Match 48.0%; Score 611; DB 1; Length 779;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 611; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 203 TTTGCTCAGTAAATTTTGTAGAACTTTTAAAGGACCTTATGCGCATGTAAACATTATTTA 262

Db 1 TTTGCTCAGTAAATTTTGTAGAACTTTTAAAGGACCTTATGCGCATGTAAACATTATTTA 60

Qy 263 TAAAGTAAGTCATGGTTAATAATTTTCTCGTCCCTCTATGATTTATTTATTCAGAAA 322

Db 61 TAAAGTAAGTCATGGTTAATAATTTTCTCGTCCCTCTATGATTTATTTATTCAGAAA 120

Qy 323 TCAGCCGTCAGACTGCTACAGCATTTACCTACCGGTACCTCGAAGTGTCCACCATCCAGA 382

Db 121 TGAGCCGTCAGACTGCTACAGCATTTACCTACCGGTACCTCGAAGTGTCCACCATCCAGA 180

Qy 383 GGGTGCCTCCCTGACTGCGCAACAACATGCAATCAAAATGACCTTGGCGAGTCTTTTGGAT 442

Db 181 GGGTGCCTCCCTGACTGCGCAACAACATGCAATCAAAATGACCTTGGCGAGTCTTTTGGAT 240

Qy 443 GTCCAGTCTGCTTGCATATGTTTACCGCCCATCTTCAATGTCAGAGTGGCCATCTTG 502

Db 241 GTCCAGTCTGCTTGCATATGTTTACCGCCCATCTTCAATGTCAGAGTGGCCATCTTG 300

Qy 503 TTTGTAGCAACTGTGCGCCCAAGCTCACATGTTGTCCAACTTGCCTGGGGGCCCTTTGGGAT 562

Db 301 TTTGTAGCAACTGTGCGCCCAAGCTCACATGTTGTCCAACTTGCCTGGGGGCCCTTTGGGAT 360

Qy 563 CCATTGCGAACTTGGCTATGAGAGAGTGGCTAAATTCAGTACTTTTCCCTCTGAATATG 622

Db 361 CCATTGCGAACTTGGCTATGAGAGAGTGGCTAAATTCAGTACTTTTCCCTCTGAATATG 420

Qy 623 GCTCTTCGTGAGTGAATAAATCTCTCCACACACAGAAAAGCAGACCATGAAGACTCT 682

Db 421 GCTCTTCGTGAGTGAATAAATCTCTCCACACACAGAAAAGCAGACCATGAAGACTCT 480

Qy 683 GTGAGTTAGGCTTATTCCTGCTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 742

Db 481 GTGAGTTAGGCTTATTCCTGCTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 540

Qy 743 TCGATGCTGTAATGCCCCATCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 802

Db 541 TCGATGCTGTAATGCCCCATCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 600

Qy 803 AGGATATAGTT 813

Db 601 AGGATATAGTT 611

RESULT 17

BI560892

LOCUS

DEFINITION

603254068F1 NIH_MGC_97 Homo sapiens cDNA clone IMAGE:5296552 5'

mrna sequence.

ACCESSION

BI560892

VERSION

EST.

KEYWORDS

SOURCE

Homo sapiens (human)

ORGANISM

Homo sapiens

REFERENCE

1 (bases 1 to 735)

AUTHORS

NIH-MGC http://mgi.nci.nih.gov/

TITLE

National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL

Unpublished (1999)

COMMENT

Contact: Robert Strausberg, Ph.D.

Tissue Procurement: Miklos Palkovits, M.D., Ph.D.

CDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki Toshiyuki and Piero Carninci (RIKEN)

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone Distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov

Plate: LLAM11750 row: 9 column: 17

High quality sequence stop: 732.

Location/Qualifiers

1. .735

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="IMAGE:5296552"

/lab_host="DH10B"

/clone_lib="NIH MGC 97"

/note="Organ: testis; Vector: BluescriptR (modified pUCscript KS+); Site: 1: BamHI; Site: 2: SalI-XhoI (gtcgag); Oligo-dT primed using primer 5'-ATTTTATTTTATTTTATTTT-3', size-selected for average

FEATURES

source

Insert size 2.2 kb and normalized to ROT 5. This is a primary library enriched for full-length clones and constructed using the Cap-trapper method (Carninci, in preparation). Library constructed by M. Brownstein (NIH/NHGRI, National Institutes of Health). Note: this is a NIH_MGC Library."

ORIGIN		Query Match		46.3%; Score 590; DB 4; Length 735;	
		Best Local Similarity		100.0%; Pred. No. 2.3e-305;	
		Matches 590; Conservative		0; Mismatches 0; Indels 0; Gaps 0;	
QY	317	CAGAATGAGCGCTGACAGTCTGACAGATTAACCTACCGGTACCTCGAAGTGTCCACCAT	376		
DB	146	CAGAATGAGCGCTGACAGTCTGACAGATTAACCTACCGGTACCTCGAAGTGTCCACCAT	205		
QY	377	CCGAGAGGTGCTGCTCCCTGACTGCGCACAACTGCAATCAACAACTGCGAGTCTTT	436		
DB	206	CCGAGAGGTGCTGCTCCCTGACTGCGCACAACTGCAATCAACAACTGCGAGTCTTT	265		
QY	437	TTGAGTGTCCAGTCTGCTTTGACTATGTTACCGCCCATTTCTCAATGTGACAGTGGCC	496		
DB	266	TTGAGTGTCCAGTCTGCTTTGACTATGTTACCGCCCATTTCTCAATGTGACAGTGGCC	325		
QY	497	ATCTTTGTTGTAGCAACTGTGCGCCCAAGCTCACATGTTGTCCAACTTGGCGGCGCCCTT	556		
DB	326	ATCTTTGTTGTAGCAACTGTGCGCCCAAGCTCACATGTTGTCCAACTTGGCGGCGCCCTT	385		
QY	557	TGGGATCCATTCGCAACTTGGCTATGGAGAAAGTGGCTAAATTCAGTCTTTCCCTGTGA	616		
DB	386	TGGGATCCATTCGCAACTTGGCTATGGAGAAAGTGGCTAAATTCAGTCTTTCCCTGTGA	445		
QY	617	ATATGCGCTTCTGAGTGTGAATAAATCTCTGCCACACACAGAAAGCAGACCATGAAG	676		
DB	446	ATATGCGCTTCTGAGTGTGAATAAATCTCTGCCACACACAGAAAGCAGACCATGAAG	505		
QY	677	AGCTCTGTGAGTTAGGCTTATCTCTGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	736		
DB	506	AGCTCTGTGAGTTAGGCTTATCTCTGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	565		
QY	737	GCTCTGTGATGCTGAATGCGCCATCTGATGATGATGATGATGATGATGATGATGATGATG	796		
DB	566	GCTCTGTGATGCTGAATGCGCCATCTGATGATGATGATGATGATGATGATGATGATGATG	625		
QY	797	AGGAGAGATATGCTTTCTGCTGACAGATAATCTCTCTGCTGCTGCTGCTGCTGCTGCTG	856		
DB	626	AGGAGAGATATGCTTTCTGCTGACAGATAATCTCTCTGCTGCTGCTGCTGCTGCTGCTG	685		
QY	857	TCATGATGAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	906		
DB	686	TCATGATGAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	735		

RESULT 18
AI971258
LOCUS
DEFINITION
similar to TR_043269 043269 HSAH1.1; mRNA sequence.
ACCESSION
AI971258
VERSION
AI971258.1
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 778)
AUTHORS
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
TITLE
Unpublished (1997)
JOURNAL
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Michael J. Brownstein, M.D., Ph.D., Michael R.

Emmert-Buck, M.D., Ph.D.
cDNA Library Preparation: M. Bento Soares, Ph.D.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Insert Length: 826 Std Error: 0.00
Seq primer: -40bp from Gibco
High quality sequence stop: 455.
Location/Qualifiers
1. 778

FEATURES
source
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:248887"
/sex="male"
/dev_stage="adult"
/lab_host="DH10B"
/clone_lib="NCI CGAP Pr28"
/note="Jordan; prostate; Vector: p7T3D-Pac (Pharmacia)
with a modified polylinker; Plasmid DNA from the
normalized library NCI CGAP Pr22 was prepared, and ss
circles were made in vitro. Following HAP purification,
this DNA was used as tracer in a subtractive hybridization
reaction. The driver was PCR-amplified cDNAs from a pool
of 5,000 clones made from the same library (clones IDs
985608-986759, 1101192-1101959, and 1217928-1220615).
Subtraction by Bento Soares and M. Fatima Bonaldo."

ORIGIN		Query Match		44.0%; Score 561; DB 1; Length 778;	
		Best Local Similarity		99.8%; Pred. No. 9.2e-290;	
		Matches 611; Conservative		0; Mismatches 1; Indels 0; Gaps 0;	
QY	193	TTCTTCCTCTTTGCTGCTGATTAATTTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	252		
DB	38	TTCTTCCTCTTTGCTGCTGATTAATTTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	97		
QY	253	ACATTAATTAATAAGTAACTGATGATTAATTTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	312		
DB	98	ACATTAATTAATAAGTAACTGATGATTAATTTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	157		
QY	313	ATTTTCAGAAATGAGCGGTGAGTCTGCTGATGATTAATTTTCTGCTGCTGCTGCTGCTGCTGCTG	372		
DB	158	ATTTTCAGAAATGAGCGGTGAGTCTGCTGATGATTAATTTTCTGCTGCTGCTGCTGCTGCTGCTG	217		
QY	373	CCATCCAGAGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	432		
DB	218	CCATCCAGAGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	277		
QY	433	CTTTTGTGAGTGTCCAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	492		
DB	278	CTTTTGTGAGTGTCCAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	337		
QY	493	GGCCATCTTTGTTGTAGCAACTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	552		
DB	338	GGCCATCTTTGTTGTAGCAACTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	397		
QY	553	CCTTTGGGATCCATTCGCAACTTGGCTATGGAGAAAGTGGCTAAATTCAGTACTTTTCCCC	612		
DB	398	CCTTTGGGATCCATTCGCAACTTGGCTATGGAGAAAGTGGCTAAATTCAGTACTTTTCCCC	457		
QY	613	TGTAATAATGCTGCTTCTGGAATGTGAATAAATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	672		
DB	458	TGTAATAATGCTGCTTCTGGAATGTGAATAAATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	517		
QY	673	GAAGAGCTCTGTGAGTTAGGCTTATTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	732		
DB	518	GAAGAGCTCTGTGAGTTAGGCTTATTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	577		
QY	733	CAAGGCTCTCTGAGTCTGTAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	792		

Db 578 CRAAGGCTCTCTGGAAGCTGTGTAATGCCCATCTGATCATCAGATAAGTCCATTACAACC 637

QY 793 CTACAGGGAGAG 804

Db 638 CTACAGGGAGAG 649

RESULT 19
CD251717/C

LOCUS
DEFINITION
AGENCOURT 14214075 NIH MGC 179 Homo sapiens cDNA clone
IMAGE:30384822 5', mRNA sequence.

ACCESSION
CD251717

VERSION
CD251717.1 GI:31012183

KEYWORDS
EST.

SOURCE
Homo sapiens (human)

ORGANISM
Homo sapiens

REFERENCE
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 980)
NIH-MGC <http://mgi.nci.nih.gov/>.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Daniela S. Gerhard, Ph.D.
Office of Cancer Genomics
National Cancer Institute / NIH
Bldg. 31 Rm10A07 Bethesda, MD 20892
Email: cgabbs-remail.nih.gov
Tissue Procurement: Dr. Michael Brownstein
CDNA Library Preparation: Invitrogen Corp
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing By: Agencourt Bioscience Corporation
Clone Distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: ND4M450 row 0 column: 07
High quality sequence stop: 557.

FEATURES
source
1. 980
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:30384822"
/tissue_type="Pituitary"
/lab_host="DH10B" (T1 and T5 phage resistances)"
/clone_lib="NIH MGC 179"
/note="Organ: brain; Vector: pCMV-SPORT6.1; Site 1: EcoRV
(destroyed); Site 2: NotI; Library is oligo-dT primed and
directionally cloned (EcoRV site is destroyed upon
cloning). Average insert size 1.1 kb. Library was
constructed by (Invitrogen). Note: this is a NIH_MGC
Library."

ORIGIN
Query Match 41.2%; Score 525; DB 6; Length 980;
Best Local Similarity 100.0%; Pred. No. 2e-270;
Matches 525; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 127 ACAGATCCCTAATAAGAGTCACATTCAGTCAATTTATTTTATATCTTTTATATCTTTTATATC 186

Db 551 ACAGATCCCTAATAAGAGTCACATTCAGTCAATTTATTTTATATCTTTTATATCTTTTATATC 492

QY 187 CTATTTTCT 246

Db 491 CTATTTTCT 432

QY 247 ATGTAAACATTTATATAAGTAAGTCATGCTGTTATATTTTCTCTCTCTCTCTCTCTCTCTCTAT 306

Db 431 ATGTAAACATTTATATAAGTAAGTCATGCTGTTATATTTTCTCTCTCTCTCTCTCTCTCTAT 372

QY 307 GTATTTATTTTCAAGATGAGCGTCAGCTGCTACAGCATTTACCTACCGGTACCTCGAG 366

Db 371 GTATTTATTTTCAAGATGAGCGTCAGCTGCTACAGCATTTACCTACCGGTACCTCGAG 312

QY 367 TGTCCACCATCCAGAGGCTGCTGCCCTGACTGGCACAACATGTCATCCAAACATGACTTG 426

Db 311 TGTCCACCATCCAGAGGCTGCTGCCCTGACTGGCACAACATGTCATCCAAACATGACTTG 252

QY 427 GCGAGTCTTTTGGAGTCTCCAGTCTGCTTTGACTATGTTACCGCCCATTTCTTCAATGT 486

Db 251 GCGAGTCTTTTGGAGTCTCCAGTCTGCTTTGACTATGTTACCGCCCATTTCTTCAATGT 192

QY 487 CAGAGTGGCCATCTTTGTTGAGCAACTGTCGCCCAAGCTCACATGTTGTCCAACTTGC 546

Db 191 CAGAGTGGCCATCTTTGTTGAGCAACTGTCGCCCAAGCTCACATGTTGTCCAACTTGC 132

QY 547 CGGGGCCCTTTGGGATCCATTCGCAACTTTGGCTATGGAGAAAGTGGCTAATTCAGTACTT 606

Db 131 CGGGGCCCTTTGGGATCCATTCGCAACTTTGGCTATGGAGAAAGTGGCTAATTCAGTACTT 72

QY 607 TTCCCTCTGTAATATATGCTCTTCTTGGATCTGAATAAATCTCTGCCA 651

Db 71 TTCCCTCTGTAATATATGCTCTTCTTGGATCTGAATAAATCTCTGCCA 27

RESULT 20
CK822873

LOCUS
DEFINITION
i195011y5 Melton Normalized Human Islet 4 N4-HIS 1 Homo sapiens
cDNA clone IMAGE:6135097 5' similar to TR:043269 O43269 HSI4H1.1;
mRNA sequence.

ACCESSION
CK822873

VERSION
CK822873.1 GI:44839798

KEYWORDS
EST.

SOURCE
Homo sapiens (human)

ORGANISM
Homo sapiens

REFERENCE
1 (bases 1 to 586)
Melton, D., Meadows, A., Clifton, S., Hillier, L., Marra, M., Pape, D.,
Wyllie, T., Martin, J., Blistain, A., Schmitt, A., Theising, B.,
Ritter, E., Ronko, J., Bennett, J., Cardenas, M., Gibbons, M.,
McCann, R., Cole, R., Tsagarishvili, R., Williams, T., Jackson, Y. and
Bowers, Y.

AUTHORS
WashU-Harvard Pancreas EST Project
Unpublished (2000)
Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue
Endocrine Pancreas Consortium
Harvard University, Howard Hughes Medical Institute
Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge,
MA 02138
Tel: 617-495-1812
Fax: 617-495-8557
Email: dmelton@biohp.harvard.edu

TITLE
JOURNAL
COMMENT
This read is a 5' RESEQUENCE of a previously sequenced pancreas
clone

FEATURES
source
1. 586
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:6135097"
/sex="Both"
/tissue_type="Islets of Langerhans"
/dev_stage="Adult"
/lab_host="DH10B"
/clone_lib="Melton Normalized Human Islet 4 N4-HIS 1"
/note="Organ: Pancreas; Vector: pSPORT1; Site 1: Not 1;
Site 2: Sal 1; Starting library constructed using
SuperScript Plasmid library kit (Life Technologies). cDNA
made by oligo-dT priming. Size-selected by column
fractionation; average insert size 1.08 kb. Library was
amplified once on solid support and plasmid DNA from

BX463976
 BX463976.2 GI:47053846
 EST.
 Homo sapiens (human)
 Homo sapiens

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 852)
Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
Full-length cDNA libraries and normalization
Unpublished (2001)
On May 22, 2003 this sequence version replaced gi:31023592.

Contact: Genoscope
Genoscope - Centre National de Sequencage
2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
Email: seqrefgenoscope.cns.fr, Web : www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoRV sites of the pCMVSPORT 6 vector. Library
was not normalized. Library was constructed by Life Technologies, a
division of Invitrogen.
This sequence belongs to sequence cluster 8104.r
For more information about this cluster, see
http://www.genoscope.cns.fr/cdna?&=CSIAF0062A01QP1&c=8104.r.

FEATURES
source

Location/Qualifiers
1. .852
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0DF021Y201"
/tissue_type="FETAL BRAIN"
/dev_stage="fetal"
/clone_lib="Homo sapiens FETAL BRAIN"
/note="Organ: brain; Vector: pCMVSPORT 6; 1st strand cDNA
was primed with a NotI-oligo(dT) primer. Five prime end
enriched, double-strand cDNA was digested with Not I and
cloned into the Not I and EcoRV sites of the pCMVSPORT 6
vector. Library was not normalized."

ORIGIN

Query Match 39.1%; Score 498; DB 5; Length 852;
Best Local Similarity 99.8%; Pred. No. 3e-256;
Matches 548; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 317 CAGAATGACCGCTGACAGCTGTACAGCAATTAACCTACCGGTACCTCGAAGTGTCCACCAT 376
DB 1 CAGAATGACCGCTGACAGCTGTACAGCAATTAACCTACCGGTACCTCGAAGTGTCCACCAT 60
QY 377 CCCAGAGGTGCTGCGCTGACTGGCACAACCTGCAATCCAAATGATGTTGGCGAGTCTTT 436
DB 61 CCCAGAGGTGCTGCGCTGACTGGCACAACCTGCAATCCAAATGATGTTGGCGAGTCTTT 120
QY 437 TTGAGTGTCCAGTCTGTTGACTATGTGTTACCGGCAATTTCTCAATGTCAGAGTGCC 496
DB 121 TTGAGTGTCCAGTCTGTTGACTATGTGTTACCGGCAATTTCTCAATGTCAGAGTGCC 180
QY 497 ATCTTGTGTTAGCACTGTGCGCCCAAGCTCAGATGTTGTCAACTTCCGGGGGCCCTT 556
DB 181 ATCTTGTGTTAGCACTGTGCGCCCAAGCTCAGATGTTGTCAACTTCCGGGGGCCCTT 240
QY 557 TGGGATCCATTCCCACTTGGGTATGAGAAAGTGCTTAATTCAGTACTTTTCCCTGTA 616
DB 241 TGGGATCCATTCCCACTTGGGTATGAGAAAGTGCTTAATTCAGTACTTTTCCCTGTA 300
QY 617 ATATGCGTCTTCTGGATGTAATTAACCTGCGCACACAGAAAGCAGACCATGAG 676
DB 301 ATATGCGTCTTCTGGATGTAATTAACCTGCGCACACAGAAAGCAGACCATGAG 360
QY 677 AGCTCTGTGAGTTTAGGCTTATCTCTGTCGTCCTGCTGCTTCTGTAATGCGAAG 736
DB 361 AGCTCTGTGAGTTTAGGCTTATCTCTGTCGTCCTGCTGCTTCTGTAATGCGAAG 420
QY 737 GCTCTCTGGATGCTGTAATGCCCACTCTGATGATCAGCATTAAGTCCATTACAACCTTAC 796
DB 421 GCTCTCTGGATGCTGTAATGCCCACTCTGATGATCAGCATTAAGTCCATTACAACCTTAC 480
QY 797 AGGAGAGAGATAGTTTTTCTTGCTACAGCAATTAATCTTCTGCTGCTGTTGACTGGG 856

Db 481 AGGAGAGAGATAGTTTTTCTTGCTACAGCAATTAATCTTCTGCTGCTGTTGACTGGG 540
QY 857 TGATGATGG 865
Db 541 TGATGATGC 549

RESULT 23
BX390856
LOCUS
DEFINITION
CDNA clone CS0DK012Y120 5-PRIME, mRNA sequence.
BX390856
ACCESSION
BX390856
VERSION
BX390856.2 GI:46875200
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
Full-length cDNA libraries and normalization
Unpublished (2001)
On May 13, 2003 this sequence version replaced gi:30619239.

Contact: Genoscope
Genoscope - Centre National de Sequencage
2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
Email: seqrefgenoscope.cns.fr, Web : www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoRV sites of the pCMVSPORT 6 vector. Library
was not normalized. Library was constructed by Life Technologies, a
division of Invitrogen. This sequence belongs to sequence cluster
8104.r
For more information about this cluster, see
http://www.genoscope.cns.fr/cdna?&=CS0BAG050ZE02_CS04717_1&c=8104.r.

FEATURES
source

Location/Qualifiers
1. .969
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0DK012Y120"
/cell_type="HELA CELLS"
/cell_line="HELA"
/clone_lib="Homo sapiens HELA CELLS COT 25-NORMALIZED"
/note="1st strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and EcoRV sites of the pCMVSPORT 6 vector. Library was normalized."

ORIGIN

Query Match 39.0%; Score 497; DB 5; Length 969;
Best Local Similarity 100.0%; Pred. No. 2.5e-255;
Matches 497; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 710 GCCCTGTGCTTCTCTGTAATGCGCAAGCTCTCTGATGCTGTAAATGCCCATCTCATGC 769
DB 1 GCCCTGTGCTTCTCTGTAATGCGCAAGCTCTCTGATGCTGTAAATGCCCATCTCATGC 60
QY 770 ATCAGATAAGTCCATTACACCCCTACAGGAGAGATATAGTTTTTCTTGCTACAGACA 829
DB 61 ATCAGATAAGTCCATTACACCCCTACAGGAGAGATATAGTTTTTCTTGCTACAGACA 120
QY 830 TTAATCTTCTGCTGCTGTTGACTGGGTGATGATCAGTCCCTGTTTGGCTTTCACTTCA 889
DB 121 TTAATCTTCTGCTGCTGTTGACTGGGTGATGATGATGCTGCTTGTGCTTTCACTTCA 180
QY 890 TGTAGTCTTTAGAGAAACAGGAAATACGATGGTCCACGAGCTTCTTCGCAATCGTAC 949
DB 181 TGTAGTCTTTAGAGAAACAGGAAATACGATGGTCCACGAGCTTCTTCGCAATCGTAC 240
QY 950 AGCTGATAGGAACACGCAAGCAAGCTGAAAATTTTCTTACCGACTTGAGCTTAATGGTC 1009

[illegible][illegible]

Db 241 CCAGCAGTCTTCCGCAATCGTACAGCTGATAGGAAACAGCAGCAAGCTGAAATTTTGC 300
QY 987 TTACCACTGAGCTAAATGGTCAATAGGCGCAAGATTGACTTGGGAAGCGACTCCTCGATC 1046
Db 301 TTACCACTGAGCTAAATGGTCAATAGGCGCAAGATTGACTTGGGAAGCGACTCCTCGATC 360
QY 1047 TATTCATGAAGGAATGCAACAGCCATTAATGAATAGCGACTGCTAGTCTTTGACACCCAG 1106
Db 361 TATTCATGAAGGAATGCAACAGCCATTAATGAATAGCGACTGCTAGTCTTTGACACCCAG 420
QY 1107 CATTCGACAGCTTTTTCGAGAAATGGCAATTTAGGCATCAATGTAATTTTCCATGTG 1166
Db 421 CATTCGACAGCTTTTTCGAGAAATGGCAATTTAGGCATCAATGTAATTTTCCATGTG 480
QY 1167 TTGAATGGCAATCAAACTTTTCGCGCAGTGTAAACATTCAGTTTCACAGAAA 1223
Db 481 TCGAATGGCAATCAAACTTTTCGCGCAGTGTAAACATTCAGTTTCACAGAAA 537

RESULT 29
BE502849
LOCUS
DEFINITION
h80b11.x1 NCI CGAP Lu24 Homo sapiens cDNA clone IMAGE:3214269 3'
similar to TR:043269 O43269 HSIAT1. ; mRNA sequence.
ACCESSION
BE502849
VERSION
BE502849.1 GI:9705257
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 647)
NCI-CCGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.
cDNA Library Preparation: M. Bento Soares, Ph.D.
cDNA Library Arrayed by: Greg Lannon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CCGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL, send email to:
info@image.llnl.gov
Seq primer: -40UP from Gibco
High quality sequence stop: 448.
Location/Qualifiers
1..647
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:3214269"
/tissue_type="carcinoid"
/lab_host="DH10B"
/clone_lib="NCI CGAP Lu24"
/note="Organ: lung; Vector: pT73D-Pac (Pharmacia) with a
modified polylinker; Plasmid DNA from the normalized
library NCI CGAP Lu5 was prepared, and ss circles were
made in vitro. Following HAP purification, this DNA was
used as tracer in a subtractive hybridization reaction.
The driver was PCR-amplified cDNAs from a pool of 5,000
clones made from the same library (clones
1414920-1417991 and 1520904-1522439). Subtraction by Bento
Soares and M. Fatima Donaldo."

FEATURES
source

Query Match 38.1%; Score 485; DB 2; Length 647;
Best Local Similarity 99.8%; Pred. No. 7e-249;
Matches 535; Conservative 0; Mismatches 1; Indels 0 Gaps 0;
QY 521 CAAAGCTACATGTTGTCCAACTTCCGCGGCGCCCTTTGGATCCATTCGCAACTTGGCTA 580

ORIGIN

Query Match 38.1%; Score 485; DB 2; Length 647;
Best Local Similarity 99.8%; Pred. No. 7e-249;
Matches 535; Conservative 0; Mismatches 1; Indels 0 Gaps 0;
QY 521 CAAAGCTACATGTTGTCCAACTTCCGCGGCGCCCTTTGGATCCATTCGCAACTTGGCTA 580

Db 1 CAAAGCTACATGTTGTCCAACTTCCGCGGCGCCCTTTGGATCCATTCGCAACTTGGCTA 60
QY 581 TGGAGAAAGTGGCTAAATCAGTACTTTTCCCTGTAAATATGCTCTTCTGGATGTGAAA 640
Db 61 TGGAGAAAGTGGCTAAATCAGTACTTTTCCCTGTAAATATGCTCTTCTGGATGTGAAA 120
QY 641 TAACTCTGCCACACACAGAAAAGAGCAGACCATGAAGAGCTCTGTGATTTAGGCTTATT 700
Db 121 TAACTCTGCCACACACAGAAAAGAGCAGACCATGAAGAGCTCTGTGATTTAGGCTTATT 180
QY 701 CTTGTCCTGCGCTGCTGCTCTCTGTAATGCAAGGCTCTCTGGAATGCTGTGTAATGCC 760
Db 181 CTTGTCCTGCGCTGCTGCTCTCTGTAATGCAAGGCTCTCTGGAATGCTGTGTAATGCC 240
QY 761 ATCTGATGATCAGCATTAAGTCCATTCAACCCCTACAGGAGAGGATATAGTTTTCTTG 820
Db 241 ATCTGATGATCAGCATTAAGTCCATTCAACCCCTACAGGAGAGGATATAGTTTTCTTG 300
QY 821 CTACAGACATTAATCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 880
Db 301 CTACAGACATTAATCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 360
QY 881 TTCACTTCACTGTTAGTCTTTAGAGAACAGGAAATATACGATGCTCACCAGCAGTCTTTC 940
Db 361 TTCACTTCACTGTTAGTCTTTAGAGAACAGGAAATATATGATGCTCACCAGCAGTCTTTC 420
QY 941 CAATCGTACAGCTGATAGGAAACACGCAAGCAGTCAAAATTTTGTACCCGACTTTGAGC 1000
Db 421 CAATCGTACAGCTGATAGGAAACACGCAAGCAGTCAAAATTTTGTACCCGACTTTGAGC 480
QY 1001 TAAATGGTTCATAGGCGCAGATTGACTTTGGAAAGCGACTCTCGATCTATTTCATGAA 1056
Db 481 TAAATGGTTCATAGGCGCAGATTGACTTTGGAAAGCGACTCTCGATCTATTTCATGAA 536

RESULT 30

BE502849
LOCUS
DEFINITION
AGENCOURT 7779845 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:6019472
5'..mRNA sequence.
ACCESSION
BE502849
VERSION
BE502849.1 GI:22705755
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 976)
NIH-MGC <http://hgsc.nhlbi.nih.gov/>.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: LLAM13222 row: a column: 09
High quality sequence stop: 446.
Location/Qualifiers
1..976
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:6019472"
/tissue_type="epithelioid carcinoma"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_70"
/note="Organ: pancreas; Vector: pCMV-SPORT6; Site_1: NotI;

FEATURES
source

Query Match 38.1%; Score 485; DB 2; Length 647;
Best Local Similarity 99.8%; Pred. No. 7e-249;
Matches 535; Conservative 0; Mismatches 1; Indels 0 Gaps 0;
QY 521 CAAAGCTACATGTTGTCCAACTTCCGCGGCGCCCTTTGGATCCATTCGCAACTTGGCTA 580

Site 2: SalI; Cloned unidirectionally. Primer: Oligo dt.
Average insert size 1.1 kb. Library constructed by Life
Technologies."

ORIGIN
Query Match 38.1%; Score 485; DB 5; Length 976;
Best Local Similarity 100.0%; Pred. No. 7.3e-249;
Matches 485; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 641 TAACTCTGCGCACACAGAAAAGAGACCATGAAGAGCTCTGTAGCTTAGGCGCTTATT 700
Db 1 TAACTCTGCGCACACAGAAAAGAGACCATGAAGAGCTCTGTAGCTTAGGCGCTTATT 60
QY 701 CTTGTCGCGGCGGCTGCTTCTCTTAATGCAAGGCTCTCTGATGCTGTAATGCCGCC 760
Db 61 CTTGTCGCGGCGGCTGCTTCTCTTAATGCAAGGCTCTCTGATGCTGTAATGCCGCC 120
QY 761 ATCTGATGATCAGCATAGTCCATTACAAACCTTACAGGAGAGATATAGTTTTCTTG 820
Db 121 ATCTGATGATCAGCATAGTCCATTACAAACCTTACAGGAGAGATATAGTTTTCTTG 180
QY 821 CTACAGACATTAATCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 880
Db 181 CTACAGACATTAATCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 240
QY 881 TTTCACTTCACTGTTAGTCTTTAGAGAACAGGAAATACGATGCTCAACAGCAGTTCTTCG 940
Db 241 TTTCACTTCACTGTTAGTCTTTAGAGAACAGGAAATACGATGCTCAACAGCAGTTCTTCG 300
QY 941 CAATCGTACAGCTGATAGAAACAGCAAGCTGAAATTTTGTCTTACCGACTTGAGC 1000
Db 301 CAATCGTACAGCTGATAGAAACAGCAAGCTGAAATTTTGTCTTACCGACTTGAGC 360
QY 1001 TAAATGCTATAGGCGACATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1060
Db 361 TAAATGCTATAGGCGACATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 420
QY 1061 TTGCAACAGCCATTATGATAGGAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1120
Db 421 TTGCAACAGCCATTATGATAGGAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 480
QY 1121 TTGCA 1125
Db 481 TTGCA 485

RESULT 31
CF551876 890 bp mRNA linear EST 22-SEP-2003
LOCUS
DEFINITION
AGENCOURT 15595245 NIH_MGC.183 Homo sapiens cDNA clone
IMAGE:30530108 5', mRNA sequence.

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

NIH-MGC http://mgi.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Daniela S. Gerhard, Ph.D.
Office of Cancer Genomics / NIH
National Cancer Institute / NIH
Bldg. 31 Rm10A07 Bethesda, MD 20892
Email: cgaps-remail.nih.gov
Tissue Procurement: Dr. Michael Brownstein
cDNA Library Preparation: Invitrogen Corp
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:

http://image.llnl.gov
Plate: NDAM618 row: 1 column: 21
High quality sequence start: 6
High quality sequence stop: 590.
Location/Qualifiers

Source

1. .890
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:30530108"
/lab_host="DH10B-Tona (T1 and T5 phage resistant)"
/clone_lib="NIH_MGC.183"
/note="Organ: Pooled muscle (cardiac and skeletal);
Vector: pCMV-SPORT6.1; Site 1: EcoRV (destroyed); Site 2:
NotI; Library is oligo-dt primed and directionally cloned
(EcoRV site is destroyed upon cloning). Average insert
size 1.7. Library was constructed by Invitrogen."

ORIGIN

Query Match 37.4%; Score 477; DB 7; Length 890;
Best Local Similarity 100.0%; Pred. No. 1.5e-244;
Matches 477; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 599 CAGTACTTTTCCCTGTAATATGCTCTCTGATGTAATTAACCTGTCACACACAG 658
Db 168 CAGTACTTTTCCCTGTAATATGCTCTCTGATGTAATTAACCTGTCACACACAG 227
QY 659 AAAAGCAGACCATGAAGAGCTCTGTGAGTTTAGGCCCTTATTCCTGTCCTGCTGGTG 718
Db 228 AAAAGCAGACCATGAAGAGCTCTGTGAGTTTAGGCCCTTATTCCTGTCCTGCTGGTG 287
QY 719 CTTCTGTAATGGAAGGCTCTCTGATGCTGTAATGCCCATCTGATGATGATGATA 778
Db 288 CTTCTGTAATGGAAGGCTCTCTGATGCTGTAATGCCCATCTGATGATGATGATA 347
QY 779 AGTCATATACACCTTACAGGAGAGGATATAGTTTTCTTGCTACAGACATTAATCTTC 838
Db 348 AGTCATATACACCTTACAGGAGAGGATATAGTTTTCTTGCTACAGACATTAATCTTC 407
QY 839 CTGTGCTGTTGACTGGGTGATGATGCTGCTGTTTGGCTTTTCACTCATGTTAGTCT 898
Db 408 CTGTGCTGTTGACTGGGTGATGATGCTGCTGTTTGGCTTTTCACTCATGTTAGTCT 467
QY 899 TAGAAGAAACAGAAAATACGATGCTCACCAGAGTCTTCCGATCTGATGATGATG 958
Db 468 TAGAAGAAACAGAAAATACGATGCTCACCAGAGTCTTCCGATCTGATGATGATG 527
QY 959 GAACAGCAAGCAAGCTGAAATTTTGTACCGACTTGAGCTAAATGCTCATAGCGAC 1018
Db 528 GAACAGCAAGCAAGCTGAAATTTTGTACCGACTTGAGCTAAATGCTCATAGCGAC 587
QY 1019 GATTGACTTGGGAAGCGACTCTCGATCTATTTTCATGAAGGAATTGCAACAGCCATTA 1075
Db 588 GATTGACTTGGGAAGCGACTCTCGATCTATTTTCATGAAGGAATTGCAACAGCCATTA 644

RESULT 32

AI803300

LOCUS

DEFINITION

AI803300

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

Unpublished (1997)

AI803300 515 bp mRNA linear EST 13-DEC-1999
tc17d08.x1 Soares NHMHP S1 Homo sapiens cDNA clone IMAGE:2064111
3' similar to TR:043269 O43269 HSA1H.1; mRNA sequence.

AI803300
AI803300.1 GI:5368772
EST.

Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 515)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)

Best Local Similarity 99.7%; Pred. No. 5.8e-243; Matches 574; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 521 CAAGCTCACAATGTTGTCACAACTTGGCGGGCCCTTTGGGATCCATTCGCAACTTGGCTA 580
|||||
Db 1 CAAGCTCACAATGTTGTCACAACTTGGCGGGCCCTTTGGGATCCATTCGCAACTTGGCTA 60
|||||

QY 581 TGGAGAAAGTGGCTAATTCAGTACTTTTCCCTGTTAAATATGCTCTTCGATGTGAAA 640
|||||

Db 61 TGGAGAAAGTGGCTAATTCAGTACTTTTCCCTGTTAAATATGCTCTTCGATGTGAAA 120
|||||

QY 641 TAACTCTGCCACACACAGAAAAGCAGACATCAAGAGCTCTCTGAGTTTGGGCTTATT 700
|||||

Db 121 TAACTCTGCCACACACAGAAAAGCAGACATCAAGAGCTCTCTGAGTTTGGGCTTATT 180
|||||

QY 701 CCTGTCCGTCGCCCTGCTCTCTGTTAAATGGAAGCTCTCTGGATGCTGTAAATGCCCC 760
|||||

Db 181 CCTGTCCGTCGCCCTGCTCTCTGTTAAATGGAAGCTCTCTGGATGCTGTAAATGCCCC 240
|||||

QY 761 ATCTGATGATCAGCATATTCATTAACACCTTACAGGAGAGGATATAGTTTCTTGG 820
|||||

Db 241 ATCTGATGATCAGCATATTCATTAACACCTTACAGGAGAGGATATAGTTTCTTGG 300
|||||

QY 821 CTACAGACATTAATCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 880
|||||

Db 301 CTACAGACATTAATCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 360
|||||

QY 881 TTCACCTTCAATGTTAGTCTTTAGAGAAACAGAAAATACAGATGCTTCCAGCAGTCTTCG 940
|||||

Db 361 TTCACCTTCAATGTTAGTCTTTAGAGAAACAGAAAATACAGATGCTTCCAGCAGTCTTCG 420
|||||

QY 941 CAATCTGACGTGATAGGAACACGCAAGCACTGAAATTTGCTTACCGACTTGGAGC 1000
|||||

Db 421 CAATCTGACGTGATAGGAACACGCAAGCACTGAAATTTGCTTACCGACTTGGAGC 480
|||||

QY 1001 TAAATGGTCATAGGACAGTTCATCTGGAACGCTCTCTCGATCTATTCATGAAGAA 1060
|||||

Db 481 TAAATGGTCATAGGACAGTTCATCTGGAACGCTCTCTCGATCTATTCATGAAGAA 540
|||||

QY 1061 TTGCAACAGCCATTATGAATAGGCACTGCTAGTCT 1096
|||||

Db 541 TTGCAACAGCCATTATGAATAGGCACTGCTAGTCT 576
|||||

RESULT 36
BI836179
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

BI836179 800 bp mRNA linear EST 04-OCT-2001
603085712F1 NIH_MGC_120 Homo sapiens cDNA clone IMAGE:5224755 5',
mRNA sequence.
BI836179
EST.
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NIH-MGC http://mgi.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
DNA Sequencing by: The I.M.A.G.E. Consortium (LLNL)
CDNA distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM1565 row: h column: 04
High quality sequence start: 2
High quality sequence stop: 800.
Location/Qualifiers

source 1. .800
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5224755"
/lab_host="DH10B"
/clone_lib="NIH_MGC_120"
/note="Organ: pooled pancreas and spleen; Vector:
pCMV-SPORT6; Site 1: NotI; Site 2: EcoRV (destroyed); RNA
source anonymous pool of spleen and pancreas from 28 yo
male. Library is oligo-dT primed and directionally cloned
(EcoRV site is destroyed upon cloning). Average insert
size 1.5 kb, insert size range 1-2.5 kb. Library is
normalized and enriched for full-length clones and was
constructed by C. Gruber (Invitrogen). Research Genetics
tracking code 025. Note: this is a NIH_MGC Library."

ORIGIN
Query Match 37.2%; Score 474; DB 4; Length 800;
Best Local Similarity 100.0%; Pred. No. 5.9e-243;
Matches 474; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 317 CAGAAATGAGCGCTCAGACTGCTACAGCATTACTTACCGGTACTCTCGAAGTGTCCACCAT 376
|||||

Db 111 CAGAAATGAGCGCTCAGACTGCTACAGCATTACTTACCGGTACTCTCGAAGTGTCCACCAT 170
|||||

QY 377 CCAGAGGGTGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 436
|||||

Db 171 CCAGAGGGTGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 230
|||||

QY 437 TTGAGTGTCAAGTCTGCTTTGACTATGTGTACCGCCCATTTCTTCAATGTCAAGTGGCC 496
|||||

Db 231 TTGAGTGTCAAGTCTGCTTTGACTATGTGTACCGCCCATTTCTTCAATGTCAAGTGGCC 290
|||||

QY 497 ATCTGTTTGTAGCACTCTGCCCAAGCTCATGTTGTGCAATGTCGCCGGGCCCTT 556
|||||

Db 291 ATCTGTTTGTAGCACTCTGCCCAAGCTCATGTTGTGCAATGTCGCCGGGCCCTT 350
|||||

QY 557 TGGGATCCCAATTCGCACTTGGCTATGAGAAAGTGGCTAAATTCAGTACTTTTCCCTGTGA 616
|||||

Db 351 TGGGATCCCAATTCGCACTTGGCTATGAGAAAGTGGCTAAATTCAGTACTTTTCCCTGTGA 410
|||||

QY 617 AATATGCGTCTTCTGGATGTGAAATAACTCTGCGCACACAGAAAAGCAGACCATGAAG 676
|||||

Db 411 AATATGCGTCTTCTGGATGTGAAATAACTCTGCGCACACAGAAAAGCAGACCATGAAG 470
|||||

QY 677 AGCTGTGCTAGTTAGGCTTATCTCTGCTGCGGCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 736
|||||

Db 471 AGCTGTGCTAGTTAGGCTTATCTCTGCTGCGGCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 530
|||||

QY 737 GCTCTCTGGATGCTGTAATGCCCCCATCTGATGATGATGATGATGATGATGATGATGATGAT 790
|||||

Db 531 GCTCTCTGGATGCTGTAATGCCCCCATCTGATGATGATGATGATGATGATGATGATGATGAT 584
|||||

RESULT 37
BX459114
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

BX459114 842 bp mRNA linear EST 06-MAY-2004
BX459114 Homo sapiens PLACENTA Homo sapiens cDNA clone CS0DE012YN22
5-PRIME, mRNA sequence.
BX459114
EST.
BX459114.2 GI:47071764
KEYWORDS
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 842)
Li, W.B., Gruber, C., Jessee, J., and Pollayes, D.
Full-length cDNA libraries and normalization
Unpublished (2001)
On May 22, 2003 this sequence version replaced gi:31035049.
Contact: Genoscope

Genoscope - Centre National de Sequencage
2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
Email: secref@genoscope.cns.fr, Web : www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo (dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoRV sites of the pCMVSPORT 6 vector. Library
was not normalized. Library was constructed by Life Technologies, a
division of Invitrogen.
This sequence belongs to sequence cluster 8104.r
For more information about this cluster, see
<http://www.genoscope.cns.fr/cdna?c=CS0DE012DG11Q1&c=8104.r>.

FEATURES
Location/Qualifiers
1. 842
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0DE012YN22"
/tissue_type="PLACENTA"
/clone_lib="Homo sapiens PLACENTA"
/note="Vector: pCMVSPORT 6; 1st strand cDNA was primed
with a NotI-oligo(dT) primer. Five prime end enriched,
double-strand cDNA was digested with Not I and cloned into
the Not I and EcoRV sites of the pCMVSPORT 6 vector.
Library was not normalized."

ORIGIN
Query Match 37.1%; Score 473; DB 5; Length 842;
Best Local Similarity 100.0%; Pred. No. 2.1e-242;
Matches 473; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 434 TTTTTCAGTGTCAGTCTGCTTTGACTATGTTACCGGCCCATTTCTCAATGTCAGAGTG 493
Db 114 TTTTTCAGTGTCAGTCTGCTTTGACTATGTTAGCGCCCATTTCTCAATGTCAGAGTG 173
QY 494 GCCATCTGTTGTAGCAACTGTGCCAAAGCTCAGTGTGTCCAACTTCGCCGGGCC 553
Db 174 GCCATCTGTTGTAGCAACTGTGCCAAAGCTCAGTGTGTCCAACTTCGCCGGGCC 233
QY 554 CTTTGGATCCATTCGCAACTTGGCTATGGAGAAAGTGGTAACTTCAGTACTTTTCCCT 613
Db 234 CTTTGGATCCATTCGCAACTTGGCTATGGAGAAAGTGGTAACTTCAGTACTTTTCCCT 293
QY 614 GTAATATGCTCTTCTGGATGTGAATAACTCTGCCACACACAGAAAAGCAGACCATG 673
Db 294 GTAAATATGCTCTTCTGGATGTGAATAACTCTGCCACACACAGAAAAGCAGACCATG 353
QY 674 AAGAGCTCTGTGATTTAGCCCTTATCTCTGCTGCCCTGCTGCTTCTCTTAATGGC 733
Db 354 AAGAGCTCTGTGATTTAGCCCTTATCTCTGCTGCCCTGCTGCTTCTCTTAATGGC 413
QY 734 AAGGCTCTGTGATGCTGTAATGCCCATCTGATGATCAGATAAGTCCATTACACCC 793
Db 414 AAGGCTCTGTGATGCTGTAATGCCCATCTGATGATCAGATAAGTCCATTACACCC 473
QY 794 TACAGGAGAGGATATAGTTTCTTCTGTACAGACATTATCTCTCTGGTGTGTTGAGT 853
Db 474 TACAGGAGAGGATATAGTTTCTTCTGTACAGACATTATCTCTCTGGTGTGTTGAGT 533
QY 854 GGGTGATGATGATGCTCTGTTTGGCTTTCACCTTCATGTTAGTCTTAGAGAA 906
Db 534 GGGTGATGATGATGCTCTGTTTGGCTTTCACCTTCATGTTAGTCTTAGAGAA 586

RESULT 38
BF573693
LOCUS 602077289F2 NIH_MGC_62 Homo sapiens cDNA clone IMAGE:4251575 5',
DEFINITION mRNA sequence.
ACCESSION BF573693
VERSION BF573693.1 GI:11647405
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 894)
NIH-MGC <http://mgc.nci.nih.gov/>.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: rcgaps@mail.nih.gov
Tissue Procurement: ATCC/DCTD/DTF
cDNA Library Preparation: CLONTECH Laboratories, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: LLCM1075 row: b column: 24
High quality sequence stop: 562.
Location/Qualifiers
1. 894
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE.4251575"
/tissue_type="melanotic melanoma, high MDR"
/lab_host="BHI0B (T1 phase-resistant)"
/clone_lib="NIH_MGC_62"
/note="Organ: skin; Vector: pDNR-LIB (Clontech); Site: 1:
SfiI (ggcccttcggcc); Site 2: SfiI (ggccattatggc);
Double-stranded cDNA was prepared from cell line RNA. 5',
3' adaptors were used in cloning as follows: 5',
adaptor sequence: 5'-ATTCTAGAGCGGAGCGGCGGACATG-dT(30)BN-3',
sequence: 5'-ATTCTAGAGCGGAGCGGCGGCGGACATG-dT(30)BN-3',
(where B = A, C, G, or T). Average
insert size 1.75 kb (range 0.9-4.0 kb). 15/15 colonies
contained inserts by PCR. This library was enriched for
full-length clones and was constructed by Clontech
Laboratories (Palo Alto, CA)."

FEATURES
source
Query Match 37.1%; Score 473; DB 2; Length 894;
Best Local Similarity 100.0%; Pred. No. 2.1e-242;
Matches 473; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 504 TTGTAGCAACTGTGCCCAAGCTCAGTGTGTCCAACTTCGCCGGGCCCTTGGGATC 563
Db 105 TTGTAGCAACTGTGCCCAAGCTCAGTGTGTTCAACTTCGCCGGGCCCTTGGGATC 164
QY 564 CATTGCGCACTTGGCTATGGAGAAAGTGGCTAACTTTCCCTCTGTAATATGCG 623
Db 165 CATTGCGCACTTGGCTATGGAGAAAGTGGCTAACTTTCCCTCTGTAATATGCG 224
QY 624 GTCTTCTGGATGTAATAACTCTGCCACACACAGAAAAGCAGACCATGAAGCTCTG 683
Db 225 GTCTTCTGGATGTAATAACTCTGCCACACACAGAAAAGCAGACCATGAAGCTCTG 284
QY 684 TGAGTTAGGCTTATCTCTGTCGCGCTGCTTCTCTGTAATATGCGAAGCTCTCT 743
Db 285 TGAGTTAGGCTTATCTCTGTCGCGCTGCTTCTCTGTAATATGCGAAGCTCTCT 344
QY 744 GGATGCTGTAATGCCCATCTGATGATCAGCATAGTCCATTACACCTCAGGGAGA 803
Db 345 GGATGCTGTAATGCCCATCTGATGATCAGCATAGTCCATTACACCTCAGGGAGA 404
QY 804 GGATATAGTTTTTCTGTGCTACAGACATTATCTTCTGCTGCTGTGATGATGAT 863
Db 405 GGATATAGTTTTTCTGTGCTACAGACATTATCTTCTGCTGCTGTGATGATGAT 464
QY 864 CGAGTCTCTTTTGGCTTTCACCTTCTGTTAGTCTTAGAGAAACAGAAAAATACCATG 923
Db 465 CGAGTCTCTTTTGGCTTTCACCTTCTGTTAGTCTTAGAGAAACAGAAAAATACCATG 524
QY 924 TCACCAAGCAGTGTCTTCGCAATCGTACAGCTGATAGAAACACGCAAGCAGCTG 976

Db 525 TCACCAGCAGTCTTCGCAATCTGTACAGCTAGGAGACGACGCAAGCCTG 577

RESULT 39
BP227842
LOCUS
DEFINITION
BP227842 Sugano cDNA library, dermoid cancer Homo sapiens CDNA
clone DMC07313, mRNA sequence.
EST.
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 583)
AUTHORS
Suzuki, Y., Yamashita, R., Shirota, M., Sakakibara, Y., Chiba, J.,
Mizushima-Sugano, J., Nakai, K. and Sugano, S.
TITLE
Sequence comparison of human and mouse genes reveals a homologous
block structure in the promoter regions
JOURNAL
Genome Res. 14 (9), 1711-1718 (2004)
CONTACT: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: ysuzuki@im.u-tokyo.ac.jp.

FEATURES
source
Location/Qualifiers
1..583
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="DMC07313"
/clone_lib="Sugano cDNA library, dermoid cancer"
/note="dermoid cancer"

ORIGIN

Query Match 36.9%; Score 470; DB 5; Length 583;
Best Local Similarity 100.0%; Pred. No. 8.2e-241;
Matches 470; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 317 CAGAAATGAGCGCTGACAGCTGTGAGCAATACCTACCGGTACCTCGAAGTGTCCACCAT 376
DB 114 CAGAAATGAGCGCTGACAGCTGTGAGCAATACCTACCGGTACCTCGAAGTGTCCACCAT 173
QY 377 CCAGAGGGTGGCTGCGCTGACTGGCACTGCAATCCAACTGATGCTGGCGAGTCTTT 436
DB 174 CCAGAGGGTGGCTGCGCTGACTGGCACTGCAATCCAACTGATGCTGGCGAGTCTTT 233
QY 437 TTGAGTGTCCAGTCTGCTTTGACTATGTGTACCGCCCAATCTTCAATGTGAGTGGCC 496
DB 234 TTGAGTGTCCAGTCTGCTTTGACTATGTGTACCGCCCAATCTTCAATGTGAGTGGCC 293
QY 497 ATCTGTTTGTAGCAACTGTGCGCCAAAGCTGATGTTGTCCAACTGCGCGGGCCCTT 556
DB 294 ATCTGTTTGTAGCAACTGTGCGCCAAAGCTGATGTTGTCCAACTGCGCGGGCCCTT 353
QY 557 TGGGATCCATTCGCACTTGGCTATGAGAAAGTGGCTAAATTCAGTACTTTTCCCTGTA 616
DB 354 TGGGATCCATTCGCACTTGGCTATGAGAAAGTGGCTAAATTCAGTACTTTTCCCTGTA 413
QY 617 AATATGCGTCTTCTGATGTGAATTAATCTCTGCGACACACAGAAAGCAGACCATGAAG 676
DB 414 AATATGCGTCTTCTGATGTGAATTAATCTCTGCGACACACAGAAAGCAGACCATGAAG 473
QY 677 AGCTCTGAGTTTAGGCTTATCTCTGCGCGCCCTGCTCTTCTCTGTAATGCGAAG 736
DB 474 AGCTCTGAGTTTAGGCTTATCTCTGCGCGCCCTGCTCTTCTCTGTAATGCGAAG 533
QY 737 GCTCTCTGATGCTGTAATGCGCCCATCTGATGATCAGCATTAAGTCCATT 786
DB 534 GCTCTCTGATGCTGTAATGCGCCCATCTGATGATCAGCATTAAGTCCATT 583

RESULT 40
BX372197/c

LOCUS
DEFINITION
BX372197 Homo sapiens HELA CELLS COT 25-NORMALIZED Homo sapiens
cDNA clone CSODK012YI20 3-PRIME, mRNA sequence.
EST.
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 957)
AUTHORS
Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
TITLE
Full-length cDNA libraries and normalization
JOURNAL
Unpublished (2001)
COMMENT
On May 8, 2003 this sequence version replaced gi:30450080.
Contact: Genoscope
Genoscope - Centre National de Sequencage
2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
Email: seqref@genoscope.cns.fr, web : www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen. This sequence belongs to sequence cluster
8104.r

For more information about this cluster, see
http://www.genoscope.cns.fr/cdna?s=CSOBAI041ZD02_CS03852_1&c=8104.r

FEATURES
source
Location/Qualifiers
1..957
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CSODK012YI20"
/cell_type="HELA CELLS COT 25-NORMALIZED"
/clone_lib="HELA"
/note="1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized."

ORIGIN

Query Match 36.3%; Score 462; DB 5; Length 957;
Best Local Similarity 100.0%; Pred. No. 1.7e-236;
Matches 462; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 813 TTTTCTTGCTACAGACATTAATCTTCTGGTGCTTTGACTGGGTGATGATGAGTCTCG 872
DB 610 TTTTCTTGCTACAGACATTAATCTTCTGGTGCTTTGACTGGGTGATGATGAGTCTCG 551
QY 873 TTTTGGCTTTCATCTTCATGTTAGTCTTAGAGAAACAGGAAATACGATGTCACGCA 932
DB 550 TTTTGGCTTTCATCTTCATGTTAGTCTTAGAGAAACAGGAAATACGATGTCACGCA 491
QY 933 GTTCTTTCGCAATCGTACAGCTGATAGGAACACGCAAGCTGAGAAATTTTCTTACCG 992
DB 490 GTTCTTTCGCAATCGTACAGCTGATAGGAACACGCAAGCTGAGAAATTTTCTTACCG 431
QY 993 ACTTGAGCTTAATGCTATAGCGACGATGATCTTGGGAAGGACTCTTCGATCTATTCA 1052
DB 430 ACTTGAGCTTAATGCTATAGCGACGATGATCTTGGGAAGGACTCTTCGATCTATTCA 371
QY 1053 TGAAGCAATTGCAACAGCCATTAATGATGACGACTGTCTAGTCTTTGACACCATTCG 1112
DB 370 TGAAGCAATTGCAACAGCCATTAATGATGACGACTGTCTAGTCTTTGACACCATTCG 311
QY 1113 ACAGCTTTTTCAGAAAATGGCAATTTTAGGCAATCAATGTAATTTTCCATGTTGAAA 1172
DB 310 ACAGCTTTTTCAGAAAATGGCAATTTTAGGCAATCAATGTAATTTTCCATGTTGAAA 251


```
QY 812 TTTTCTTCTGCTACAGCAATTAATCTTCTGGTGTCTGTGACTGGTGTGATGATGATGCTCT 871
Db 457 TTTTCTTCTGCTACAGCAATTAATCTTCTGGTGTCTGTGACTGGTGTGATGATGATGCTCT 398
QY 872 GTTTTGGCTTTCTACTTTCATCTTGTAGTCTTGTAGAGAAACAGGAGAAATACGATGGTCAACGAGC 931
Db 397 GTTTTGGCTTTCTACTTTCATCTTGTAGTCTTGTAGAGAAACAGGAGAAATACGATGGTCAACGAGC 338
QY 932 AGTTCTTCCGATCGTACAGCTGATAGGAAACAGCGAAGCAAGCTGAAATTTTGTCTTACC 991
Db 337 AGTTCTTCCGAAATCGTACAGCTGATAGGAAACAGCGAAGCAAGCTGAAATTTTGTCTTACC 278
QY 992 GACTTGCAGCTTAAATGTTGATAGCGAGATTTGCTTGGGAGCGACTCTCTCGATCTATTTC 1051
Db 277 GACTTGCAGCTTAAATGTTGATAGCGAGATTTGCTTGGGAGCGACTCTCTCGATCTATTTC 218
QY 1052 ATGAAGGAATGCAACAGCGCAATTTGAATAGCGACTGTCTAGTCTTTTGACACAGCAATTTG 1111
Db 217 ATGAAGGAATGCAACAGCGCAATTTGAATAGCGACTGTCTAGTCTTTTGACACAGCAATTTG 158
QY 1112 CACAGCTTTTTCAGAGAAATGGCAATTTAGGCATCAATGTAATTTTCCATGTTGAA 1171
Db 157 CACAGCTTTTTCAGAGAAATGGCAATTTAGGCATCAATGTAATTTTCCATGTTGAA 98
QY 1172 ATGGCAATCAACATTTCTGGCCAGCTTTTAATCTTCACTTTTCAGAGAAATAGGCA 1231
Db 97 ATGGCAATCAACATTTCTGGCCAGCTTTTAATCTTCACTTTTCAGAGAAATAGGCA 38
QY 1232 CCATCTGTCTGCAACCTTAAACTCTTTCCGTAGGT 1268
Db 37 CCATCTGTCTGCAACCTTAAACTCTTTCCGTAGGT 1
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```
RESULT 43
LOCUS AI698102 608 bp mRNA linear EST 03-JUN-1999
DEFINITION we20h10.x1 NCI CGAP Lu24 Homo sapiens cDNA clone IMAGE:2341699 3'
similar to TR:043269 O43269 HSA1H1.1; mRNA sequence.
```

```
AI698102
AI698102
AI698102.1 GI:4986002
EST.
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 608)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.
cDNA Library Preparation: M. Bento Soares, Ph.D.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www.bio.llnl.gov/bbrp/image/image.html
Seq primer: -400P from Glbco
High quality sequence stop: 445.
Location/Qualifiers
1. .608
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:2341699"
/tissue_type="carcinoid"
/lab_host="DH10B"
/clone_lib="NCI CGAP Lu24"
/note="Organ: lung; Vector: pT73D-Pac (Pharmacia) with a
modified polylinker; Plasmid DNA from the normalized
```

FEATURES
source

RESULT 44
BF839462

LOCUS BF839462
DEFINITION RC4-HT0132-281100-011-h11 HT0132 Homo sapiens cDNA, mRNA sequence.
ACCESSION BF839462
VERSION BF839462.1
KEYWORDS EST.
SOURCE Homo sapiens (human)

ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 487)

REFERENCE

AUTHORS

Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R.,

Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F.,

Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H.,

Brunstein, A., de Oliveira, P.S., Bucher, P., Jongeneel, C.V.,

O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and

Simpson, A.J.

Shotgun sequencing of the human transcriptome with ORF expressed

sequence tags

Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)

20020663

10737800

PUBMED

COMMENT

Contact: Simpson A.J.G.

Laboratory of Cancer Genetics

Ludwig Institute for Cancer Research

Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,

library NCI CGAP Lu5 was prepared, and as circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from a pool of 5,000 clones made from the same library (cloneIDs 1414920-1417991 and 1520904-1522439). Subtraction by Bento Soares and M. Fatima Donaldo.

ORIGIN

Query Match 35.8%; Score 456; DB 1; Length 608;
Best Local Similarity 100.0%; Pred. No. 2.8e-233;
Matches 456; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 527 TCACATGTTGTCACATTTGCCGGGGCCCTTTGGGATCCATTTGCCAACTTGGCTATGGAGA 586
Db 7 TCACATGTTGTCACATTTGCCGGGGCCCTTTGGGATCCATTTGCCAACTTGGCTATGGAGA 66
QY 587 AAGTGGCTAATTCAGTACTTTCCCTCTGTAATATGCTCTTCTGATGTGAATAAATTC 646
Db 67 AAGTGGCTAATTCAGTACTTTCCCTCTGTAATATGCTCTTCTGATGTGAATAAATTC 126
QY 647 TGCCACACACAGAAAAAGCAGACCATGAAGAGCTCTGTGAGTTTAGGCCCTTATTCCTGTC 706
Db 127 TGCCACACACAGAAAAAGCAGACCATGAAGAGCTCTGTGAGTTTAGGCCCTTATTCCTGTC 186
QY 707 CFTGCCCTGCTCTCTCTGTAATGCAAGGCTCTCTGGATGCTGTAATGCCCATCTGA 766
Db 187 CFTGCCCTGCTCTCTCTGTAATGCAAGGCTCTCTGGATGCTGTAATGCCCATCTGA 246
QY 767 TGCATCAGCAATAAGTCCATTACACCCCTACAGGAGAGATATAGTTTTCTTGTCTACAG 826
Db 247 TGCATCAGCAATAAGTCCATTACACCCCTACAGGAGAGATATAGTTTTCTTGTCTACAG 306
QY 827 ACATTAATCTTCTGCTGCTGTTGACTGGTGTGATGATGATGATGATGATGATGATGATGAT 886
Db 307 ACATTAATCTTCTGCTGCTGTTGACTGGTGTGATGATGATGATGATGATGATGATGATGAT 366
QY 887 TCATGTTAGTCTTTAGAGAAACAGGAGAAATACGATGGTCCACGACAGTTTCTTCGCAATCG 946
Db 367 TCATGTTAGTCTTTAGAGAAACAGGAGAAATACGATGGTCCACGACAGTTTCTTCGCAATCG 426
QY 947 TACAGCTGTAGTGAACACGACCAAGCTGAAAAAT 982
Db 427 TACAGCTGTAGTGAACACGACCAAGCTGAAAAAT 462

BF839462 487 bp mRNA linear EST 13-JAN-2001
RC4-HT0132-281100-011-h11 HT0132 Homo sapiens cDNA, mRNA sequence.

BF839462.1 GI:12191845

EST.

Source

Homo sapiens (human)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 487)

Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R.,

Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F.,

Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H.,

Brunstein, A., de Oliveira, P.S., Bucher, P., Jongeneel, C.V.,

O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and

Simpson, A.J.

Shotgun sequencing of the human transcriptome with ORF expressed

sequence tags

Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)

20020663

10737800

PUBMED

COMMENT

Contact: Simpson A.J.G.

Laboratory of Cancer Genetics

Ludwig Institute for Cancer Research

Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,


```
Db 431 AGAAGTGGCTAATCAGTACTTTTCCCTGTAATATGCTTCTCGGATGGAATAA 490
Qy 644 CTCGCGCACACAGAAAAAGCAGACCATGAAGAGCTCTGTGAGTTTAGGCCCTTATTCCT 703
Db 491 CTCGCGCACACAGAAAAAGCAGACCATGAAGAGCTCTGTGAGTTTAGGCCCTTATTCCT 550
Qy 704 GTCCGTGCCCT 714
Db 551 GTCCGTGCCCT 561

RESULT 46
BX356371 1058 bp mRNA linear EST 08-APR-2004
LOCUS BX356371 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA
DEFINITION clone CS0D1011Y112 5-PRIME, mRNA sequence.
ACCESSION BX356371
VERSION BX356371.2 GI:46306467
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
TITLE 1 (bases 1 to 1058)
JOURNAL Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
COMMENT Full-length cDNA libraries and normalization
Unpublished (2001)
On May 5, 2003 this sequence version replaced gi:30376057.
Contact: Genoscope
Genoscope - Centre National de Sequencage
2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
Email: seqref@genoscope.cns.fr, Web: www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen. This sequence belongs to sequence cluster
8104.r
For more information about this cluster, see
http://www.genoscope.cns.fr/cdna?s=CS0D1011B06QP1&c=8104.r.

FEATURES
Location/Qualifiers
1..1058
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0D1011Y112"
/tissue_type="PLACENTA COT 25-NORMALIZED"
/clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/note="1st strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized."

ORIGIN
Query Match 33.8%; Score 430; DB 5; Length 1058;
Best Local Similarity 99.3%; Pred. No. 2.9e-219;
Matches 680; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 590 TGGCTAATTCAGTACTTTTCCCTGTAATATGCGTCTCTGGATGTGAAATAACTCTGC 649
Db 1 TGGCTAATTCAGTACTTTTCCCTGTAATATGCGTCTCTGGATGTGAAATAACTCTGC 60
Qy 650 CACACACAAAAAGCAGACCATGAAGAGCTCTGTGAGTTTAGGCCCTTATTCCTGCCGT 709
Db 61 CACACACAAAAAGCAGACCATGAAGAGCTCTGTGAGTTTAGGCCCTTATTCCTGCCGT 120
Qy 710 GCCCTGGTCTTCTCTGTAATGCGAGGCTCTCTGATGCTGTATGATGCCCATCTGATGC 769
Db 121 GCCCTGGTCTTCTCTGTAATGCGAGGCTCTCTGATGCTGTATGATGCCCATCTGATGC 180
Qy 770 ATCAGCATTAAGTCCATTACACCCCTACAGGAGAGATATGTTTTCTTGCTACAGACA 829
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```
Db 181 ATCAGCATTAAGTCCATTACACCCCTACAGGAGAGATATAGTTTTTCTTGCTACAGACA 240
Qy 830 TTAATCTTCTCGTGTGCTGTGATGCGGTGATGATGAGTCCTGCTTTTGGCTTTCACCTTCA 889
Db 241 TTAATCTTCTCGTGTGCTGTGATGCGGTGATGATGAGTCCTGCTTTTGGCTTTCACCTTCA 300
Qy 890 TGTAGTCTTTAGAGAAACAGGAAAAATACGATGGTCCAGCAGTTCTTTCGCAATCGTAC 949
Db 301 TGTAGTCTTTAGAGAAACAGGAAAAATACGATGGTCCAGCAGTTCTTTCGCAATCGTAC 360
Qy 950 AGCTGATAGAAACACGCAAGCAAGCTGAAAAATTTTCTTACCGACTTGAAGTCTTAAATGGTC 1009
Db 361 AGCTGATAGAAACACGCAAGCAAGCTGAAAAATTTTCTTACCGACTTGAAGTCTTAAATGGTC 420
Qy 1010 ATAGGCGACGATTTGACTTTGGGAAGGCGACTCTCTCGATCTATTTCATGAAGAAATTCGAACAG 1069
Db 421 ATAGGCGACGCTKBKCTTTGGGAAGGCGACTCTCTCGATCTATTTCATGAAGAAATTCGAACAG 480
Qy 1070 CCATTATGAATAGCGACTGTCTGTCTTTGACACCGCAATTCGACAGCTTTTTCGAGAAA 1129
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RESULT 47
BX340272 882 bp mRNA linear EST 07-APR-2004
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DEFINITION clone CS0D1084YJ01 5-PRIME, mRNA sequence.
ACCESSION BX340272
VERSION BX340272.2 GI:46264520
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
TITLE 1 (bases 1 to 882)
JOURNAL Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
COMMENT Full-length cDNA libraries and normalization
Unpublished (2001)
On May 1, 2003 this sequence version replaced gi:30310869.
Contact: Genoscope
Genoscope - Centre National de Sequencage
2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
Email: seqref@genoscope.cns.fr, Web: www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen. This sequence belongs to sequence cluster
8104.r
For more information about this cluster, see
http://www.genoscope.cns.fr/cdna?s=CS0D1084CE01QP1&c=8104.r.

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primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized."

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Db 874 CTCCTGGA 882

RESULT 48
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DEFINITION BP332871
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VERSION BP332871
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SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Euthera; Primates; Catarrhini; Homiidae; Homo.
TITLE Suzuki, Y., Yamashita, R., Hirota, M., Sakakibara, Y., Chiba, J.,
Mizushima-Sugano, J., Nakai, K. and Sugano, S.
JOURNAL Sequence comparison of human and mouse genes reveals a homologous
COMMENT Block structure in the promoter regions
Genome Res. 14 (9), 1711-1718 (2004)
Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: yusuzuki@ims.u-tokyo.ac.jp.
FEATURES
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ACCESSION BP332871
VERSION BP332871
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
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AUTHORS Mammalia; Euthera; Primates; Catarrhini; Homiidae; Homo.
TITLE NIH-MGC http://mgc.nci.nih.gov/.
JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC)
COMMENT Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: CLONTECH Laboratories, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM1379 row: b column: 23
High quality sequence stop: 644.
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256	17	1.3	601	4	US-09-949-016-152648	Sequence 152648, A	329	17	1.3	7070	4	US-09-949-016-2808	Sequence 2808, Ap
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C 259	17	1.3	601	4	US-09-949-016-158588	Sequence 158588, A	332	17	1.3	7070	4	US-09-949-016-2811	Sequence 2811, Ap
C 260	17	1.3	601	4	US-09-949-016-158592	Sequence 158592, A	333	17	1.3	7070	4	US-09-949-016-2812	Sequence 2812, Ap
261	17	1.3	601	4	US-09-949-016-176114	Sequence 176114, A	334	17	1.3	7109	4	US-09-949-016-2813	Sequence 2813, Ap
262	17	1.3	601	4	US-09-949-016-176115	Sequence 176115, A	335	17	1.3	7109	4	US-09-949-016-2814	Sequence 2814, Ap
263	17	1.3	601	4	US-09-949-016-176116	Sequence 176116, A	336	17	1.3	7109	4	US-09-949-016-2815	Sequence 2815, Ap
264	17	1.3	601	4	US-09-949-016-186551	Sequence 186551, A	337	17	1.3	7109	4	US-09-949-016-2816	Sequence 2816, Ap
265	17	1.3	601	4	US-09-949-016-188275	Sequence 188275, A	338	17	1.3	7109	4	US-09-949-016-2817	Sequence 2817, Ap
C 266	17	1.3	601	4	US-09-949-016-192464	Sequence 192464, A	339	17	1.3	7109	4	US-09-949-016-2818	Sequence 2818, Ap
C 267	17	1.3	601	4	US-09-949-016-198891	Sequence 198891, A	340	17	1.3	7109	4	US-09-949-016-2819	Sequence 2819, Ap
C 268	17	1.3	601	4	US-09-949-016-201044	Sequence 201044, A	341	17	1.3	7109	4	US-09-949-016-2820	Sequence 2820, Ap
C 269	17	1.3	601	4	US-09-949-016-201045	Sequence 201045, A	342	17	1.3	7109	4	US-09-949-016-2821	Sequence 2821, Ap
C 270	17	1.3	647	3	US-09-109-204-26	Sequence 26, Appl	343	17	1.3	7141	4	US-09-949-016-2822	Sequence 2822, Ap
C 271	17	1.3	647	4	US-09-490-032-26	Sequence 26, Appl	344	17	1.3	7141	4	US-09-949-016-2823	Sequence 2823, Ap
C 272	17	1.3	648	4	US-09-248-796A-5974	Sequence 5974, Ap	345	17	1.3	7141	4	US-09-949-016-2824	Sequence 2824, Ap
C 273	17	1.3	956	4	US-09-949-016-3447	Sequence 3447, Ap	346	17	1.3	7141	4	US-09-949-016-2825	Sequence 2825, Ap
C 274	17	1.3	1008	3	US-08-235-836C-53	Sequence 53, Appl	347	17	1.3	7190	4	US-09-902-540-843	Sequence 843, App
C 275	17	1.3	1008	3	US-08-235-836C-130	Sequence 130, App	348	17	1.3	10204	4	US-09-949-016-14104	Sequence 14104, A
C 276	17	1.3	1008	3	US-08-235-836C-131	Sequence 131, App	349	17	1.3	11543	4	US-09-949-016-12071	Sequence 12071, A
C 277	17	1.3	1011	3	US-08-235-836C-51	Sequence 51, App	C 350	17	1.3	11543	4	US-09-949-016-12673	Sequence 12673, A
C 278	17	1.3	1014	3	US-09-257-179-32	Sequence 32, Appl	C 351	17	1.3	11544	4	US-09-949-016-16172	Sequence 16172, A
C 279	17	1.3	1024	4	US-09-328-475C-61	Sequence 61, Appl	C 352	17	1.3	11544	4	US-09-949-016-16173	Sequence 16173, A
C 280	17	1.3	1024	4	US-09-328-475C-62	Sequence 62, Appl	C 353	17	1.3	11544	4	US-09-949-016-16174	Sequence 16174, A
281	17	1.3	1459	3	US-09-020-956-174	Sequence 174, App	C 354	17	1.3	11544	4	US-09-949-016-16175	Sequence 16175, A
282	17	1.3	1459	3	US-09-030-607-174	Sequence 174, App	C 355	17	1.3	11725	2	US-08-756-506-1	Sequence 1, Appli
283	17	1.3	1459	3	US-09-439-313-174	Sequence 174, App	356	17	1.3	11725	4	US-09-328-925-50	Sequence 50, Appl
284	17	1.3	1459	3	US-09-352-616A-174	Sequence 174, App	357	17	1.3	11725	4	US-09-054-272-31	Sequence 31, Appl
285	17	1.3	1459	3	US-09-232-149A-174	Sequence 174, App	358	17	1.3	12284	4	US-09-949-016-15243	Sequence 15243, A
286	17	1.3	1459	4	US-09-159-812-174	Sequence 174, App	359	17	1.3	13977	3	US-09-484-970B-60	Sequence 60, Appl
287	17	1.3	1459	4	US-09-636-215-174	Sequence 174, App	C 360	17	1.3	14977	4	US-09-949-016-16088	Sequence 16088, A
288	17	1.3	1459	4	US-09-685-166A-174	Sequence 174, App	C 361	17	1.3	14902	4	US-09-949-016-16753	Sequence 16753, A
289	17	1.3	1459	4	US-09-115-453-174	Sequence 174, App	C 362	17	1.3	17901	4	US-09-949-016-14064	Sequence 14064, A
290	17	1.3	1459	4	US-09-688-489-174	Sequence 174, App	C 363	17	1.3	24563	4	US-09-949-016-13492	Sequence 13492, A
291	17	1.3	1459	4	US-09-679-426-174	Sequence 174, App	C 364	17	1.3	24803	4	US-09-949-016-11966	Sequence 11966, A
292	17	1.3	1459	4	US-09-759-143-174	Sequence 174, App	C 365	17	1.3	24804	4	US-09-949-016-16377	Sequence 16377, A
293	17	1.3	1459	4	US-09-651-236-174	Sequence 174, App	C 366	17	1.3	24945	4	US-09-949-016-16255	Sequence 16255, A
294	17	1.3	1464	4	US-09-248-796A-6275	Sequence 6275, Ap	C 367	17	1.3	25041	4	US-09-949-016-17400	Sequence 17400, A
295	17	1.3	1527	4	US-09-328-352-2341	Sequence 2341, Ap	C 368	17	1.3	26852	4	US-09-949-016-12736	Sequence 12736, A
C 296	17	1.3	1923	4	US-09-884-324-7	Sequence 884-324-7	C 369	17	1.3	26852	4	US-09-949-016-15823	Sequence 15823, A
C 297	17	1.3	2167	3	US-08-884-324-7	Sequence 884-324-7	C 370	17	1.3	28994	3	US-08-884-324-14	Sequence 14, Appl
C 298	17	1.3	2167	3	US-09-479-862-7	Sequence 7, Appli	C 371	17	1.3	28994	4	US-09-479-862-14	Sequence 14, Appl
C 299	17	1.3	2224	3	US-09-109-204-6	Sequence 6, Appli	C 372	17	1.3	38059	4	US-09-328-925-4	Sequence 4, Appli
C 300	17	1.3	2224	4	US-09-490-032-6	Sequence 6, Appli	C 373	17	1.3	38059	4	US-09-328-925-4	Sequence 4, Appli
301	17	1.3	2259	4	US-09-023-655-796	Sequence 796, App	C 374	17	1.3	38059	4	US-09-328-925-4	Sequence 4, Appli
C 302	17	1.3	2421	4	US-09-902-540-7795	Sequence 7795, Ap	C 375	17	1.3	37815	4	US-09-949-016-17566	Sequence 17566, A
303	17	1.3	2595	4	US-09-919-497-12	Sequence 12, Appl	C 376	17	1.3	37815	4	US-09-949-016-17566	Sequence 17566, A
304	17	1.3	2727	4	US-09-620-312D-218	Sequence 218, App	C 377	17	1.3	38059	4	US-09-328-925-4	Sequence 4, Appli
C 305	17	1.3	3031	3	US-09-556-877-87	Sequence 87, Appl	C 378	17	1.3	38059	4	US-09-328-925-4	Sequence 4, Appli
C 306	17	1.3	3031	3	US-09-620-412C-87	Sequence 87, Appl	C 379	17	1.3	41736	4	US-09-949-016-17381	Sequence 17381, A
C 307	17	1.3	3031	4	US-09-410-568-87	Sequence 87, Appl	C 380	17	1.3	42917	4	US-09-949-016-13795	Sequence 13795, A
C 308	17	1.3	3031	3	US-09-598-419-87	Sequence 87, Appl	C 381	17	1.3	43576	4	US-09-949-016-15364	Sequence 15364, A
C 309	17	1.3	3136	3	US-09-443-184-43	Sequence 43, Appl	C 382	17	1.3	43577	4	US-09-949-016-12183	Sequence 12183, A
C 310	17	1.3	3136	4	US-09-806-536A-27	Sequence 27, Appl	C 383	17	1.3	46253	4	US-09-949-016-11890	Sequence 11890, A
C 311	17	1.3	3224	3	US-09-526-993-2	Sequence 2, Appli	C 384	17	1.3	46257	4	US-09-949-016-13711	Sequence 13711, A
C 312	17	1.3	3812	1	US-08-188-582-19	Sequence 19, Appl	C 385	17	1.3	47471	4	US-09-949-016-12271	Sequence 12271, A
C 313	17	1.3	3812	1	US-08-646-715-19	Sequence 19, Appl	C 386	17	1.3	47787	4	US-09-949-016-11969	Sequence 11969, A
314	17	1.3	3857	4	US-09-710-279-3480	Sequence 3480, Ap	C 387	17	1.3	51273	4	US-09-949-016-13018	Sequence 13018, A
315	17	1.3	4079	4	US-09-016-434-1257	Sequence 1257, Ap	C 388	17	1.3	54711	4	US-09-949-016-17489	Sequence 17489, A
316	17	1.3	4105	3	US-08-121-446-1	Sequence 1, Appli	C 389	17	1.3	56516	2	US-08-996-306-1	Sequence 1, Appli
317	17	1.3	4105	4	US-09-931-157-1	Sequence 1, Appli	390	17	1.3	56516	3	US-09-338-907-1	Sequence 1, Appli
318	17	1.3	4232	4	US-09-270-767-12086	Sequence 12086, A	391	17	1.3	56516	3	US-09-218-207-1	Sequence 1, Appli
319	17	1.3	4877	4	US-09-566-921-8	Sequence 8, Appli	392	17	1.3	56520	3	US-09-338-907-179	Sequence 179, App

393	17	1.3	56520	3	US-09-218-207-179	Sequence 179, Appl	c 466	17	1.3	172677	4	US-09-949-016-13444	Sequence 13444, A
394	17	1.3	60317	4	US-09-949-016-12638	Sequence 12638, A	467	17	1.3	177797	4	US-09-949-016-14125	Sequence 14125, A
395	17	1.3	60917	4	US-09-949-016-16057	Sequence 16057, A	c 468	17	1.3	187136	4	US-09-949-016-17231	Sequence 17231, A
c 396	17	1.3	65962	4	US-09-949-016-17152	Sequence 17152, A	469	17	1.3	192302	4	US-09-949-016-15270	Sequence 15270, A
c 397	17	1.3	72662	4	US-09-949-016-17073	Sequence 17073, A	470	17	1.3	192506	4	US-09-949-016-15830	Sequence 15830, A
c 398	17	1.3	74730	4	US-09-949-016-15189	Sequence 15189, A	c 471	17	1.3	198632	4	US-09-949-016-12781	Sequence 12781, A
c 399	17	1.3	78846	4	US-09-949-016-12396	Sequence 12396, A	c 472	17	1.3	198637	4	US-09-949-016-17393	Sequence 17393, A
400	17	1.3	78846	4	US-09-949-016-12391	Sequence 12391, A	c 473	17	1.3	212449	4	US-09-949-016-15419	Sequence 15419, A
401	17	1.3	78846	4	US-09-949-016-12792	Sequence 12792, A	c 474	17	1.3	221545	4	US-09-949-016-13875	Sequence 13875, A
402	17	1.3	78846	4	US-09-949-016-12793	Sequence 12793, A	c 475	17	1.3	227750	4	US-09-949-016-17175	Sequence 17175, A
403	17	1.3	78850	4	US-09-949-016-12793	Sequence 12793, A	476	17	1.3	227979	4	US-09-949-016-11842	Sequence 11842, A
404	17	1.3	78850	4	US-09-949-016-16013	Sequence 16013, A	477	17	1.3	263693	4	US-09-949-016-12386	Sequence 12386, A
405	17	1.3	78850	4	US-09-949-016-16014	Sequence 16014, A	478	17	1.3	263694	4	US-09-949-016-16915	Sequence 16915, A
406	17	1.3	78850	4	US-09-949-016-16016	Sequence 16016, A	479	17	1.3	278866	4	US-09-949-016-13922	Sequence 13922, A
407	17	1.3	78850	4	US-09-949-016-16201	Sequence 16201, A	480	17	1.3	278866	4	US-09-949-016-13924	Sequence 13924, A
408	17	1.3	78850	4	US-09-949-016-16202	Sequence 16202, A	481	17	1.3	278866	4	US-09-949-016-13925	Sequence 13925, A
409	17	1.3	78850	4	US-09-949-016-16203	Sequence 16203, A	482	17	1.3	278866	4	US-09-949-016-13926	Sequence 13926, A
410	17	1.3	78850	4	US-09-949-016-16204	Sequence 16204, A	483	17	1.3	278866	4	US-09-949-016-14699	Sequence 14699, A
411	17	1.3	79824	4	US-09-949-016-12019	Sequence 12019, A	484	17	1.3	278866	4	US-09-949-016-14701	Sequence 14701, A
412	17	1.3	80246	3	US-09-078-294-4	Sequence 4, Appl	485	17	1.3	278866	4	US-09-949-016-14702	Sequence 14702, A
c 413	17	1.3	80411	4	US-09-949-016-15777	Sequence 15777, A	486	17	1.3	278866	4	US-09-949-016-14703	Sequence 14703, A
c 414	17	1.3	80595	3	US-09-078-294-3	Sequence 3, Appl	487	17	1.3	278866	4	US-09-949-016-14704	Sequence 14704, A
415	17	1.3	86945	4	US-09-949-016-13849	Sequence 13849, A	488	17	1.3	278866	4	US-09-949-016-14705	Sequence 14705, A
416	17	1.3	86945	4	US-09-949-016-13850	Sequence 13850, A	489	17	1.3	336024	4	US-09-949-016-12373	Sequence 12373, A
417	17	1.3	86945	4	US-09-949-016-13851	Sequence 13851, A	490	17	1.3	390890	4	US-09-949-016-14720	Sequence 14720, A
418	17	1.3	86945	4	US-09-949-016-13852	Sequence 13852, A	491	17	1.3	392000	4	US-10-027-983-11	Sequence 11, Appl
419	17	1.3	86945	4	US-09-949-016-13853	Sequence 13853, A	492	17	1.3	393753	4	US-09-949-016-14573	Sequence 14573, A
420	17	1.3	86945	4	US-09-949-016-13854	Sequence 13854, A	493	17	1.3	393753	4	US-09-949-016-14574	Sequence 14574, A
421	17	1.3	86945	4	US-09-949-016-13855	Sequence 13855, A	c 494	17	1.3	451924	4	US-09-949-016-12896	Sequence 12896, A
422	17	1.3	86945	4	US-09-949-016-13856	Sequence 13856, A	c 495	17	1.3	451925	4	US-09-949-016-12896	Sequence 12896, A
423	17	1.3	86945	4	US-09-949-016-13857	Sequence 13857, A	c 496	17	1.3	451925	4	US-09-949-016-17305	Sequence 17305, A
424	17	1.3	86945	4	US-09-949-016-13858	Sequence 13858, A	c 497	17	1.3	454726	4	US-09-949-016-14157	Sequence 14157, A
c 425	17	1.3	86945	4	US-09-949-016-13859	Sequence 13859, A	c 498	17	1.3	640681	4	US-09-790-988-1	Sequence 1, Appl
426	17	1.3	94879	4	US-09-949-016-12101	Sequence 12101, A	c 499	17	1.3	670690	4	US-09-949-016-12505	Sequence 12505, A
427	17	1.3	94884	4	US-09-949-016-12101	Sequence 12101, A	c 500	17	1.3	670690	4	US-09-949-016-14207	Sequence 14207, A
428	17	1.3	95621	4	US-09-949-016-13237	Sequence 13237, A	c 501	17	1.3	678533	4	US-09-949-016-14577	Sequence 14577, A
429	17	1.3	99830	4	US-09-949-016-16859	Sequence 16859, A	c 502	17	1.3	678533	4	US-09-949-016-14578	Sequence 14578, A
430	17	1.3	101357	4	US-09-949-016-12364	Sequence 12364, A	c 503	17	1.3	767677	4	US-09-949-016-12147	Sequence 12147, A
431	17	1.3	101357	4	US-09-949-016-12364	Sequence 12364, A	c 504	17	1.3	767677	4	US-09-949-016-17361	Sequence 17361, A
432	17	1.3	101357	4	US-09-949-016-15648	Sequence 15648, A	c 505	17	1.3	786431	4	US-09-751-389-3	Sequence 3, Appl
c 433	17	1.3	104520	4	US-09-949-016-13303	Sequence 13303, A	c 506	17	1.3	818128	4	US-09-949-016-14546	Sequence 14546, A
c 434	17	1.3	105050	4	US-09-949-016-15953	Sequence 15953, A	c 507	17	1.3	818128	4	US-09-949-016-14547	Sequence 14547, A
435	17	1.3	113060	4	US-09-949-016-14773	Sequence 14773, A	c 508	17	1.3	818128	4	US-09-949-016-14548	Sequence 14548, A
436	17	1.3	113060	4	US-09-949-016-14774	Sequence 14774, A	c 509	17	1.3	818128	4	US-09-949-016-14549	Sequence 14549, A
437	17	1.3	113283	4	US-09-949-016-16976	Sequence 16976, A	c 510	17	1.3	818128	4	US-09-949-016-14550	Sequence 14550, A
438	17	1.3	113283	4	US-09-949-016-16977	Sequence 16977, A	c 511	17	1.3	818128	4	US-09-949-016-14551	Sequence 14551, A
c 439	17	1.3	113876	4	US-09-949-016-14828	Sequence 14828, A	c 512	17	1.3	818128	4	US-09-949-016-14552	Sequence 14552, A
c 440	17	1.3	113876	4	US-09-949-016-14829	Sequence 14829, A	c 513	17	1.3	818128	4	US-09-949-016-14553	Sequence 14553, A
c 441	17	1.3	115508	4	US-09-949-016-11800	Sequence 11800, A	c 514	17	1.3	818128	4	US-09-949-016-14554	Sequence 14554, A
c 442	17	1.3	115508	4	US-09-949-016-14826	Sequence 14826, A	c 515	17	1.3	818128	4	US-09-949-016-14555	Sequence 14555, A
c 443	17	1.3	115508	4	US-09-949-016-14827	Sequence 14827, A	c 516	17	1.3	818128	4	US-09-949-016-14556	Sequence 14556, A
444	17	1.3	116592	4	US-09-818-512-3	Sequence 3, Appl	c 517	17	1.3	818128	4	US-09-949-016-14557	Sequence 14557, A
c 445	17	1.3	119032	4	US-09-949-016-12160	Sequence 12160, A	c 518	17	1.3	818128	4	US-09-949-016-14558	Sequence 14558, A
c 446	17	1.3	119032	4	US-09-949-016-17268	Sequence 17268, A	c 519	17	1.3	818128	4	US-09-949-016-14559	Sequence 14559, A
447	17	1.3	119594	4	US-09-949-016-12080	Sequence 12080, A	c 520	17	1.3	818128	4	US-09-949-016-14560	Sequence 14560, A
448	17	1.3	119601	4	US-09-949-016-15952	Sequence 15952, A	c 521	17	1.3	818128	4	US-09-949-016-14561	Sequence 14561, A
449	17	1.3	119649	4	US-09-949-016-12537	Sequence 12537, A	c 522	17	1.3	818128	4	US-09-949-016-14562	Sequence 14562, A
450	17	1.3	124264	4	US-09-949-016-16396	Sequence 16396, A	c 523	17	1.3	818128	4	US-09-949-016-14563	Sequence 14563, A
c 451	17	1.3	126029	4	US-09-949-016-14731	Sequence 14731, A	c 524	17	1.3	818128	4	US-09-949-016-14564	Sequence 14564, A
c 452	17	1.3	135667	4	US-09-949-016-15051	Sequence 15051, A	c 525	17	1.3	818128	4	US-09-949-016-14565	Sequence 14565, A
453	17	1.3	138693	4	US-09-949-016-16724	Sequence 16724, A	c 526	17	1.3	818128	4	US-09-949-016-14566	Sequence 14566, A
454	17	1.3	146095	4	US-09-949-016-12872	Sequence 12872, A	c 527	17	1.3	1664976	4	US-09-949-016-14567	Sequence 14567, A
455	17	1.3	146104	4	US-09-949-016-13239	Sequence 13239, A	c 528	17	1.3	1664976	4	US-08-916-421B-1	Sequence 1, Appl
456	17	1.3	147840	4	US-09-949-016-15236	Sequence 15236, A	c 529	17	1.3	1664976	4	US-09-552-570-1	Sequence 1, Appl
c 457	17	1.3	148609	4	US-09-949-016-12860	Sequence 12860, A	c 530	17	1.3	1664976	4	US-09-557-884-1	Sequence 1, Appl
c 458	17	1.3	148609	4	US-09-949-016-16787	Sequence 16787, A	c 531	17	1.3	1830121	4	US-09-643-990A-1	Sequence 1, Appl
c 459	17	1.3	150597	4	US-09-949-016-15379	Sequence 15379, A	c 532	17	1.3	1830121	4	US-09-396-196G-120398	Sequence 120398, A
c 460	17	1.3	152486	4	US-09-949-016-12869	Sequence 12869, A	c 533	17	1.3	25	4	US-09-396-196G-120399	Sequence 120399, A
461	17	1.3	155019	4	US-09-949-016-11929	Sequence 11929, A	c 534	17	1.3	25	4	US-09-396-196G-120410	Sequence 120410, A
462	17	1.3	158735	4	US-09-949-016-11689	Sequence 11689, A	c 535	17	1.3	25	4	US-09-396-196G-120411	Sequence 120411, A
463	17	1.3	158735	4	US-09-949-016-17130	Sequence 17130, A	c 536	17	1.3	106	4	US-09-396-196G-120412	Sequence 120412, A
464	17	1.3	160759	4	US-09-949-016-16514	Sequence 16514, A	c 537	17	1.3	109	4	US-09-621-976-18048	Sequence 18048, A
465	17	1.3	161124	4	US-09-949-016-16514	Sequence 16514, A	c 538	17	1.3	120	4	US-09-621-976-18075	Sequence 18075, A
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539	16	1.3	160	4	US-09-621-976-18066	Sequence 18066, A	612	16	1.3	601	4	US-09-949-016-40470	Sequence 40470, A
540	16	1.3	160	4	US-09-621-976-18071	Sequence 18071, A	C 613	16	1.3	601	4	US-09-949-016-40896	Sequence 40896, A
541	16	1.3	162	4	US-09-621-976-18068	Sequence 18068, A	C 614	16	1.3	601	4	US-09-949-016-40897	Sequence 40897, A
C 542	16	1.3	170	4	US-08-956-1718-4697	Sequence 4697, Ap	C 615	16	1.3	601	4	US-09-949-016-40898	Sequence 40898, A
C 543	16	1.3	170	4	US-09-270-767-2673	Sequence 2673, A	C 616	16	1.3	601	4	US-09-949-016-40899	Sequence 40899, A
C 544	16	1.3	170	4	US-08-781-986A-4697	Sequence 4697, Ap	C 617	16	1.3	601	4	US-09-949-016-44071	Sequence 44071, A
545	16	1.3	179	4	US-09-621-976-18054	Sequence 18054, A	C 618	16	1.3	601	4	US-09-949-016-52558	Sequence 52558, A
546	16	1.3	190	4	US-09-513-999C-30241	Sequence 30241, A	C 619	16	1.3	601	4	US-09-949-016-53737	Sequence 53737, A
547	16	1.3	195	4	US-09-621-976-18062	Sequence 18062, A	C 620	16	1.3	601	4	US-09-949-016-53738	Sequence 53738, A
548	16	1.3	196	4	US-09-513-999C-24370	Sequence 24370, A	C 621	16	1.3	601	4	US-09-949-016-53739	Sequence 53739, A
C 549	16	1.3	202	4	US-09-513-999C-14672	Sequence 14672, A	C 622	16	1.3	601	4	US-09-949-016-57310	Sequence 57310, A
C 550	16	1.3	202	4	US-09-513-999C-23906	Sequence 23906, A	C 623	16	1.3	601	4	US-09-949-016-60189	Sequence 60189, A
551	16	1.3	220	3	US-09-109-204-29	Sequence 29, Appl	C 624	16	1.3	601	4	US-09-949-016-62056	Sequence 62056, A
552	16	1.3	220	4	US-09-490-032-29	Sequence 29, Appl	C 625	16	1.3	601	4	US-09-949-016-69556	Sequence 69556, A
553	16	1.3	240	4	US-09-513-999C-30933	Sequence 30933, A	C 626	16	1.3	601	4	US-09-949-016-69598	Sequence 69598, A
554	16	1.3	252	4	US-09-601-198-34	Sequence 34, Appl	C 627	16	1.3	601	4	US-09-949-016-70668	Sequence 70668, A
555	16	1.3	252	4	US-09-601-198-48	Sequence 48, Appl	C 628	16	1.3	601	4	US-09-949-016-73941	Sequence 73941, A
556	16	1.3	258	4	US-09-248-796A-4107	Sequence 4107, Ap	C 629	16	1.3	601	4	US-09-949-016-73942	Sequence 73942, A
557	16	1.3	266	4	US-09-023-655-799	Sequence 799, App	C 630	16	1.3	601	4	US-09-949-016-74047	Sequence 74047, A
558	16	1.3	349	4	US-09-513-999C-10056	Sequence 10056, A	C 631	16	1.3	601	4	US-09-949-016-74048	Sequence 74048, A
559	16	1.3	354	4	US-09-513-999C-34934	Sequence 34934, A	C 632	16	1.3	601	4	US-09-949-016-74609	Sequence 74609, A
560	16	1.3	359	4	US-09-513-999C-11853	Sequence 11853, A	C 633	16	1.3	601	4	US-09-949-016-82167	Sequence 82167, A
561	16	1.3	372	4	US-09-401-064-361	Sequence 361, App	C 634	16	1.3	601	4	US-09-949-016-84891	Sequence 84891, A
562	16	1.3	377	4	US-09-513-999C-3808	Sequence 3808, Ap	C 635	16	1.3	601	4	US-09-949-016-85288	Sequence 85288, A
C 563	16	1.3	389	4	US-09-621-976-3333	Sequence 3333, Ap	C 636	16	1.3	601	4	US-09-949-016-85289	Sequence 85289, A
564	16	1.3	394	3	US-09-221-017B-49	Sequence 49, Appl	C 637	16	1.3	601	4	US-09-949-016-88127	Sequence 88127, A
C 565	16	1.3	419	3	US-09-641-638-431	Sequence 431, App	C 638	16	1.3	601	4	US-09-949-016-88128	Sequence 88128, A
C 566	16	1.3	419	4	US-10-170-097-431	Sequence 431, App	C 639	16	1.3	601	4	US-09-949-016-88301	Sequence 88301, A
C 567	16	1.3	438	4	US-09-479-040-4	Sequence 4, Appl	C 640	16	1.3	601	4	US-09-949-016-88375	Sequence 88375, A
C 568	16	1.3	450	4	US-09-107-532A-2078	Sequence 2078, Ap	C 641	16	1.3	601	4	US-09-949-016-88976	Sequence 88976, A
C 569	16	1.3	477	4	US-09-248-796A-742	Sequence 742, App	C 642	16	1.3	601	4	US-09-949-016-89377	Sequence 89377, A
C 570	16	1.3	489	4	US-09-642-796A-8695	Sequence 8695, Ap	C 643	16	1.3	601	4	US-09-949-016-91442	Sequence 91442, A
571	16	1.3	507	4	US-09-583-110-1380	Sequence 1380, Ap	C 644	16	1.3	601	4	US-09-949-016-92450	Sequence 92450, A
C 572	16	1.3	508	4	US-09-621-976-3096	Sequence 3096, Ap	C 645	16	1.3	601	4	US-09-949-016-92451	Sequence 92451, A
C 573	16	1.3	513	4	US-09-270-767-6659	Sequence 6659, Ap	C 646	16	1.3	601	4	US-09-949-016-93183	Sequence 93183, A
C 574	16	1.3	513	4	US-09-270-767-21941	Sequence 21941, A	C 647	16	1.3	601	4	US-09-949-016-93184	Sequence 93184, A
575	16	1.3	519	4	US-09-107-433-1218	Sequence 1218, Ap	C 648	16	1.3	601	4	US-09-949-016-93820	Sequence 93820, A
576	16	1.3	523	4	US-09-270-767-7077	Sequence 7077, Ap	C 649	16	1.3	601	4	US-09-949-016-94081	Sequence 94081, A
577	16	1.3	523	4	US-09-270-767-22359	Sequence 22359, A	C 650	16	1.3	601	4	US-09-949-016-110804	Sequence 110804, A
578	16	1.3	525	3	US-09-221-017B-673	Sequence 673, App	C 651	16	1.3	601	4	US-09-949-016-110965	Sequence 110965, A
579	16	1.3	529	3	US-09-109-204-28	Sequence 28, Appl	C 652	16	1.3	601	4	US-09-949-016-11126	Sequence 11126, A
580	16	1.3	529	4	US-09-490-032-28	Sequence 28, Appl	C 653	16	1.3	601	4	US-09-949-016-111287	Sequence 111287, A
581	16	1.3	532	3	US-09-221-017B-161	Sequence 161, App	C 654	16	1.3	601	4	US-09-949-016-13343	Sequence 13343, A
582	16	1.3	542	4	US-09-621-976-2601	Sequence 2601, Ap	C 655	16	1.3	601	4	US-09-949-016-133414	Sequence 133414, A
583	16	1.3	548	3	US-08-642-274D-21	Sequence 21, Appl	C 656	16	1.3	601	4	US-09-949-016-133607	Sequence 133607, A
584	16	1.3	548	3	US-08-952-014C-21	Sequence 21, Appl	C 657	16	1.3	601	4	US-09-949-016-134283	Sequence 134283, A
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C 586	16	1.3	601	4	US-09-949-016-18622	Sequence 18622, A	C 659	16	1.3	601	4	US-09-949-016-137941	Sequence 137941, A
C 587	16	1.3	601	4	US-09-949-016-18628	Sequence 20048, A	C 660	16	1.3	601	4	US-09-949-016-137942	Sequence 137942, A
C 588	16	1.3	601	4	US-09-949-016-26008	Sequence 26008, A	C 661	16	1.3	601	4	US-09-949-016-143911	Sequence 143911, A
C 589	16	1.3	601	4	US-09-949-016-26083	Sequence 26083, A	C 662	16	1.3	601	4	US-09-949-016-143910	Sequence 143910, A
C 590	16	1.3	601	4	US-09-949-016-26084	Sequence 26084, A	C 663	16	1.3	601	4	US-09-949-016-144820	Sequence 144820, A
C 591	16	1.3	601	4	US-09-949-016-26085	Sequence 26085, A	C 664	16	1.3	601	4	US-09-949-016-144825	Sequence 144825, A
C 592	16	1.3	601	4	US-09-949-016-26086	Sequence 26086, A	C 665	16	1.3	601	4	US-09-949-016-145773	Sequence 145773, A
C 593	16	1.3	601	4	US-09-949-016-26087	Sequence 26087, A	C 666	16	1.3	601	4	US-09-949-016-146041	Sequence 146041, A
C 594	16	1.3	601	4	US-09-949-016-26088	Sequence 26088, A	C 667	16	1.3	601	4	US-09-949-016-146309	Sequence 146309, A
C 595	16	1.3	601	4	US-09-949-016-26089	Sequence 26089, A	C 668	16	1.3	601	4	US-09-949-016-146840	Sequence 146840, A
C 596	16	1.3	601	4	US-09-949-016-27583	Sequence 27583, A	C 669	16	1.3	601	4	US-09-949-016-146841	Sequence 146841, A
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598	16	1.3	601	4	US-09-949-016-28050	Sequence 28050, A	C 671	16	1.3	601	4	US-09-949-016-147267	Sequence 147267, A
599	16	1.3	601	4	US-09-949-016-28050	Sequence 28050, A	C 672	16	1.3	601	4	US-09-949-016-149390	Sequence 149390, A
600	16	1.3	601	4	US-09-949-016-29065	Sequence 29065, A	C 673	16	1.3	601	4	US-09-949-016-149391	Sequence 149391, A
601	16	1.3	601	4	US-09-949-016-30681	Sequence 30681, A	C 674	16	1.3	601	4	US-09-949-016-149392	Sequence 149392, A
602	16	1.3	601	4	US-09-949-016-31022	Sequence 31022, A	C 675	16	1.3	601	4	US-09-949-016-151226	Sequence 151226, A
C 603	16	1.3	601	4	US-09-949-016-31023	Sequence 31023, A	C 676	16	1.3	601	4	US-09-949-016-151490	Sequence 151490, A
C 604	16	1.3	601	4	US-09-949-016-31024	Sequence 31024, A	C 677	16	1.3	601	4	US-09-949-016-151807	Sequence 151807, A
C 605	16	1.3	601	4	US-09-949-016-31025	Sequence 31025, A	C 678	16	1.3	601	4	US-09-949-016-155862	Sequence 155862, A
C 606	16	1.3	601	4	US-09-949-016-31795	Sequence 31795, A	C 679	16	1.3	601	4	US-09-949-016-157189	Sequence 157189, A
C 607	16	1.3	601	4	US-09-949-016-31796	Sequence 31796, A	C 680	16	1.3	601	4	US-09-949-016-158062	Sequence 158062, A
C 608	16	1.3	601	4	US-09-949-016-39803	Sequence 39803, A	C 681	16	1.3	601	4	US-09-949-016-158683	Sequence 158683, A
609	16	1.3	601	4	US-09-949-016-39804	Sequence 39804, A	C 682	16	1.3	601	4	US-09-949-016-158780	Sequence 158780, A
C 610	16	1.3	601	4	US-09-949-016-39980	Sequence 39980, A	C 683	16	1.3	601	4	US-09-949-016-161310	Sequence 161310, A
C 611	16	1.3	601	4	US-09-949-016-39981	Sequence 39981, A	C 684	16	1.3	601	4	US-09-949-016-162144	Sequence 162144, A

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C 686	16	1.3	601	4	US-09-949-016-166747	Sequence 166747,	C 759	16	1.3	1001	4	US-10-170-097-265	Sequence 265, App
C 687	16	1.3	601	4	US-09-949-016-168046	Sequence 168046,	C 760	16	1.3	1001	4	US-10-170-097-266	Sequence 266, App
C 688	16	1.3	601	4	US-09-949-016-168326	Sequence 168326,	C 761	16	1.3	1047	4	US-09-107-532A-2496	Sequence 2496, App
C 689	16	1.3	601	4	US-09-949-016-168327	Sequence 168327,	C 762	16	1.3	1062	3	US-08-961-527-197	Sequence 197, App
C 690	16	1.3	601	4	US-09-949-016-169637	Sequence 169637,	C 763	16	1.3	1128	4	US-08-583-110-2289	Sequence 2289, App
C 691	16	1.3	601	4	US-09-949-016-169638	Sequence 169638,	C 764	16	1.3	1149	4	US-09-107-433-1234	Sequence 1234, App
C 692	16	1.3	601	4	US-09-949-016-171856	Sequence 171856,	C 765	16	1.3	1188	4	US-09-540-236-617	Sequence 617, App
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C 694	16	1.3	601	4	US-09-949-016-171858	Sequence 171858,	C 767	16	1.3	1218	4	US-09-270-767-14792	Sequence 14792, A
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C 696	16	1.3	601	4	US-09-949-016-173345	Sequence 173345,	C 769	16	1.3	1230	4	US-09-710-279-3257	Sequence 3257, App
C 697	16	1.3	601	4	US-09-949-016-173346	Sequence 173346,	C 770	16	1.3	1314	3	US-08-936-165A-153	Sequence 153, App
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C 699	16	1.3	601	4	US-09-949-016-175016	Sequence 175016,	C 772	16	1.3	1382	4	US-09-369-247-32	Sequence 32, Appl
C 700	16	1.3	601	4	US-09-949-016-175017	Sequence 175017,	C 773	16	1.3	1389	4	US-09-602-787A-77	Sequence 77, Appl
C 701	16	1.3	601	4	US-09-949-016-175018	Sequence 175018,	C 774	16	1.3	1392	3	US-09-257-584-1	Sequence 1, Appli
C 702	16	1.3	601	4	US-09-949-016-175791	Sequence 175791,	C 775	16	1.3	1434	4	US-09-710-279-3249	Sequence 3249, App
C 703	16	1.3	601	4	US-09-949-016-173345	Sequence 173345,	C 776	16	1.3	1493	4	US-09-620-312D-728	Sequence 728, App
C 704	16	1.3	601	4	US-09-949-016-180723	Sequence 180723,	C 777	16	1.3	1524	3	US-09-134-001C-2234	Sequence 2234, App
C 705	16	1.3	601	4	US-09-949-016-180724	Sequence 180724,	C 778	16	1.3	1551	4	US-09-614-221A-531	Sequence 531, App
C 706	16	1.3	601	4	US-09-949-016-182088	Sequence 182088,	C 779	16	1.3	1551	4	US-09-583-110-2384	Sequence 2384, App
C 707	16	1.3	601	4	US-09-949-016-182089	Sequence 182089,	C 780	16	1.3	1572	4	US-09-107-433-770	Sequence 770, App
C 708	16	1.3	601	4	US-09-949-016-183193	Sequence 183193,	C 781	16	1.3	1578	4	US-09-328-352-3641	Sequence 3641, App
C 709	16	1.3	601	4	US-09-949-016-183194	Sequence 183194,	C 782	16	1.3	1578	4	US-09-107-532A-984	Sequence 984, App
C 710	16	1.3	601	4	US-09-949-016-185858	Sequence 185858,	C 783	16	1.3	1588	3	US-08-858-207A-58	Sequence 58, Appl
C 711	16	1.3	601	4	US-09-949-016-186874	Sequence 186874,	C 784	16	1.3	1602	1	US-08-948-176-1	Sequence 1, Appli
C 712	16	1.3	601	4	US-09-949-016-187835	Sequence 187835,	C 785	16	1.3	1602	2	US-09-356-806-117	Sequence 117, App
C 713	16	1.3	601	4	US-09-949-016-189666	Sequence 189666,	C 786	16	1.3	1602	1	US-09-848-723-6	Sequence 6, Appli
C 714	16	1.3	601	4	US-09-949-016-189711	Sequence 189711,	C 787	16	1.3	1602	5	PCT-US91-09160-1	Sequence 1, Appli
C 715	16	1.3	601	4	US-09-949-016-189712	Sequence 189712,	C 788	16	1.3	1602	4	US-09-426-793-6	Sequence 6, Appli
C 716	16	1.3	601	4	US-09-949-016-190970	Sequence 190970,	C 789	16	1.3	1716	4	US-09-252-991A-11978	Sequence 11978, A
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C 718	16	1.3	601	4	US-09-949-016-196259	Sequence 196259,	C 791	16	1.3	1818	3	US-09-357-206A-6	Sequence 6, Appli
C 719	16	1.3	601	4	US-09-949-016-196854	Sequence 196854,	C 792	16	1.3	1850	3	US-09-848-723-6	Sequence 6, Appli
C 720	16	1.3	601	4	US-09-949-016-198855	Sequence 198855,	C 793	16	1.3	1855	3	US-09-150-141-6	Sequence 6, Appli
C 721	16	1.3	601	4	US-09-949-016-198856	Sequence 198856,	C 794	16	1.3	1855	3	US-09-374-493-6	Sequence 6, Appli
C 722	16	1.3	601	4	US-09-949-016-198857	Sequence 198857,	C 795	16	1.3	1855	3	US-09-374-824-6	Sequence 6, Appli
C 723	16	1.3	601	4	US-09-949-016-198858	Sequence 198858,	C 796	16	1.3	1855	3	US-09-374-492-6	Sequence 6, Appli
C 724	16	1.3	601	4	US-09-949-016-198859	Sequence 198859,	C 797	16	1.3	1855	3	US-09-785-343-6	Sequence 6, Appli
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C 726	16	1.3	601	4	US-09-949-016-198904	Sequence 198904,	C 799	16	1.3	1855	4	US-10-411-976-6	Sequence 6, Appli
C 727	16	1.3	601	4	US-09-949-016-205428	Sequence 205428,	C 800	16	1.3	1855	4	US-09-949-016-519	Sequence 519, App
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C 730	16	1.3	601	4	US-09-949-016-205431	Sequence 205431,	C 803	16	1.3	1930	3	US-09-404-390-1	Sequence 1, Appli
C 731	16	1.3	603	4	US-09-949-016-205431	Sequence 205431,	C 804	16	1.3	1968	4	US-09-248-796A-13252	Sequence 13252, A
C 732	16	1.3	648	3	US-09-774-639-42	Sequence 722, App	C 805	16	1.3	1970	4	US-09-385-219A-25	Sequence 25, Appl
C 733	16	1.3	655	3	US-09-109-204-27	Sequence 42, Appl	C 806	16	1.3	1983	4	US-09-583-110-1817	Sequence 1817, App
C 734	16	1.3	655	4	US-09-109-204-27	Sequence 27, Appl	C 807	16	1.3	1995	4	US-09-107-433-887	Sequence 887, App
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C 741	16	1.3	783	4	US-09-270-767-18795	Sequence 18795, A	C 814	16	1.3	2340	4	US-09-949-016-1663	Sequence 1663, App
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C 746	16	1.3	873	3	US-09-134-001C-1207	Sequence 1207, App	C 819	16	1.3	2497	6	5185259-2	Patent No. 5185259
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C 749	16	1.3	900	4	US-09-252-991A-1168	Sequence 1168, App	C 822	16	1.3	2515	3	US-09-724-864-4	Sequence 4, Appli
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C 756	16	1.3	990	4	US-09-404-390-2	Sequence 2, Appli	C 829	16	1.3	2707	4	US-09-949-016-4096	Sequence 4096, App
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C 839	16	1.3	3182	4	US-09-809-665A-72	Sequence 72, Appl	C 912	16	1.3	7626	3	US-09-949-016-15705	Sequence 15705, A
C 840	16	1.3	3209	4	US-09-766-594-671	Sequence 671, App	C 913	16	1.3	7685	3	US-09-221-017B-1092	Sequence 1092, Ap
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C 855	16	1.3	3735	3	US-09-295-028-43	Sequence 43, Appl	C 928	16	1.3	11466	4	US-08-956-171E-444	Sequence 444, App
C 856	16	1.3	3735	3	US-09-106-582-43	Sequence 43, Appl	C 929	16	1.3	11466	4	US-08-781-986A-444	Sequence 444, App
C 857	16	1.3	3735	4	US-09-159-469-43	Sequence 43, Appl	C 930	16	1.3	11466	3	US-09-410-464-9	Sequence 9, Appl
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C 863	16	1.3	3818	4	US-09-710-279-3367	Sequence 3367, Ap	C 936	16	1.3	12308	4	US-09-854-133-422	Sequence 422, App
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C 876	16	1.3	5066	4	US-09-799-451-558	Sequence 558, App	C 949	16	1.3	16595	3	US-09-146-053-7	Sequence 7, Appl
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C 880	16	1.3	5552	3	US-08-155-888-1	Sequence 1, Appl	C 953	16	1.3	19157	4	US-09-949-016-13142	Sequence 13142, A
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C 882	16	1.3	5632	3	US-09-560-594-3	Sequence 3, Appl	C 955	16	1.3	20023	4	US-09-949-016-12604	Sequence 12604, A
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C 888	16	1.3	6095	3	US-09-357-206A-18	Sequence 18, Appl	C 961	16	1.3	24553	4	US-09-949-016-16901	Sequence 16901, A
C 889	16	1.3	6153	4	US-09-949-016-14584	Sequence 14584, A	C 962	16	1.3	24740	4	US-09-949-016-13528	Sequence 13528, A
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C 892	16	1.3	6272	4	US-08-956-171E-140	Sequence 140, App	C 965	16	1.3	26355	4	US-09-949-016-17602	Sequence 17602, A
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C 896	16	1.3	6866	4	US-09-949-016-15807	Sequence 15807, A	C 969	16	1.3	27360	4	US-09-949-016-17502	Sequence 17502, A
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C 899	16	1.3	7351	1	US-08-484-304-83	Sequence 83, Appl	C 972	16	1.3	28585	4	US-09-949-016-16482	Sequence 16482, A
C 900	16	1.3	7351	2	US-08-184-009-127	Sequence 127, App	C 973	16	1.3	28806	4	US-09-949-016-13217	Sequence 13217, A
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US-09-591-694-1
; Application US/09591694
; Patent No. 6638734
; GENERAL INFORMATION:
; APPLICANT: John C. Reed
; APPLICANT: Shu-ichi Matsuzawa
; TITLE OF INVENTION: Nucleic Acid Encoding Proteins Involved
; TITLE OF INVENTION: in Protein Degradation, Products and Methods Related Thereto
; FILE REFERENCE: P-LJ 4220
; CURRENT APPLICATION NUMBER: US/09/591,694
; CURRENT FILING DATE: 2000-06-09
; EARLIER APPLICATION NUMBER: US 09/330,517
; EARLIER FILING DATE: 1999-06-11
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 1274
; TYPE: DNA
; ORGANISM: Homo sapien
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (274)...(1167)
US-09-591-694-1

Query Match 100.0%; Score 1274; DB 4; Length 1274;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1274; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1081 AGCGACTGTCTAGTCTTTGACACAGCATTTGACAGCTTTTTCGAGAAATGGCAATTTA 1140

QY 1141 GGCATCAATGTAATTTTCCATGTTGAAATGGCAATTTGCAACAGCCATTTTCTGCCAGTCT 1200
Db 1141 GGCATCAATGTAATTTTCCATGTTGAAATGGCAATTTGCAACAGCCATTTTCTGCCAGTCT 1200

QY 1201 TTAATAACTTCAGTTTTCACAGAAATAAGGCAAGCCATCTGCTGCTGCTGCTGCTGCTGCT 1260
Db 1201 TTAATAACTTCAGTTTTCACAGAAATAAGGCAAGCCATCTGCTGCTGCTGCTGCTGCTGCT 1260

QY 1261 CGGTAGGTGGAAGC 1274
Db 1261 CGGTAGGTGGAAGC 1274

RESULT 2
 US-09-023-655-588
 ; Sequence 588, Application US/09023655
 ; Patent No. 6607879
 ; GENERAL INFORMATION:
 ; APPLICANT: Cocks, Benjamin G.
 ; APPLICANT: Susan G. Stuart
 ; APPLICANT: Jeffrey J. Seilhamer
 ; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL GENE
 ; TITLE OF INVENTION: EXPRESSION
 ; NUMBER OF SEQUENCES: 1508
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
 ; STREET: 3174 PORTER DRIVE
 ; CITY: PALO ALTO
 ; STATE: CALIFORNIA
 ; COUNTRY: USA
 ; ZIP: 94304
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/023,655
 ; FILING DATE: HEREWITH
 ; CLASSIFICATION:
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER:
 ; FILING DATE:
 ; CLASSIFICATION:
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Zeller, Karen J.
 ; REGISTRATION NUMBER: 37,071
 ; REFERENCE/DOCKET NUMBER: PA-0001 US
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (650) 855-0555
 ; TELEFAX: (650) 845-4166
 ; INFORMATION FOR SEQ ID NO: 588:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 2440 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; IMMEDIATE SOURCE:
 ; LIBRARY: SPLNFT01
 ; CLONE: 29244
 ; US-09-023-655-588
 Query Match 81.7%; Score 1041; DB 4; Length 2440;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1041; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 234 AAGGACTTATGGCATGTAACATATTATTAAGTAAGTCATGGTTATTAATTATTTTCT 293
 DB 467 AAGGACTTATGGCATGTAACATATTATTAAGTAAGTCATGGTTATTAATTATTTTCT 526
 QY 294 CCGTCTCTCTTATGTTATTTATTCAGAAATGAGCGCTGAGCTGCTACAGCACTTACCTAC 353
 DB 527 CCGTCTCTCTTATGTTATTTATTCAGAAATGAGCGCTGAGCTGCTACAGCACTTACCTAC 586
 QY 354 CGGTACTCGAAGTGTCCACCATCCAGAGGGTCCCTGACCTGACGCGGACCACTGCATC 413
 DB 587 CGGTACTCGAAGTGTCCACCATCCAGAGGGTCCCTGACCTGACGCGGACCACTGCATC 646
 QY 414 CAACATATGCTGGCAGTCTTTTTCAGTGTCCAGTGTCCAGTGTCTGTTGATGTGTTACCGCC 473
 DB 647 CAACATATGCTGGCAGTCTTTTTCAGTGTCCAGTGTCCAGTGTCTGTTGATGTGTTACCGCC 706
 QY 474 CATTCTTCAATGTCAGAGTGGCCATCTTTTGTAGCAACTGTCCGCCAAAGCTCACATG 533
 DB 707 CATTCTTCAATGTCAGAGTGGCCATCTTTTGTAGCAACTGTCCGCCAAAGCTCACATG 766

QY 534 TTGTCCAACTTGC CGGGGCCCTTTTGGGATCCATTTCGCAACTTGGGCTATGGAGAAAGTGCC 593
 DB 767 TTGTCCAACTTGC CGGGGCCCTTTTGGGATCCATTTCGCAACTTGGGCTATGGAGAAAGTGCC 826
 QY 594 TAATTTCAGTACTTTTCCCGCTGTAAATATGCGTCTTCTGGATGTGAATTAACCTCTGCCACA 653
 DB 827 TAATTTCAGTACTTTTCCCGCTGTAAATATGCGTCTTCTGGATGTGAATTAACCTCTGCCACA 886
 QY 654 CACAGAAAAGCAGACCACTGAAGAGCTCTGTGAGTTTAGGCTTTATCTCTGTCGCGGCC 713
 DB 887 CACAGAAAAGCAGACCACTGAAGAGCTCTGTGAGTTTAGGCTTTATCTCTGTCGCGGCC 946
 QY 714 TGGTGTCTCTGTAAATGCAAGGCTCTCTGGATGTGAATTAACCTCTGATGATCA 773
 DB 947 TGGTGTCTCTGTAAATGCAAGGCTCTCTGGATGTGAATTAACCTCTGATGATCA 1006
 QY 774 GCATAAGTCCATTACAAACCTACAGGAGAGGATATAGTTTTCTTGTCTACACATTA 833
 DB 1007 GCATAAGTCCATTACAAACCTACAGGAGAGGATATAGTTTTCTTGTCTACACATTA 1066
 QY 834 TCTTCTGTGTCTGTGACTGGGTGATGATGAGTCTCTGTCTTGGCTTTTCACTTTCATGTT 893
 DB 1067 TCTTCTGTGTCTGTGACTGGGTGATGATGAGTCTCTGTCTTGGCTTTTCACTTTCATGTT 1126
 QY 894 AGTCTTAGAGAAACAGGAAAAATACGATGGTCAACGAGTCTTTCGCAATGTCAGCT 953
 DB 1127 AGTCTTAGAGAAACAGGAAAAATACGATGGTCAACGAGTCTTTCGCAATGTCAGCT 1186
 QY 954 GATAGAACACGACAGCTGAAAAATTTTCTTACCGACTTACGCTAAATGGTCTATAG 1013
 DB 1187 GATAGAACACGACAGCTGAAAAATTTTCTTACCGACTTACGCTAAATGGTCTATAG 1246
 QY 1014 GCGACGATTGACTTGGGAAGCAGCTCTCGATCTATTCAATGAAGAAATGCAACAGCCAT 1073
 DB 1247 GCGACGATTGACTTGGGAAGCAGCTCTCGATCTATTCAATGAAGAAATGCAACAGCCAT 1306
 QY 1074 TATGAATAGCGACTGTCTAGTCTTTGACACCAAGCTTTCAGCTTTTTCGAGAAAATGG 1133
 DB 1307 TATGAATAGCGACTGTCTAGTCTTTGACACCAAGCTTTCAGCTTTTTCGAGAAAATGG 1366
 QY 1134 CAATTAGGCATCAATGTAACCTATTTCATGTTTGAATGCAATCAACATTTTCTGG 1193
 DB 1367 CAATTAGGCATCAATGTAACCTATTTCATGTTTGAATGCAATCAACATTTTCTGG 1426
 QY 1194 CCAGTGTTTTAAACTTCAGTTTTCAGAAAAATAAGGCAACCCATCTCTGCGCAACCTAAA 1253
 DB 1427 CCAGTGTTTTAAACTTCAGTTTTCAGAAAAATAAGGCAACCCATCTCTGCGCAACCTAAA 1486
 QY 1254 ACTCTTTCGCTAGGTGGAAGC 1274
 DB 1487 ACTCTTTCGCTAGGTGGAAGC 1507
 RESULT 3
 US-09-544-618-11
 ; Sequence 11, Application US/09544618
 ; Patent No. 6503502
 ; GENERAL INFORMATION:
 ; APPLICANT: Telemar, Adam
 ; APPLICANT: Amson, Robert
 ; APPLICANT: Cohen, Daniel
 ; TITLE OF INVENTION: NUCLEOTIDE SEQUENCES, PROTEINS, DRUGS AND DIAGNOSTIC
 ; TITLE OF INVENTION: AGENTS OF USE IN TREATING CANCER
 ; FILE REFERENCE: 065691-0139
 ; CURRENT APPLICATION NUMBER: US/09/544,618
 ; CURRENT FILING DATE: 2000-03-06
 ; NUMBER OF SEQ ID NOS: 22
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 11
 ; LENGTH: 1884
 ; TYPE: DNA
 ; ORGANISM: TSAP 3

```

; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1) .. (846)
US-09-544-618-11

Query Match      61.2%; Score 780; DB 4; Length 1884;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 780; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 322 ATGAGCGCTCAGACTGCTACAGCATTACCTACCGGTACCTCGAAGTGTCCACATCCCGAG 381
Db 1 ATGAGCGGTGACAGCTGCTACAGATTACCTACCGGTACCTCGAAGTGTCCACATCCCGAG 60

QY 382 AGGGTGCCTGCCCTGACTGGCACAATGCTCATCAATGACTTGGCGAGTCTTTTGGAG 441
Db 61 AGGGTGCCTGCCCTGACTGGCACAATGCTCATCAATGACTTGGCGAGTCTTTTGGAG 120

QY 442 TGTCCAGTCTGCTTTGAGTATGTGTACCGCCCATCTTCAATGTACAGATGGCCATCTT 501
Db 121 TGTCCAGTCTGCTTTGAGTATGTGTACCGCCCATCTTCAATGTACAGATGGCCATCTT 180

QY 502 GTTGTAGCACTGTGCGCCCAAGCTCACATGTGTCCAACTTGTCCGCGGCCCTTTGGGA 561
Db 181 GTTGTAGCACTGTGCGCCCAAGCTCACATGTGTCCAACTTGTCCGCGGCCCTTTGGGA 240

QY 562 TCCATTGCAACTTGGCTATGAGAAAGTGGCTAATTCAGTACTTTTCCCTGTAAATAT 621
Db 241 TCCATTGCAACTTGGCTATGAGAAAGTGGCTAATTCAGTACTTTTCCCTGTAAATAT 300

QY 622 GCGCTTCTGGATGTGAATAAATCTGCGCACACACAGAAAAAGCAGACCATGAAGAGCTC 681
Db 301 GCGCTTCTGGATGTGAATAAATCTGCGCACACACAGAAAAAGCAGACCATGAAGAGCTC 360

QY 682 TGTGAGTTTAGGCTTATCTCTGCGCTGCTGCTTCTGCTGCTGCTGCTGCTGCTGCTGCT 741
Db 361 TGTGAGTTTAGGCTTATCTCTGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 420

QY 742 CTGGATGCTGTAATGCCCATCTGATGATGATGATGATGATGATGATGATGATGATGATG 801
Db 421 CTGGATGCTGTAATGCCCATCTGATGATGATGATGATGATGATGATGATGATGATGATG 480

QY 802 GAGGATATAGTTTCTGCTACAGACATTAATCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 861
Db 481 GAGGATATAGTTTCTGCTACAGACATTAATCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 540

QY 862 ATGCACTGCTGTTTGGCTTTTCACTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 921
Db 541 ATGCACTGCTGTTTGGCTTTTCACTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 600

QY 922 GGTCAACGAGTCTTTCGCAATGCTACAGCTGATAGGAACACGCAAGCAAGCTGAAAT 981
Db 601 GGTCAACGAGTCTTTCGCAATGCTACAGCTGATAGGAACACGCAAGCAAGCTGAAAT 660

QY 982 TTTGCTTACGACTTACGATTAATGTGTATAGCGAGGATGATGCTGGAAGGAGCTCTT 1041
Db 661 TTTGCTTACGACTTACGATTAATGTGTATAGCGAGGATGATGCTGGAAGGAGCTCTT 720

QY 1042 CGATCTATTATGAGGAATGCAAGCAATGATGATGATGATGATGATGATGATGATGATGAT 1101
Db 721 CGATCTATTATGAGGAATGCAAGCAATGATGATGATGATGATGATGATGATGATGATGAT 780

RESULT 4
US-09-949-016-15300/c
; Sequence 15300, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14

; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1) .. (846)
US-09-544-618-11

Query Match      61.2%; Score 780; DB 4; Length 1884;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 780; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 322 ATGAGCGCTCAGACTGCTACAGCATTACCTACCGGTACCTCGAAGTGTCCACATCCCGAG 381
Db 1 ATGAGCGGTGACAGCTGCTACAGATTACCTACCGGTACCTCGAAGTGTCCACATCCCGAG 60

QY 382 AGGGTGCCTGCCCTGACTGGCACAATGCTCATCAATGACTTGGCGAGTCTTTTGGAG 441
Db 61 AGGGTGCCTGCCCTGACTGGCACAATGCTCATCAATGACTTGGCGAGTCTTTTGGAG 120

QY 442 TGTCCAGTCTGCTTTGAGTATGTGTACCGCCCATCTTCAATGTACAGATGGCCATCTT 501
Db 121 TGTCCAGTCTGCTTTGAGTATGTGTACCGCCCATCTTCAATGTACAGATGGCCATCTT 180

QY 502 GTTGTAGCACTGTGCGCCCAAGCTCACATGTGTCCAACTTGTCCGCGGCCCTTTGGGA 561
Db 181 GTTGTAGCACTGTGCGCCCAAGCTCACATGTGTCCAACTTGTCCGCGGCCCTTTGGGA 240

QY 562 TCCATTGCAACTTGGCTATGAGAAAGTGGCTAATTCAGTACTTTTCCCTGTAAATAT 621
Db 241 TCCATTGCAACTTGGCTATGAGAAAGTGGCTAATTCAGTACTTTTCCCTGTAAATAT 300

QY 622 GCGCTTCTGGATGTGAATAAATCTGCGCACACACAGAAAAAGCAGACCATGAAGAGCTC 681
Db 301 GCGCTTCTGGATGTGAATAAATCTGCGCACACACAGAAAAAGCAGACCATGAAGAGCTC 360

QY 682 TGTGAGTTTAGGCTTATCTCTGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 741
Db 361 TGTGAGTTTAGGCTTATCTCTGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 420

QY 742 CTGGATGCTGTAATGCCCATCTGATGATGATGATGATGATGATGATGATGATGATGATG 801
Db 421 CTGGATGCTGTAATGCCCATCTGATGATGATGATGATGATGATGATGATGATGATGATG 480

QY 802 GAGGATATAGTTTCTGCTACAGACATTAATCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 861
Db 481 GAGGATATAGTTTCTGCTACAGACATTAATCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 540

QY 862 ATGCACTGCTGTTTGGCTTTTCACTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 921
Db 541 ATGCACTGCTGTTTGGCTTTTCACTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 600

QY 922 GGTCAACGAGTCTTTCGCAATGCTACAGCTGATAGGAACACGCAAGCAAGCTGAAAT 981
Db 601 GGTCAACGAGTCTTTCGCAATGCTACAGCTGATAGGAACACGCAAGCAAGCTGAAAT 660

QY 982 TTTGCTTACGACTTACGATTAATGTGTATAGCGAGGATGATGCTGGAAGGAGCTCTT 1041
Db 661 TTTGCTTACGACTTACGATTAATGTGTATAGCGAGGATGATGCTGGAAGGAGCTCTT 720

QY 1042 CGATCTATTATGAGGAATGCAAGCAATGATGATGATGATGATGATGATGATGATGATGAT 1101
Db 721 CGATCTATTATGAGGAATGCAAGCAATGATGATGATGATGATGATGATGATGATGATGAT 780

RESULT 5
US-09-591-694-42
; Sequence 42, Application US/09591694
; Patent No. 6638734
; GENERAL INFORMATION:
; APPLICANT: John C. Reed
; APPLICANT: Shu-ichi Matsuzawa
; TITLE OF INVENTION: Nucleic Acid Encoding Proteins Involved
; IN PROTEIN DEGRADATION, PRODUCTS AND METHODS RELATED THERETO
; FILE REFERENCE: P-LJ 4220
; CURRENT APPLICATION NUMBER: US/09/591,694
; CURRENT FILING DATE: 2000-06-09
; EARLIER APPLICATION NUMBER: US 09/330,517
; EARLIER FILING DATE: 1999-06-11
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 42
; LENGTH: 28
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Primer
US-09-591-694-42

Query Match      1.6%; Score 20; DB 4; Length 28;
Best Local Similarity 100.0%; Pred. No. 5.9;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 236 GGACTTATGGCATGTAACA 255
Db 9 GGACTTATGGCATGTAACA 28

RESULT 6
US-09-016-434-397
; Sequence 397, Application US/09016434
; Patent No. 6500938
; GENERAL INFORMATION:
; APPLICANT: Janice Au-Young
; APPLICANT: Jeffrey J. Seilhamer
; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING
; PATHWAY GENE EXPRESSION
; NUMBER OF SEQUENCES: 1490
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
; STREET: 3174 PORTER DRIVE
; CITY: PALO ALTO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94304
```

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/016,434
FILING DATE: HEREWITH
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Zeller, Karen J.
REGISTRATION NUMBER: 37,071
REFERENCE/DOCKET NUMBER: PA-0002 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 855-0555
TELEFAX: (650) 845-4166
INFORMATION FOR SEQ ID NO: 397:
SEQUENCE CHARACTERISTICS:
LENGTH: 257 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: BRAITUT03
CLONE: 2113436
US-09-016-434-397

Query Match 1.6%; Score 20; DB 4; Length 257;
Best Local Similarity 100.0%; Pred. No. 6.4;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 850 GACTGGGTGATGATGCAGTC 869
|||||
Db 222 GACTGGGTGATGATGCAGTC 241

RESULT 7
US-08-545-860D-63/c
Sequence 63, Application US/08545860D
Patent No. 6040140
GENERAL INFORMATION:
APPLICANT: Croce, Carlo
APPLICANT: Canaani, Eli
TITLE OF INVENTION: Diagnostics, Therapeutics and Methods
TITLE OF INVENTION: for Detection and Treatment of Acute Leukemias
TITLE OF INVENTION: Resulting from Chromosome Abnormalities in the All-1 Region
NUMBER OF SEQUENCES: 94
CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock, Washburn, Kurtz, Mackiewicz &
ADDRESSEE: No. 6040140ris
STREET: One Liberty Place, 46th floor
CITY: Philadelphia
STATE: Pennsylvania
COUNTRY: USA
ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/545,860D
FILING DATE: 07-MAR-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/04496
FILING DATE: 22-APR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/10930

FILING DATE: 09-DEC-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/327,392
FILING DATE: 19-OCT-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/320,559
FILING DATE: 11-OCT-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/062,443
FILING DATE: 14-MAY-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/971,094
FILING DATE: 30-OCT-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/888,839
FILING DATE: 27-MAY-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/805,093
FILING DATE: 11-DEC-1991
ATTORNEY/AGENT INFORMATION:
NAME: Deluca Esq., Mark
REGISTRATION NUMBER: 33,229
REFERENCE/DOCKET NUMBER: TJU-1262
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 568-3100
TELEFAX: (215) 568-3439
INFORMATION FOR SEQ ID NO: 63:
SEQUENCE CHARACTERISTICS:
LENGTH: 8342 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
FEATURE:
NAME/KEY: CDS
LOCATION: 2..265
FEATURE:
NAME/KEY: CDS
LOCATION: 595..666
FEATURE:
NAME/KEY: CDS
LOCATION: 2353..2484
FEATURE:
NAME/KEY: CDS
LOCATION: 3032..3145
FEATURE:
NAME/KEY: CDS
LOCATION: 6788..6934
FEATURE:
NAME/KEY: CDS
LOCATION: 7967..8062
FEATURE:
NAME/KEY: CDS
LOCATION: 8304..8342
US-08-545-860D-63

Query Match 1.6%; Score 20; DB 3; Length 8342;
Best Local Similarity 100.0%; Pred. No. 7.4;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 154 TGTAAATTTTATTTTAAAT 173
|||||
Db 6400 TGTAAATTTTATTTTAAAT 6381

RESULT 8
PCT-US94-04496-63/c
Sequence 63, Application PC/TUS9404496
GENERAL INFORMATION:
APPLICANT: Croce, Carlo
APPLICANT: Canaani, Eli

;; TITLE OF INVENTION: Diagnostics, Therapeutics and Methods
;; TITLE OF INVENTION: for Detection and Treatment of Acute Leukemias
;; TITLE OF INVENTION: Resulting from Chromosome Abnormalities in the All-1
;; NUMBER OF SEQUENCES: 86
;; CORRESPONDENCE ADDRESS:
;; ADDRESSER: Woodcock, Washburn, Kurtz, Mackiewicz &
;; ADDRESSER: Norris
;; STREET: One Liberty Place, 46th floor
;; CITY: Philadelphia
;; STATE: Pennsylvania
;; COUNTRY: USA
;; ZIP: 19103
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: Patent In Release #1.0, Version #1.25
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: PCT/US94/04496
;; FILING DATE:
;; CLASSIFICATION:
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Deluca Esq., Mark
;; REGISTRATION NUMBER: 33,229
;; REFERENCE/DOCKET NUMBER: TJU-1242
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (215) 568-3100
;; TELEFAX: (215) 568-3439
;; INFORMATION FOR SEQ ID NO: 63:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 8342 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: CDNA
;; HYPOTHETICAL: NO
;; ANTI-SENSE: NO
;; FEATURE:
;; NAME/KEY: CDS
;; LOCATION: 2..265
;; FEATURE:
;; NAME/KEY: CDS
;; LOCATION: 595..666
;; FEATURE:
;; NAME/KEY: CDS
;; LOCATION: 2353..2484
;; FEATURE:
;; NAME/KEY: CDS
;; LOCATION: 3032..3145
;; FEATURE:
;; NAME/KEY: CDS
;; LOCATION: 6788..6934
;; FEATURE:
;; NAME/KEY: CDS
;; LOCATION: 7967..8062
;; FEATURE:
;; NAME/KEY: CDS
;; LOCATION: 8304..8342
PCT-US94-04496-63

Query Match 1.6%; Score 20; DB 5; Length 8342;
Best Local Similarity 100.0%; Pred. No. 7.4;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 154 TGTAAATTTATTTTAAAT 173
Db 6400 TGTAAATTTATTTTAAAT 6381

RESULT 9
US-08-080-255-6/c
; Sequence 6, Application US/08080255
; Patent No. 5487970

;; GENERAL INFORMATION:
;; APPLICANT: Rowley, Janet D.
;; APPLICANT: Diaz, Manuel O.
;; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR
;; TITLE OF INVENTION: DETECTING GENE REARRANGEMENTS AND
;; NUMBER OF SEQUENCES: 8
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Arnold, White & Durkee
;; STREET: P. O. Box 4433
;; CITY: Houston
;; STATE: Texas
;; COUNTRY: USA
;; ZIP: 77210
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: Patent In Release #1.0, Version #1.25
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/080,255
;; FILING DATE: 19930617
;; CLASSIFICATION: 435
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Parker, David L.
;; REGISTRATION NUMBER: 32,165
;; REFERENCE/DOCKET NUMBER: ARCD:072/PAR
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (512) 320-7200
;; TELEFAX: (512) 474-7577
;; INFORMATION FOR SEQ ID NO: 6:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 8392 base pairs
;; TYPE: NUCLEIC ACID
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: DNA (genomic)
US-08-080-255-6

Query Match 1.6%; Score 20; DB 1; Length 8392;
Best Local Similarity 100.0%; Pred. No. 7.4;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 154 TGTAAATTTATTTTAAAT 173
Db 6450 TGTAAATTTATTTTAAAT 6431

RESULT 10
US-08-465-713-6/c
; Sequence 6, Application US/08465713
; Patent No. 6121419
;; GENERAL INFORMATION:
;; APPLICANT: Rowley, Janet D.
;; APPLICANT: Diaz, Manuel O.
;; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR
;; TITLE OF INVENTION: DETECTING GENE REARRANGEMENTS AND
;; NUMBER OF SEQUENCES: 8
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Arnold, White & Durkee
;; STREET: P. O. Box 4433
;; CITY: Houston
;; STATE: Texas
;; COUNTRY: USA
;; ZIP: 77210
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: Patent In Release #1.0, Version #1.25
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/465,713

;; FILING DATE: 06-JUN-1995
;; CLASSIFICATION: 530
;; PRIOR APPLICATION NUMBER: US/08/080,255
;; FILING DATE: 17 JUNE 1993
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Parker, David L.
;; REGISTRATION NUMBER: 32,165
;; REFERENCE/DOCKET NUMBER: ARCD:072/PAR
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (512) 320-7200
;; TELEFAX: (512) 474-7577
;; INFORMATION FOR SEQ ID NO: 6:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 8392 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: DNA (genomic)
US-08-465-713-6

Query Match 1.6%; Score 20; DB 3; Length 8392;
Best Local Similarity 100.0%; Pred. No. 7.4;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 154 TGTAAATTTTATTTTAAAT 173
DB 6450 TGTAAATTTTATTTTAAAT 6431

RESULT 11
PCT-US93-05857-6/c
;; Sequence 6, Application PC/TUS9305857
;; GENERAL INFORMATION:
;; APPLICANT: Board of Regents
;; APPLICANT: The University of Texas System
;; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DETECTING
;; TITLE OF INVENTION: GENE REARRANGEMENTS AND TRANSLOCATIONS
;; NUMBER OF SEQUENCES: 8
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Arnold, White & Durkee
;; STREET: P. O. Box 4433
;; CITY: Houston
;; STATE: Texas
;; COUNTRY: USA
;; ZIP: 77210
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: Patent In Release #1.0, Version #1.25
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: PCT/US93/05857
;; FILING DATE: 19930617
;; CLASSIFICATION:
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 07/900,689
;; FILING DATE: 17/06/92
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Parker, David L.
;; REGISTRATION NUMBER: 32,165
;; REFERENCE/DOCKET NUMBER: ARCD:072/PAR
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (512) 320-7200
;; TELEFAX: (512) 474-7577
;; INFORMATION FOR SEQ ID NO: 6:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 8392 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: DNA (genomic)
PCT-US93-05857-6

Query Match 1.6%; Score 20; DB 5; Length 8392;
Best Local Similarity 100.0%; Pred. No. 7.4;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 154 TGTAAATTTTATTTTAAAT 173
DB 6450 TGTAAATTTTATTTTAAAT 6431

RESULT 12
US-09-591-694-43/c
;; Sequence 43, Application US/09591694
;; Patent No. 6638734
;; GENERAL INFORMATION:
;; APPLICANT: John C. Reed
;; APPLICANT: Shu-Tchi Matsuzawa
;; TITLE OF INVENTION: Nucleic Acid Encoding Proteins Involved
;; TITLE OF INVENTION: in Protein Degradation, Products and Methods Related Thereto
;; FILE REFERENCE: P-LJ 4220
;; CURRENT APPLICATION NUMBER: US/09/591,694
;; EARLIER FILING DATE: 2000-06-09
;; EARLIER APPLICATION NUMBER: US 09/330,517
;; EARLIER FILING DATE: 1999-06-11
;; NUMBER OF SEQ ID NOS: 49
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO 43
;; LENGTH: 19
;; TYPE: DNA
;; ORGANISM: Artificial Sequence
;; FEATURE:
;; OTHER INFORMATION: Primer
US-09-591-694-43

Query Match 1.5%; Score 19; DB 4; Length 19;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 562 TCCATTGCGCAACTTGGCTA 580
DB 19 TCCATTGCGCAACTTGGCTA 1

RESULT 13
US-09-252-991A-10103
;; Sequence 10103, Application US/09252991A
;; Patent No. 6551795
;; GENERAL INFORMATION:
;; APPLICANT: Marc J. Rubenfield et al.
;; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
;; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
;; FILE REFERENCE: 107196.136
;; CURRENT APPLICATION NUMBER: US/09/252,991A
;; CURRENT FILING DATE: 1999-02-18
;; PRIOR APPLICATION NUMBER: US 60/074,788
;; PRIOR FILING DATE: 1998-02-18
;; PRIOR APPLICATION NUMBER: US 60/094,190
;; PRIOR FILING DATE: 1998-07-27
;; NUMBER OF SEQ ID NOS: 33142
;; SEQ ID NO 10103
;; LENGTH: 345
;; TYPE: DNA
;; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-10103

Query Match 1.5%; Score 19; DB 4; Length 345;
Best Local Similarity 100.0%; Pred. No. 21;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 918 CGATGGTCACGACGATTC 936
DB 98 CGATGGTCACGACGATTC 116

```
RESULT 14
US-09-949-016-19538
; Sequence 19538, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 19538
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-19538

Query Match          1.5%; Score 19; DB 4; Length 601;
Best Local Similarity 100.0%; Pred. No. 22;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 155 GTAATTTTATTTTAAAT 173
Db 40 GTAATTTTATTTTAAAT 58

RESULT 15
US-09-949-016-19539
; Sequence 19539, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 19539
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-19539

Query Match          1.5%; Score 19; DB 4; Length 601;
Best Local Similarity 100.0%; Pred. No. 22;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 155 GTAATTTTATTTTAAAT 173
Db 241 GTAATTTTATTTTAAAT 259

RESULT 16
US-09-949-016-94799
; Sequence 94799, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 94799
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-94799

Query Match          1.5%; Score 19; DB 4; Length 601;
Best Local Similarity 100.0%; Pred. No. 22;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 155 GTAATTTTATTTTAAAT 173
Db 241 GTAATTTTATTTTAAAT 259
```

```
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 94799
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-94799

Query Match          1.5%; Score 19; DB 4; Length 601;
Best Local Similarity 100.0%; Pred. No. 22;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 155 GTAATTTTATTTTAAAT 173
Db 40 GTAATTTTATTTTAAAT 58

RESULT 17
US-09-949-016-94800
; Sequence 94800, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 94800
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-94800

Query Match          1.5%; Score 19; DB 4; Length 601;
Best Local Similarity 100.0%; Pred. No. 22;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 155 GTAATTTTATTTTAAAT 173
Db 241 GTAATTTTATTTTAAAT 259

RESULT 18
US-09-949-016-164402
; Sequence 164402, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
```


; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 164402
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-164402

Query Match 1.5%; Score 19; DB 4; Length 601;
Best Local Similarity 100.0%; Pred. No. 22;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 972 AGCTGAAATTTTGCTTAC 990
|||
DB 556 AGCTGAAATTTTGCTTAC 574

RESULT 19
US-09-949-016-164403
; Sequence 164403, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 164403
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-164403

Query Match 1.5%; Score 19; DB 4; Length 601;
Best Local Similarity 100.0%; Pred. No. 22;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 972 AGCTGAAATTTTGCTTAC 990
|||
DB 74 AGCTGAAATTTTGCTTAC 92

RESULT 20
US-09-252-991A-10002/c
; Sequence 10002, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190

; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 10002
; LENGTH: 636
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-10002

Query Match 1.5%; Score 19; DB 4; Length 636;
Best Local Similarity 100.0%; Pred. No. 22;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 918 CGATGTCACACGAGTTC 936
|||
DB 368 CGATGTCACACGAGTTC 350

RESULT 21
US-08-277-031B-14
; Sequence 14, Application US/08277031B
; Patent No. 6620593
; GENERAL INFORMATION:
; APPLICANT: Havaashi, Koji
; APPLICANT: Sakaki, Toshiyuki
; APPLICANT: Yabusaki, Yoshiyasu
; APPLICANT: Komai, Koichiro
; APPLICANT: Kaneko, Hideo
; APPLICANT: Nakatsuoka, Iwao
; TITLE OF INVENTION: METHOD FOR SAFETY EVALUATION OF
; TITLE OF INVENTION: CHEMICAL COMPOUND USING RECOMBINANT YEAST EXPRESSING
; NUMBER OF INVENTION: HUMAN CYTOCHROME P450
; NUMBER OF SEQUENCES: 42
; CORRESPONDENCE ADDRESS:
; ADDRESS: Birch, Stewart, Kolasch & Birch
; STREET: P.O. Box 747
; CITY: Falls Church
; STATE: Virginia
; COUNTRY: USA
; ZIP: 22040-0747
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5inch, 1.44MB
; COMPUTER: IBM PC
; OPERATING SYSTEM: Dos 5.0
; SOFTWARE: WordPerfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/277,031B
; FILING DATE: 19-JULY-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP-201120/1993
; APPLICATION NUMBER: JP-180246/1993
; APPLICATION NUMBER: JP-208279/1993
; FILING DATE: 20-07-1993
; FILING DATE: 21-07-1993
; FILING DATE: 30-07-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Raymond C. Stewart
; REGISTRATION NUMBER: 21,066
; REFERENCE/DOCKET NUMBER: 20-3530P
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-205-8000
; TELEFAX: 703-205-8050
; TELEX:
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1473
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
US-08-277-031B-14

Query Match 1.5%; Score 19; DB 4; Length 1473;
Best Local Similarity 100.0%; Pred. No. 23;

```

; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 855-0555
; TELEFAX: (650) 845-4166
; INFORMATION FOR SEQ ID NO: 1055:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1995 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GENBANK
; CLONE: g181299
;
; US-09-023-655-1055
;
; Query Match 1.5%; Score 19; DB 4; Length 1995;
; Best Local Similarity 100.0%; Pred. No. 23;
; Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
;
; QY 972 AGCTGAAAAATTTGCTTAC 990
; | | | | | | | | | | | | | | | |
; Db 898 AGCTGAAAAATTTGCTTAC 916
;
; RESULT 24
; US-09-949-016-4610
; Sequence 4610, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH THE INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4610
; LENGTH: 1995
; TYPE: DNA
; ORGANISM: Human
;
; US-09-949-016-4610
;
; Query Match 1.5%; Score 19; DB 4; Length 1995;
; Best Local Similarity 100.0%; Pred. No. 23;
; Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
;
; QY 972 AGCTGAAAAATTTGCTTAC 990
; | | | | | | | | | | | | | | | |
; Db 898 AGCTGAAAAATTTGCTTAC 916
;
; RESULT 25
; US-08-201-118-6
; Sequence 6, Application US/08201118
; Patent No. 5786191
; GENERAL INFORMATION:
; APPLICANT: GOLDSTEIN, Joyce A.
; TITLE OF INVENTION: CLONING AND EXPRESSION OF COMPLEMENTARY
; DNA FOR MULTIPLE MEMBERS OF THE HUMAN CYTOCHROME P450 2C
; TITLE OF INVENTION: DNAS FOR MULTIPLE MEMBERS OF THE HUMAN CYTOCHROME P450 2C
; TITLE OF INVENTION: SUBFAMILY
; NUMBER OF SEQUENCES: 44
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Khourie and Crew
; STREET: 379 Lytton Avenue
; CITY: Palo Alto
; STATE: California
;

```

; COUNTRY: US
; ZIP: 94301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/201,118
; FILING DATE: 22-FEB-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/864,962
; FILING DATE: 09-APR-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Liebeschuetz, Joe
; REGISTRATION NUMBER: 37,505
; REFERENCE/DOCKET NUMBER: 15280-192-1
; TELEPHONE: (415) 326-2400
; TELEFAX: (415) 326-2422
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2009 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
US-08-201-118-6

Query Match 1.5%; Score 19; DB 1; Length 2009;
Best Local Similarity 100.0%; Pred. No. 23;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 972 AGCTGAAATTTTGCTTAC 990
|||||
DB 898 AGCTGAAATTTTGCTTAC 916
|||||

RESULT 26
US-08-238-821B-6
; Sequence 6, Application US/08238821B
; Patent No. 5912120
; GENERAL INFORMATION:
; APPLICANT: GOLDSTEIN, Joyce A.
; APPLICANT: ROMKES-SPARKS, Marjorie
; APPLICANT: DE MORAIS, Sonia M.F.
; TITLE OF INVENTION: CLONING, EXPRESSION AND DIAGNOSIS OF HUMAN
; TITLE OF INVENTION: CYTOCHROME P450 2C19: THE PRINCIPAL DETERMINANT OF S-
; TITLE OF INVENTION: MEPHENYTOIN METABOLISM
; NUMBER OF SEQUENCES: 61
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: US
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/238,821B
; FILING DATE: 06-MAY-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/201,118
; FILING DATE: 22-FEB-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/864,962

; FILING DATE: 09-APR-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Liebeschuetz, Joe
; REGISTRATION NUMBER: 37,505
; REFERENCE/DOCKET NUMBER: 15280-192110US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 326-2400
; TELEFAX: (650) 326-2422
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2009 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: Region
; LOCATION: 1..199
; OTHER INFORMATION: /note= "Corresponds to positions -199to -
; OTHER INFORMATION: 1 for 29c of Figure 2."
US-08-238-821B-6

Query Match 1.5%; Score 19; DB 2; Length 2009;
Best Local Similarity 100.0%; Pred. No. 23;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 972 AGCTGAAATTTTGCTTAC 990
|||||
DB 898 AGCTGAAATTTTGCTTAC 916
|||||

RESULT 27
PCT-US95-05744-6
; Sequence 6, Application PC/TUS9505744
; GENERAL INFORMATION:
; APPLICANT: GOLDSTEIN, Joyce A.
; APPLICANT: ROMKES-SPARKS, Marjorie
; APPLICANT: DE MORAIS, Sonia M.F.
; TITLE OF INVENTION: CLONING, EXPRESSION AND DIAGNOSIS OF HUMAN
; TITLE OF INVENTION: CYTOCHROME P450 2C19: THE PRINCIPAL DETERMINANT
; TITLE OF INVENTION: OF S-MEPHENYTOIN METABOLISM
; NUMBER OF SEQUENCES: 61
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Khourie and Crew
; STREET: 379 Lytton Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: US
; ZIP: 94301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/05744
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/238,821
; FILING DATE: 06-MAY-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/201,118
; FILING DATE: 22-FEB-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/864,962
; FILING DATE: 09-APR-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Dow, Karen B.
; REGISTRATION NUMBER: 29,684
; REFERENCE/DOCKET NUMBER: 15280-192-1-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 326-2400

```
; TELEFAX: (415) 326-2422
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2009 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
PCT-US95-05744-6

Query Match 1.5%; Score 19; DB 5; Length 2009;
Best Local Similarity 100.0%; Pred. No. 23;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 972 AGCTGAAAATTTTGCTTAC 990
Db 898 AGCTGAAAATTTTGCTTAC 916

RESULT 28
US-08-201-118-12
; Sequence 12, Application US/08201118
; Patent No. 5786191
; GENERAL INFORMATION:
; APPLICANT: GOLDSTEIN, Joyce A.
; APPLICANT: ROMKES-SPARKS, Marjorie
; TITLE OF INVENTION: CLONING AND EXPRESSION OF COMPLEMENTARY
; TITLE OF INVENTION: DNAS FOR MULTIPLE MEMBERS OF THE HUMAN CYTOCHROME P450 2C
; NUMBER OF SEQUENCES: 44
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Khourie and Crew
; STREET: 379 Lytton Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: US
; ZIP: 94301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/201,118
; FILING DATE: 22-FEB-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/864,962
; FILING DATE: 09-APR-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Liebeschuetz, Joe
; REGISTRATION NUMBER: 37,505
; REFERENCE/DOCKET NUMBER: 15280-192-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 326-2400
; TELEFAX: (415) 326-2422
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2258 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
US-08-201-118-12

Query Match 1.5%; Score 19; DB 1; Length 2258;
Best Local Similarity 100.0%; Pred. No. 23;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 972 AGCTGAAAATTTTGCTTAC 990
Db 741 AGCTGAAAATTTTGCTTAC 759

US-08-201-118-12

Query Match 1.5%; Score 19; DB 1; Length 2258;
Best Local Similarity 100.0%; Pred. No. 23;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 972 AGCTGAAAATTTTGCTTAC 990
Db 741 AGCTGAAAATTTTGCTTAC 759
```

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RESULT 29
US-08-238-821B-12
; Sequence 12, Application US/08238821B
; Patent No. 5912120
; GENERAL INFORMATION:
; APPLICANT: GOLDSTEIN, Joyce A.
; APPLICANT: ROMKES-SPARKS, Marjorie
; APPLICANT: DE MORAIS, Sonia M.F.
; TITLE OF INVENTION: CLONING, EXPRESSION AND DIAGNOSIS OF HUMAN
; TITLE OF INVENTION: CYTOCHROME P450 2C19: THE PRINCIPAL DETERMINANT OF S-
; NUMBER OF SEQUENCES: 61
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: US
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/238,821B
; FILING DATE: 06-MAY-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/201,118
; FILING DATE: 22-FEB-1994
; CLASSIFICATION: 435
; APPLICATION NUMBER: US 07/864,962
; FILING DATE: 09-APR-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Liebeschuetz, Joe
; REGISTRATION NUMBER: 37,505
; REFERENCE/DOCKET NUMBER: 15280-192110US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 326-2400
; TELEFAX: (650) 326-2422
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2258 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: Region
; LOCATION: 1..18
; OTHER INFORMATION: /note= "Corresponds to positions -18 to-1
; OTHER INFORMATION: for 6b of Figure 2."
US-08-238-821B-12

Query Match 1.5%; Score 19; DB 2; Length 2258;
Best Local Similarity 100.0%; Pred. No. 23;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 972 AGCTGAAAATTTTGCTTAC 990
Db 741 AGCTGAAAATTTTGCTTAC 759

RESULT 30
US-09-023-655-995
; Sequence 995, Application US/09023655
; Patent No. 6607879
; GENERAL INFORMATION:
; APPLICANT: Cocks, Benjamin G.
; APPLICANT: Susan G. Stuart
```

```
; APPLICANT: Jeffrey J. Seilhamer
; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL GENE
; TITLE OF INVENTION: EXPRESSION
; NUMBER OF SEQUENCES: 1508
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
; STREET: 3174 PORTER DRIVE
; CITY: PALO ALTO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
; CURRENT APPLICATION DATA:
; FILING DATE: HEREWITH
; APPLICATION NUMBER: US/09/023,655
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; FILING DATE:
; APPLICATION NUMBER:
; ATTORNEY/AGENT INFORMATION:
; NAME: Zeller, Karen J.
; REGISTRATION NUMBER: 37,071
; REFERENCE/DOCKET NUMBER: PA-0001 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 855-0555
; TELEFAX: (650) 845-4166
; INFORMATION FOR SEQ ID NO: 995:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2258 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GENBANK
; CLONE: g171181
;
US-09-023-655-995

Query Match 1.5%; Score 19; DB 4; Length 2258;
Best Local Similarity 100.0%; Pred. No. 23;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 972 AGCTGAAATTTTGCTTAC 990
Db 741 AGCTGAAATTTTGCTTAC 759

RESULT 31
PCT-US95-05744-12
; Sequence 12, Application PC/TUS9505744
; GENERAL INFORMATION:
; APPLICANT: GOLDSTEIN, Joyce A.
; APPLICANT: ROMKES-SPARKS, Marjorie
; APPLICANT: DE MORAIS, Sonia M.F.
; TITLE OF INVENTION: CLONING, EXPRESSION AND DIAGNOSIS OF HUMAN
; TITLE OF INVENTION: CYTOCHROME P450 2C19: THE PRINCIPAL DETERMINANT
; NUMBER OF SEQUENCES: 61
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Khourie and Crew
; STREET: 379 Lytton Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: US
; ZIP: 94301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
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; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/05744
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA: US 08/238,821
; FILING DATE: 06-MAY-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/201,118
; FILING DATE: 22-FEB-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/864,962
; FILING DATE: 09-APR-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Dow, Karen B.
; REGISTRATION NUMBER: 29,684
; REFERENCE/DOCKET NUMBER: 15280-192-1-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 326-2400
; TELEFAX: (415) 326-2422
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2258 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
;
PCT-US95-05744-12

Query Match 1.5%; Score 19; DB 5; Length 2258;
Best Local Similarity 100.0%; Pred. No. 23;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 972 AGCTGAAATTTTGCTTAC 990
Db 741 AGCTGAAATTTTGCTTAC 759

RESULT 32
US-09-539-333D-220
; Sequence 220, Application US/09539333D
; Patent No. 6476208
; GENERAL INFORMATION:
; APPLICANT: Cohen, Daniel
; APPLICANT: Blumenfeld, Marta
; APPLICANT: Chumakov, Ilya
; APPLICANT: Bougueret, Lydie
; APPLICANT: Bihain, Bernard
; APPLICANT: Essioux, Laurent
; TITLE OF INVENTION: SCHIZOPHRENIA ASSOCIATED GENES, PROTEINS AND BIALLELIC MARKERS
; FILE REFERENCE: GENSET.047AUS
; CURRENT APPLICATION NUMBER: US/09/539,333D
; CURRENT FILING DATE: 2000-03-30
; PRIOR APPLICATION NUMBER: US 60/126,903
; PRIOR FILING DATE: 1999-03-30
; PRIOR APPLICATION NUMBER: US 60/131,971
; PRIOR FILING DATE: 1999-04-30
; PRIOR APPLICATION NUMBER: US 60/132,065
; PRIOR FILING DATE: 1999-04-30
; PRIOR APPLICATION NUMBER: US 60/143,928
; PRIOR FILING DATE: 1999-07-14
; PRIOR APPLICATION NUMBER: US 60/145,915
; PRIOR FILING DATE: 1999-07-27
; PRIOR APPLICATION NUMBER: US 60/146,453
; PRIOR FILING DATE: 1999-07-29
; PRIOR APPLICATION NUMBER: US 60/146,452
; PRIOR FILING DATE: 1999-07-29
; PRIOR APPLICATION NUMBER: US 60/162,288
; PRIOR FILING DATE: 1999-10-28
; PRIOR APPLICATION NUMBER: US 09/416,384
; PRIOR FILING DATE: 1999-10-12
; NUMBER OF SEQ ID NOS: 231
```

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; SOFTWARE: Patent.pm
; SEQ ID NO 220
; LENGTH: 3001
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: allele
; LOCATION: 1501
; OTHER INFORMATION: 99-27335-191 : polymorphic base A or C
; FEATURE:
; NAME/KEY: misc.binding
; LOCATION: 1481..1500
; OTHER INFORMATION: 99-27335-191.misl,
; FEATURE:
; NAME/KEY: misc.binding
; LOCATION: 1502..1521
; OTHER INFORMATION: 99-27335-191.mis2, complement
; FEATURE:
; NAME/KEY: primer.bnd
; LOCATION: 1322..1342
; OTHER INFORMATION: upstream amplification primer
; FEATURE:
; NAME/KEY: primer.bnd
; LOCATION: 1768..1788
; OTHER INFORMATION: downstream amplification primer, complement
; FEATURE:
; NAME/KEY: misc.binding
; LOCATION: 1489..1513
; OTHER INFORMATION: 99-27335-191 probe
; US-09-333D-220

Query Match 1.5%; Score 19; DB 4; Length 3001;
Best Local Similarity 100.0%; Pred. No. 23;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 156 TAATTTTATTTTAAATA 174
Db 765 TAATTTTATTTTAAATA 783

RESULT 33
US-09-252-991A-10037
; Sequence 10037, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; PRIOR FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 10037
; LENGTH: 4515
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
; US-09-252-991A-10037

Query Match 1.5%; Score 19; DB 4; Length 4515;
Best Local Similarity 100.0%; Pred. No. 24;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 918 CGATGTCACCAAGTTC 936
Db 240 CGATGTCACCAAGTTC 258

RESULT 34
US-09-949-016-11829/c
; Sequence 11829, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11829
; LENGTH: 44248
; TYPE: DNA
; ORGANISM: Human
; US-09-949-016-11829

Query Match 1.5%; Score 19; DB 4; Length 44248;
Best Local Similarity 100.0%; Pred. No. 26;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 155 GTAATTTTATTTTAAAT 173
Db 9413 GTAATTTTATTTTAAAT 9395

RESULT 35
US-09-949-016-14485/c
; Sequence 14485, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14485
; LENGTH: 44249
; TYPE: DNA
; ORGANISM: Human
; US-09-949-016-14485

Query Match 1.5%; Score 19; DB 4; Length 44249;
Best Local Similarity 100.0%; Pred. No. 26;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 155 GTAATTTTATTTTAAAT 173
Db 9413 GTAATTTTATTTTAAAT 9395

RESULT 36
US-09-949-016-14491/c
; Sequence 14491, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
```

```
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1491
; LENGTH: 44249
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-14491

Query Match          1.5%; Score 19; DB 4; Length 44249;
Best Local Similarity 100.0%; Pred. No. 26;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 155 GTAATTTTATTTTAAAT 173
   |||||||
Db 9413 GTAATTTTATTTTAAAT 9395

RESULT 37
US-09-949-016-16352
; Sequence 16352, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 16352
; LENGTH: 56147
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-16352

Query Match          1.5%; Score 19; DB 4; Length 56147;
Best Local Similarity 100.0%; Pred. No. 26;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 972 AGCTGAAAATTTTGCTTAC 990
   |||||||
Db 25216 AGCTGAAAATTTTGCTTAC 25234

RESULT 38
US-09-557-884-1/c
; Sequence 1, Application US/09557884
; Patent No. 6506581
; GENERAL INFORMATION:
; APPLICANT: Fleischmann et al.
; TITLE OF INVENTION: The Nucleotide sequence of
; the Haemophilus influenzae Rd Genome, Fragments
; Thereof, and Uses Thereof
; NUMBER OF SEQUENCES: 1
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Human Genome Sciences, Inc.
US-09-557-884-1
```

```
; STREET: 9410 Key West Avenue
; CITY: Rockville
; STATE: MD
; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3 1/2 inch diskette
; COMPUTER: Dell Pentium
; OPERATING SYSTEM: MS DOS v6.22
; SOFTWARE: ASCII Text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/557,884
; FILING DATE: 25-Apr-2000
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/476,102
; FILING DATE: JUN-5-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Michelle S. Marks
; REGISTRATION NUMBER: 41,971
; REFERENCE/DOCKET NUMBER: PB186P3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 301-309-8504
; TELEFAX: 301-309-8439
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1830121 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-557-884-1

Query Match          1.5%; Score 19; DB 4; Length 1830121;
Best Local Similarity 100.0%; Pred. No. 29;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 586 AAAGTGGCTAATTCAGTAC 604
   |||||||
Db 1402767 AAAGTGGCTAATTCAGTAC 1402749

RESULT 39
US-09-643-990A-1/c
; Sequence 1, Application US/09643990A
; Patent No. 6528289
; GENERAL INFORMATION:
; APPLICANT: Robert D. Fleischmann
; Mark D. Adams
; Owen White
; Hamilton O. Smith
; J. Craig Venter
; TITLE OF INVENTION: The Nucleotide sequence of
; the Haemophilus influenzae Rd Genome, Fragments
; Thereof, and Uses Thereof
; NUMBER OF SEQUENCES: 1
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville,
; STATE: MD
; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3 1/2 inch diskette
; COMPUTER: Dell Pentium
; OPERATING SYSTEM: MS DOS v6.22
; SOFTWARE: ASCII Text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/643,990A
; FILING DATE: 23-Aug-2000
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
```

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; APPLICATION NUMBER: 08/487,429
; FILING DATE: 1995-06-07
; APPLICATION NUMBER: 08/426,787
; FILING DATE: 1995-04-21
; ATTORNEY/AGENT INFORMATION:
;   NAME: Kenley K. Hoover
;   REGISTRATION NUMBER: 40,302
;   REFERENCE/DOCKET NUMBER: PB186PIC1
; TELECOMMUNICATION INFORMATION:
;   TELEPHONE: 301-610-5790
;   TELEFAX: 310-309-8439
; INFORMATION FOR SEQ ID NO: 1:
;   SEQUENCE CHARACTERISTICS:
;     LENGTH: 1830121 base pairs
;     TYPE: nucleic acid
;     STRANDEDNESS: double
;     TOPOLOGY: linear
;   SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-643-990A-1

Query Match      1.5%; Score 19; DB 4; Length 1830121;
Best Local Similarity 100.0%; Pred. No. 29;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      586 AAAGTGCTAAATTCAGTAC 604
DB      1402767 AAAGTGCTAAATTCAGTAC 1402749

RESULT 40
US-09-248-796A-7164/c
; Sequence 7164, Application US/09248796A
; Patent No. 6747137
; GENERAL INFORMATION:
; APPLICANT: Keith Weinstock et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
; FILE REFERENCE: 107196.132
; CURRENT APPLICATION NUMBER: US/09/248,796A
; CURRENT FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: US 60/074,725
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/096,409
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 28208
; SEQ ID NO 7164
; LENGTH: 303
; TYPE: DNA
; ORGANISM: Candida albicans
US-09-248-796A-7164

Query Match      1.4%; Score 18; DB 4; Length 303;
Best Local Similarity 100.0%; Pred. No. 70;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      30 ATTTAGCATTATTATT 47
DB      47 ATTTAGCATTATTATT 30

RESULT 41
US-09-248-796A-852
; Sequence 852, Application US/09248796A
; Patent No. 6747137
; GENERAL INFORMATION:
; APPLICANT: Keith Weinstock et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
; FILE REFERENCE: 107196.132
; CURRENT APPLICATION NUMBER: US/09/248,796A
; CURRENT FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: US 60/074,725
; PRIOR FILING DATE: 1998-02-13
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; PRIOR APPLICATION NUMBER: US 60/096,409
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 28208
; SEQ ID NO 852
; LENGTH: 414
; TYPE: DNA
; ORGANISM: Candida albicans
US-09-248-796A-852

Query Match      1.4%; Score 18; DB 4; Length 414;
Best Local Similarity 100.0%; Pred. No. 71;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      167 TTTTAATATCTTTTTTAA 184
DB      389 TTTTAATATCTTTTTTAA 406

RESULT 42
US-09-621-976-14723
; Sequence 14723, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Jobert, S.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
; FILE REFERENCE: GENSET.054PR2
; CURRENT APPLICATION NUMBER: US/09/621,976
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.pm
; SEQ ID NO 14723
; LENGTH: 420
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-621-976-14723

Query Match      1.4%; Score 18; DB 4; Length 420;
Best Local Similarity 100.0%; Pred. No. 71;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      156 TAAATTTATTTTAAAT 173
DB      55 TAAATTTATTTTAAAT 72

RESULT 43
US-09-513-999C-31455
; Sequence 31455, Application US/09513999C
; Patent No. 6783961
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Duclert, A.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; Patent No. 6783961
; FILE REFERENCE: 59.US2.REG
; CURRENT APPLICATION NUMBER: US/09/513,999C
; CURRENT FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/122,487
; PRIOR FILING DATE: 1999-02-26
; NUMBER OF SEQ ID NOS: 36681
; SOFTWARE: Patent.pm
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; ORGANISM: Homo sapiens
; FEATURE:
;   NAME/KEY: misc.feature
;   LOCATION: 119
;   OTHER INFORMATION: r=a or g
;   FEATURE:
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FEATURE: CDS
NAME/KEY: 1.498
LOCATION: 1.498
OTHER INFORMATION: /product= "soluble human kit ligand"
OTHER INFORMATION: (amino acids 1-165)"
PCT-US95-03866-1

Query Match 1.4%; Score 18; DB 5; Length 495;
Best Local Similarity 100.0%; Pred. No. 71;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 411 ATCCAAATGACTTGGC 428
Db 134 ATCCAAATGACTTGGC 117

RESULT 47
PCT-US95-03866-17/c
Sequence 17, Application PC/TUS9503866
GENERAL INFORMATION:
APPLICANT: CytoMed, Inc. (all states except US)
APPLICANT: Nocka, Karl (US only)
APPLICANT: Lobell, Robert B (US only)
TITLE OF INVENTION: STABILIZED DIMER OF KIT LIGAND AND
TITLE OF INVENTION: FLT-3/FLK-2 LIGAND
NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Neave
STREET: 1251 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: United States of America
ZIP: 10020
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/03866
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/220,379
FILING DATE: 28-MAR-1994
ATTORNEY/AGENT INFORMATION:
NAME: Haley Jr, James F
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: CytoMed/2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-596-9000
TELEFAX: 212-596-9090
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 498 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
FEATURE:
NAME/KEY: CDS
LOCATION: 1.498
FEATURE:
NAME/KEY: mat_peptide
LOCATION: 4.498
OTHER INFORMATION: /product= "human KL w/Tyr->Cys"
OTHER INFORMATION: substitution at aa 26"
PCT-US95-03866-17

Query Match 1.4%; Score 18; DB 5; Length 498;
Best Local Similarity 100.0%; Pred. No. 71;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 411 ATCCAAATGACTTGGC 428
Db 137 ATCCAAATGACTTGGC 120

RESULT 48
PCT-US95-03866-35/c
Sequence 35, Application PC/TUS9503866
GENERAL INFORMATION:
APPLICANT: CytoMed, Inc. (all states except US)
APPLICANT: Nocka, Karl (US only)
APPLICANT: Lobell, Robert B (US only)
TITLE OF INVENTION: STABILIZED DIMER OF KIT LIGAND AND
TITLE OF INVENTION: FLT-3/FLK-2 LIGAND
NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Neave
STREET: 1251 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: United States of America
ZIP: 10020
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/03866
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/220,379
FILING DATE: 28-MAR-1994
ATTORNEY/AGENT INFORMATION:
NAME: Haley Jr, James F
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: CytoMed/2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-596-9000
TELEFAX: 212-596-9090
INFORMATION FOR SEQ ID NO: 35:
SEQUENCE CHARACTERISTICS:
LENGTH: 498 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
FEATURE:
NAME/KEY: CDS
LOCATION: 1.498
FEATURE:
NAME/KEY: mat_peptide
LOCATION: 4.498
OTHER INFORMATION: /product= "human KL with Cys->Ser"
OTHER INFORMATION: substitution at aa 138"
PCT-US95-03866-35

Query Match 1.4%; Score 18; DB 5; Length 498;
Best Local Similarity 100.0%; Pred. No. 71;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 411 ATCCAAATGACTTGGC 428
Db 137 ATCCAAATGACTTGGC 120

RESULT 49
PCT-US95-03866-19/c

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; Sequence 19, Application PC/TUS9503866
; GENERAL INFORMATION:
; APPLICANT: CytoMed, Inc. (all states except US)
; APPLICANT: Nocka, Karl (US only)
; APPLICANT: Lobell, Robert B (US only)
; TITLE OF INVENTION: STABILIZED DIMER OF KIT LIGAND AND
; TITLE OF INVENTION: FLT-3/FLK-2 LIGAND
; NUMBER OF SEQUENCES: 36
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Neave
; STREET: 1251 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: United States of America
; ZIP: 10020
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/03866
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/220,379
; FILING DATE: 28-MAR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Haley Jr, James F
; REGISTRATION NUMBER: 27,794
; REFERENCE/DOCKET NUMBER: Cytomed/2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-596-9000
; TELEFAX: 212-596-9090
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 501 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..501
; FEATURE:
; NAME/KEY: mat_peptide
; LOCATION: 4..501
; OTHER INFORMATION: /product= "human KL w/extra Cys
; OTHER INFORMATION: inserted at aa 27"
PCT-US95-03866-19

Query Match 1.4%; Score 18; DB 5; Length 501;
Best Local Similarity 100.0%; Pred.No.71;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 411 ATCCAAACATGACTTGGC 428
DB 140 ATCCAAACATGACTTGGC 123

RESULT 50
US-08-955-848A-58/c
; Sequence 58, Application US/08955848A
; Patent No. 5969105
; GENERAL INFORMATION:
; APPLICANT: Mc Wherter, Charles
; APPLICANT: Feng, Yiding
; TITLE OF INVENTION: No. 5969105el Stem Cell Factor Receptor
; TITLE OF INVENTION: Agonists
; NUMBER OF SEQUENCES: 86
; CORRESPONDENCE ADDRESS:
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; ADDRESSEE: G. D. Seartle & Co.
; STREET: P.O. Box 5110
; CITY: Chicago
; STATE: IL
; COUNTRY: U. S. A.
; ZIP: 60680
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/955,848A
; FILING DATE: 21-OCT-1997
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/029,165
; FILING DATE: 25-OCT-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Bennett, Dennis A
; REGISTRATION NUMBER: 34,547
; REFERENCE/DOCKET NUMBER: C-2992/1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 314-737-6986
; TELEFAX: 314-737-6972
; TELEX:
; INFORMATION FOR SEQ ID NO: 58:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 506 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-955-848A-58

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Best Local Similarity 100.0%; Pred.No.71;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 411 ATCCAAACATGACTTGGC 428
DB 448 ATCCAAACATGACTTGGC 431

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Title: US-10-679-246-1

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6	1223	96.0	2829	17 US-10-108-260A-269	Sequence 269, App
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8	356	27.9	1535	9 US-09-925-297-84	Sequence 84, Appli
9	159	12.5	405	18 US-10-357-930-38440	Sequence 38440, A
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c 96	19	1.5	7728	15	US-10-311-455-50	Sequence 50, Appl	c 169	18	1.4	678	13	US-10-027-632-283359	Sequence 283359, A
c 97	19	1.5	9983	17	US-10-257-166-154	Sequence 154, App	c 170	18	1.4	678	17	US-10-027-632-283359	Sequence 283359, A
c 98	19	1.5	13249	15	US-10-311-455-89	Sequence 89, Appl	c 171	18	1.4	690	17	US-10-242-535A-14419	Sequence 14419, A
c 99	19	1.5	17211	15	US-10-311-455-627	Sequence 627, App	c 172	18	1.4	690	17	US-10-085-783A-14419	Sequence 14419, A
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c 113	19	1.5	71517	17	US-10-027-632-53712	Sequence 53712, A	c 186	18	1.4	822	18	US-10-384-339C-134	Sequence 134, App
c 114	19	1.5	1830121	17	US-10-329-670-1	Sequence 1, Appli	c 187	18	1.4	828	18	US-10-363-345A-5931	Sequence 5931, Ap
c 115	19	1.5	1830121	18	US-10-158-865-1	Sequence 1, Appli	c 188	18	1.4	828	18	US-10-363-345A-5931	Sequence 5931, Ap
c 116	19	1.5	3011208	17	US-10-398-221-2058	Sequence 2058, Ap	c 189	18	1.4	828	19	US-10-363-483A-5932	Sequence 5932, Ap
c 117	19	1.5	3673778	16	US-10-312-841-1	Sequence 1, Appli	c 190	18	1.4	863	14	US-10-198-846-3308	Sequence 3308, Ap
c 118	19	1.4	25	19	US-10-719-900-453080	Sequence 453080, A	c 191	18	1.4	879	17	US-10-424-599-87973	Sequence 87973, A
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c 121	18	1.4	179	17	US-09-237-183A-2287	Sequence 2287, Ap	c 194	18	1.4	935	14	US-10-198-846-11734	Sequence 11734, A
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c 123	18	1.4	244	17	US-10-424-599-58139	Sequence 58139, A	c 196	18	1.4	945	18	US-10-363-345A-7008	Sequence 7008, Ap
c 124	18	1.4	253	10	US-09-237-183A-2513	Sequence 2513, Ap	c 197	18	1.4	945	19	US-10-363-483A-7007	Sequence 7007, Ap
c 125	18	1.4	270	10	US-09-237-183A-2478	Sequence 2478, Ap	c 198	18	1.4	945	19	US-10-363-483A-7008	Sequence 7008, Ap
c 126	18	1.4	306	18	US-10-425-115-134898	Sequence 134898, A	c 199	18	1.4	948	18	US-10-363-483A-7008	Sequence 7008, Ap
c 127	18	1.4	326	17	US-10-424-599-139819	Sequence 139819, A	c 200	18	1.4	951	15	US-10-128-714-1525	Sequence 1525, Ap
c 128	18	1.4	342	18	US-10-357-930-7849	Sequence 7849, Ap	c 201	18	1.4	968	13	US-10-027-632-31270	Sequence 31270, A
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232	18	1.4	1263	17	US-10-027-632-177458	Sequence 177458,	305	18	1.4	7625	15	US-10-311-455-1403	Sequence 1403, Ap
233	18	1.4	1321	18	US-10-688-843-86	Sequence 86, Appl	306	18	1.4	7703	9	US-09-764-887-415	Sequence 415, App
234	18	1.4	1404	9	US-09-005-243-60	Sequence 60, Appl	307	18	1.4	7703	9	US-09-764-887-456	Sequence 456, App
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237	18	1.4	1404	18	US-10-620-642-60	Sequence 60, Appl	310	18	1.4	7781	15	US-10-311-455-1141	Sequence 1141, Ap
238	18	1.4	1405	17	US-10-305-720-1316	Sequence 1316, Ap	311	18	1.4	7857	18	US-10-433-793-105	Sequence 105, App
239	18	1.4	1501	17	US-10-424-599-135896	Sequence 135896,	312	18	1.4	8794	10	US-09-764-891-8933	Sequence 8933, Ap
240	18	1.4	1575	18	US-10-793-639-216	Sequence 216, App	313	18	1.4	8962	15	US-10-311-455-659	Sequence 659, App
241	18	1.4	1735	9	US-09-805-020-1	Sequence 1, Appli	314	18	1.4	9741	15	US-10-311-455-1296	Sequence 1296, Ap
242	18	1.4	1822	13	US-10-027-632-97295	Sequence 97295, A	315	18	1.4	10855	15	US-10-311-455-1461	Sequence 1461, Ap
243	18	1.4	1822	17	US-10-027-632-97295	Sequence 97295, A	316	18	1.4	10886	15	US-10-311-455-2107	Sequence 2107, Ap
244	18	1.4	2133	13	US-10-027-632-263650	Sequence 263650,	317	18	1.4	11155	15	US-09-984-827-5	Sequence 5, Appli
245	18	1.4	2133	13	US-10-027-632-263651	Sequence 263651,	318	18	1.4	11754	10	US-09-984-827-5	Sequence 5, Appli
246	18	1.4	2133	13	US-10-027-632-263652	Sequence 263652,	319	18	1.4	14987	15	US-10-311-455-603	Sequence 603, App
247	18	1.4	2133	13	US-10-027-632-263653	Sequence 263653,	320	18	1.4	15387	15	US-10-311-455-158	Sequence 158, App
248	18	1.4	2133	17	US-10-027-632-263650	Sequence 263650,	321	18	1.4	15789	14	US-10-103-313-600	Sequence 600, App
249	18	1.4	2133	17	US-10-027-632-263651	Sequence 263651,	322	18	1.4	17213	15	US-10-311-455-1455	Sequence 1455, Ap
250	18	1.4	2133	17	US-10-027-632-263652	Sequence 263652,	323	18	1.4	17213	15	US-10-311-455-1456	Sequence 1456, Ap
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252	18	1.4	2173	17	US-10-424-599-122311	Sequence 122311,	325	18	1.4	17959	16	US-10-240-452-42	Sequence 42, Appl
253	18	1.4	2210	17	US-10-425-114-9776	Sequence 9776, Ap	326	18	1.4	18283	17	US-10-221-613-326	Sequence 326, App
254	18	1.4	2222	17	US-10-425-114-8413	Sequence 8413, Ap	327	18	1.4	30781	14	US-10-092-908-37	Sequence 37, Appl
255	18	1.4	2489	17	US-10-424-599-72698	Sequence 72698, A	328	18	1.4	31842	11	US-09-997-722-232	Sequence 232, App
256	18	1.4	2616	17	US-10-282-122A-18056	Sequence 18056, A	329	18	1.4	35962	18	US-10-473-126-98	Sequence 98, Appl
257	18	1.4	2750	17	US-10-424-599-49499	Sequence 49499, A	330	18	1.4	35962	18	US-10-473-126-98	Sequence 244, App
258	18	1.4	2772	17	US-10-425-114-6460	Sequence 6460, Ap	331	18	1.4	40862	15	US-10-311-455-2045	Sequence 2045, Ap
259	18	1.4	2951	15	US-10-128-714-5295	Sequence 525, App	332	18	1.4	41454	13	US-10-087-192-1642	Sequence 1642, Ap
260	18	1.4	2979	15	US-10-128-714-331	Sequence 331, App	333	18	1.4	41454	13	US-10-087-192-1642	Sequence 721, App
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262	18	1.4	2996	15	US-10-128-714-5331	Sequence 5331, Ap	335	18	1.4	43411	18	US-10-450-826-76	Sequence 76, Appl
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264	18	1.4	3303	9	US-09-833-790-421	Sequence 421, App	337	18	1.4	56153	17	US-10-221-714A-519	Sequence 519, App
265	18	1.4	3304	19	US-10-304-124-4	Sequence 4, Appli	338	18	1.4	60486	18	US-10-719-993-6842	Sequence 6842, Ap
266	18	1.4	3304	19	US-10-768-030-2	Sequence 2, Appli	339	18	1.4	60486	19	US-10-741-600-17713	Sequence 17713, A
267	18	1.4	3310	14	US-10-097-340-362	Sequence 362, App	340	18	1.4	64125	18	US-10-322-281-350	Sequence 350, App
268	18	1.4	3360	17	US-10-424-599-11458	Sequence 11458, A	341	18	1.4	65559	13	US-10-087-192-841	Sequence 841, App
269	18	1.4	3614	17	US-10-240-425-1571	Sequence 1571, Ap	342	18	1.4	82938	10	US-09-818-657-3	Sequence 3, Appli
270	18	1.4	3684	18	US-10-437-963-33451	Sequence 33451, A	343	18	1.4	82952	18	US-10-416-898-7	Sequence 7, Appli
271	18	1.4	3720	18	US-10-437-963-46223	Sequence 46223, A	344	18	1.4	88576	17	US-10-085-117-319	Sequence 319, App
272	18	1.4	3807	9	US-09-005-243-43	Sequence 43, Appl	345	18	1.4	88624	16	US-10-292-081A-1	Sequence 1, Appli
273	18	1.4	3807	9	US-09-224-683-43	Sequence 43, Appl	346	18	1.4	88624	17	US-10-608-397-1	Sequence 1, Appli
274	18	1.4	3807	18	US-10-175-608-43	GENERAL INFORMA	347	18	1.4	90798	18	US-10-318-819A-4	Sequence 4, Appli
275	18	1.4	3807	19	US-10-620-642-43	GENERAL INFORMA	348	18	1.4	122624	13	US-10-087-192-1726	Sequence 1726, Ap
276	18	1.4	4335	17	US-10-282-122A-24793	Sequence 24793, A	349	18	1.4	122923	13	US-10-087-192-268	Sequence 268, App
277	18	1.4	4452	18	US-10-425-115-19940	Sequence 19940, A	350	18	1.4	159138	18	US-10-719-993-6777	Sequence 6777, Ap
278	18	1.4	4647	18	US-10-425-115-19943	Sequence 19943, A	351	18	1.4	159138	19	US-10-741-600-17613	Sequence 17613, A
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280	18	1.4	4699	19	US-10-958-382-2	Sequence 2, Appli	353	18	1.4	183999	18	US-10-745-377-1	Sequence 1, Appli
281	18	1.4	4736	17	US-10-452-510-15	Sequence 15, Appl	354	18	1.4	183999	18	US-10-872-113-1	Sequence 1, Appli
282	18	1.4	4736	17	US-10-617-334-15	Sequence 15, Appl	355	18	1.4	185695	14	US-10-020-141-11	Sequence 11, Appl
283	18	1.4	4736	18	US-10-744-465-15	Sequence 15, Appl	356	18	1.4	185695	14	US-10-017-721-1	Sequence 1, Appli
284	18	1.4	4736	18	US-10-833-679-15	Sequence 15, Appl	357	18	1.4	195071	19	US-10-741-600-17991	Sequence 17991, A
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286	18	1.4	5416	15	US-10-311-455-1769	Sequence 1769, Ap	359	18	1.4	321491	13	US-10-087-192-532	Sequence 532, App
287	18	1.4	5447	17	US-10-221-714A-484	Sequence 484, App	360	18	1.4	518360	18	US-10-367-094-125	Sequence 125, App
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289	18	1.4	5864	9	US-09-005-243-47	Sequence 47, Appl	362	18	1.4	1503841	9	US-09-795-668-1	Sequence 1, Appli
290	18	1.4	5864	9	US-09-224-683-47	Sequence 47, Appl	363	18	1.4	1503841	9	US-09-946-807-1	Sequence 1, Appli
291	18	1.4	5864	18	US-10-175-608-47	GENERAL INFORMA	364	18	1.4	1691139	14	US-10-067-514-1	Sequence 1, Appli
292	18	1.4	5864	19	US-10-620-642-47	GENERAL INFORMA	365	18	1.4	1691139	17	US-10-419-723-1	Sequence 1, Appli
293	18	1.4	5883	15	US-10-311-455-1705	Sequence 1705, Ap	366	18	1.4	1980090	18	US-10-719-993-6815	Sequence 6815, Ap
294	18	1.4	5976	17	US-10-221-714A-24	Sequence 24, Appl	367	18	1.4	1980090	19	US-10-741-600-17676	Sequence 17676, A
295	18	1.4	5976	18	US-10-311-507-94	Sequence 94, Appl	368	18	1.4	3673778	16	US-10-312-461-2	Sequence 2, Appli
296	18	1.4	6049	15	US-10-311-455-202	Sequence 202, App	369	18	1.4	9025608	15	US-10-356-761-1	Sequence 1, Appli
297	18	1.4	6222	15	US-10-311-455-666	Sequence 666, App	370	18	1.3	153	18	US-10-430-201-4202	Sequence 4202, Ap
298	18	1.4	6255	15	US-10-311-455-933	Sequence 933, App	371	17	1.3	153	18	US-10-430-201-4203	Sequence 4203, Ap
299	18	1.4	6351	15	US-10-311-455-933	Sequence 1147, Ap	372	17	1.3	165	9	US-09-960-352-1045	Sequence 1045, Ap
300	18	1.4	6365	15	US-10-311-455-97	Sequence 97, Appl	373	17	1.3	179	9	US-09-878-134-137	Sequence 137, App
301	18	1.4	6487	16	US-10-292-081A-8	Sequence 8, Appli	374	17	1.3	196	18	US-10-674-124A-18155	Sequence 18155, A
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378	17	1.3	201	18	US-10-719-933-13972	Sequence 13972, A	451	17	1.3	429	17	US-10-424-599-22560	Sequence 22560, A
379	17	1.3	201	18	US-10-719-933-22123	Sequence 22123, A	c 452	17	1.3	431	9	US-09-983-965-3592	Sequence 3592, Ap
380	17	1.3	201	18	US-10-719-933-22124	Sequence 22124, A	453	17	1.3	431	13	US-10-027-632-278290	Sequence 278290, Ap
381	17	1.3	201	18	US-10-719-933-36245	Sequence 36245, A	454	17	1.3	431	17	US-10-027-632-278290	Sequence 278290, Ap
382	17	1.3	201	18	US-10-719-933-37062	Sequence 37062, A	455	17	1.3	431	17	US-10-027-632-278290	Sequence 278290, Ap
383	17	1.3	201	18	US-10-719-933-44748	Sequence 44748, A	456	17	1.3	434	9	US-09-735-705-26	Sequence 26, Ap
384	17	1.3	201	18	US-10-719-933-50149	Sequence 50149, A	457	17	1.3	434	9	US-09-850-716A-26	Sequence 26, Ap
385	17	1.3	201	18	US-10-719-933-50150	Sequence 50150, A	458	17	1.3	434	9	US-09-897-778-26	Sequence 26, Ap
386	17	1.3	201	19	US-10-741-600-9430	Sequence 9430, Ap	459	17	1.3	434	14	US-09-466-396A-26	Sequence 26, Ap
387	17	1.3	201	19	US-10-741-600-34549	Sequence 34549, A	460	17	1.3	434	15	US-10-117-982-26	Sequence 26, Ap
388	17	1.3	201	19	US-10-741-600-35052	Sequence 35052, A	461	17	1.3	434	17	US-10-313-986-26	Sequence 26, Ap
389	17	1.3	201	19	US-10-741-600-41956	Sequence 41956, A	462	17	1.3	434	18	US-10-775-972-26	Sequence 26, Ap
390	17	1.3	201	19	US-10-741-600-41957	Sequence 41957, A	463	17	1.3	436	9	US-09-867-701-2032	Sequence 2032, Ap
391	17	1.3	201	19	US-10-741-600-52117	Sequence 52117, A	464	17	1.3	437	9	US-09-735-705-74	Sequence 74, Ap
392	17	1.3	201	19	US-10-741-600-52119	Sequence 52119, A	465	17	1.3	437	9	US-09-850-716A-74	Sequence 74, Ap
393	17	1.3	201	19	US-10-741-600-52122	Sequence 52122, A	466	17	1.3	437	9	US-09-897-778-74	Sequence 74, Ap
394	17	1.3	201	19	US-10-741-600-67297	Sequence 67297, A	467	17	1.3	437	10	US-09-466-396A-74	Sequence 74, Ap
395	17	1.3	201	19	US-10-741-600-67298	Sequence 67298, A	468	17	1.3	437	14	US-10-007-700-74	Sequence 74, Ap
396	17	1.3	206	18	US-10-674-124A-14204	Sequence 14204, A	469	17	1.3	437	15	US-10-117-982-74	Sequence 74, Ap
397	17	1.3	221	9	US-09-983-965-5845	Sequence 5845, Ap	470	17	1.3	437	17	US-10-313-986-74	Sequence 74, Ap
398	17	1.3	222	9	US-09-933-797-671	Sequence 671, Ap	471	17	1.3	437	18	US-10-775-972-74	Sequence 74, Ap
399	17	1.3	232	9	US-09-960-352-4577	Sequence 4577, Ap	c 472	17	1.3	437	18	US-10-357-930-13134	Sequence 13134, A
400	17	1.3	233	17	US-10-242-535A-57047	Sequence 57047, A	c 473	17	1.3	438	13	US-10-040-739-575	Sequence 575, App
401	17	1.3	233	17	US-10-085-783A-57047	Sequence 57047, A	c 474	17	1.3	444	13	US-09-814-353-21978	Sequence 21978, A
402	17	1.3	251	17	US-10-242-535A-9435	Sequence 9435, Ap	c 475	17	1.3	447	13	US-10-027-632-74611	Sequence 74611, A
403	17	1.3	251	17	US-10-085-783A-9435	Sequence 9435, Ap	c 476	17	1.3	447	13	US-10-027-632-299562	Sequence 299562, A
404	17	1.3	255	17	US-10-424-599-9069	Sequence 9069, Ap	c 477	17	1.3	447	17	US-10-027-632-74611	Sequence 74611, A
405	17	1.3	261	10	US-09-237-183A-2497	Sequence 2497, Ap	c 478	17	1.3	447	17	US-10-027-632-299562	Sequence 299562, A
406	17	1.3	267	18	US-10-437-963-155	Sequence 155, App	c 479	17	1.3	451	18	US-10-357-930-48932	Sequence 48932, A
407	17	1.3	279	18	US-10-674-124A-23007	Sequence 23007, A	c 480	17	1.3	464	13	US-10-027-632-66783	Sequence 66783, A
408	17	1.3	302	17	US-10-242-535A-56462	Sequence 56462, A	c 481	17	1.3	464	13	US-10-027-632-67327	Sequence 67327, A
409	17	1.3	302	17	US-10-085-783A-56462	Sequence 56462, A	c 482	17	1.3	464	13	US-10-027-632-66783	Sequence 66783, A
410	17	1.3	308	17	US-10-424-599-100302	Sequence 100302, A	c 483	17	1.3	464	17	US-10-027-632-66783	Sequence 66783, A
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412	17	1.3	311	17	US-10-085-783A-58595	Sequence 58595, A	c 485	17	1.3	464	17	US-10-027-632-311240	Sequence 311240, A
413	17	1.3	318	18	US-10-437-963-50449	Sequence 50449, A	c 486	17	1.3	464	17	US-10-424-599-2314	Sequence 2314, Ap
414	17	1.3	322	18	US-10-425-115-162462	Sequence 162462, A	c 487	17	1.3	465	18	US-10-357-930-34281	Sequence 34281, A
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416	17	1.3	323	17	US-10-085-783A-37619	Sequence 37619, A	c 489	17	1.3	466	9	US-09-864-761-9	Sequence 9, Appli
417	17	1.3	326	9	US-09-960-352-1631	Sequence 1631, Ap	c 490	17	1.3	469	18	US-10-437-963-5372	Sequence 5372, Ap
418	17	1.3	326	18	US-10-425-115-35986	Sequence 35986, A	c 491	17	1.3	470	13	US-10-027-632-35796	Sequence 35796, A
419	17	1.3	331	17	US-10-242-535A-32558	Sequence 32558, A	c 492	17	1.3	470	13	US-10-027-632-35796	Sequence 35796, A
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421	17	1.3	335	18	US-10-425-115-37944	Sequence 37944, A	c 494	17	1.3	478	9	US-09-991-936-940	Sequence 940, App
422	17	1.3	339	17	US-10-424-599-138100	Sequence 138100, Ap	c 495	17	1.3	479	9	US-09-960-352-14432	Sequence 14432, A
423	17	1.3	348	17	US-10-149-736-31	Sequence 31, Appl	c 496	17	1.3	480	10	US-09-918-995-3334	Sequence 3334, Ap
424	17	1.3	348	17	US-10-964-536-31	Sequence 31, Appl	c 497	17	1.3	480	10	US-09-770-961-954	Sequence 954, App
425	17	1.3	356	17	US-10-424-599-48056	Sequence 48056, A	c 498	17	1.3	480	17	US-10-242-535A-29395	Sequence 29395, A
426	17	1.3	357	9	US-09-867-701-7378	Sequence 7378, Ap	c 499	17	1.3	480	17	US-10-085-783A-29395	Sequence 29395, A
427	17	1.3	363	18	US-10-425-115-147959	Sequence 147959, Ap	c 500	17	1.3	482	18	US-10-357-930-3965	Sequence 3965, A
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429	17	1.3	370	17	US-10-425-114-7414	Sequence 7414, Ap	c 502	17	1.3	489	10	US-09-918-995-9361	Sequence 9361, Ap
430	17	1.3	370	17	US-10-425-114-7414	Sequence 7414, Ap	c 503	17	1.3	489	17	US-10-276-774-644	Sequence 644, App
431	17	1.3	373	10	US-09-814-353-18991	Sequence 18991, A	c 504	17	1.3	490	14	US-10-052-283-238	Sequence 238, App
432	17	1.3	376	9	US-09-974-300-8213	Sequence 8213, Ap	c 505	17	1.3	492	14	US-10-062-674-365	Sequence 365, App
433	17	1.3	376	9	US-09-974-300-8225	Sequence 8225, Ap	c 506	17	1.3	494	9	US-09-864-761-4394	Sequence 4394, Ap
434	17	1.3	376	10	US-09-803-713-2074	Sequence 2074, Ap	c 507	17	1.3	494	17	US-10-424-599-18680	Sequence 18680, A
435	17	1.3	378	18	US-10-425-115-67094	Sequence 67094, A	c 508	17	1.3	498	18	US-10-437-963-26272	Sequence 26272, A
436	17	1.3	387	18	US-10-357-930-13230	Sequence 13230, A	c 509	17	1.3	500	14	US-10-052-283-214	Sequence 214, App
437	17	1.3	408	18	US-10-357-930-19126	Sequence 19126, A	c 510	17	1.3	504	13	US-10-040-739-922	Sequence 922, App
438	17	1.3	413	13	US-10-027-632-182883	Sequence 182883, A	c 511	17	1.3	504	13	US-10-027-632-62778	Sequence 62778, A
439	17	1.3	413	10	US-09-918-995-36285	Sequence 36285, A	c 512	17	1.3	504	17	US-10-027-632-62778	Sequence 62778, A
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443	17	1.3	418	17	US-10-027-632-297609	Sequence 297609, A	c 516	17	1.3	514	17	US-10-027-632-6478	Sequence 6478, Ap
444	17	1.3	421	18	US-10-357-930-34376	Sequence 34376, A	c 517	17	1.3	514	17	US-10-027-632-6478	Sequence 6478, Ap
445	17	1.3	423	9	US-09-960-352-11252	Sequence 11252, A	c 518	17	1.3	516	13	US-10-027-632-90993	Sequence 90993, A
446	17	1.3	423	17	US-10-424-599-118097	Sequence 118097, A	c 519	17	1.3	516	13	US-10-027-632-90994	Sequence 90994, A
447	17	1.3	423	17	US-09-918-995-17769	Sequence 17769, A	c 520	17	1.3	516	13	US-10-027-632-317600	Sequence 317600, A
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525	17	1.3	516	17	US-10-027-632-317600	Sequence 317600, A	598	17	1.3	614	17	US-10-424-599-40083	Sequence 40083, A
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529	17	1.3	527	18	US-10-437-963-48094	Sequence 48094, A	c 602	17	1.3	616	13	US-10-027-632-303147	Sequence 303147, A
c 530	17	1.3	531	19	US-10-696-639-2091	Sequence 2091, Ap	603	17	1.3	616	17	US-10-027-632-46116	Sequence 46116, A
531	17	1.3	532	9	US-09-864-761-13120	Sequence 13120, A	604	17	1.3	616	17	US-10-027-632-46117	Sequence 46117, A
532	17	1.3	532	17	US-10-425-114-36308	Sequence 36308, A	605	17	1.3	616	17	US-10-027-632-46118	Sequence 46118, A
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c 535	17	1.3	542	9	US-09-736-457-551	Sequence 551, App	608	17	1.3	624	17	US-10-027-632-224732	Sequence 224732, A
c 536	17	1.3	542	9	US-09-302-941-551	Sequence 551, App	c 609	17	1.3	626	13	US-10-027-632-291655	Sequence 291655, A
c 537	17	1.3	542	9	US-09-849-626-551	Sequence 551, App	c 610	17	1.3	626	13	US-10-027-632-291656	Sequence 291656, A
c 538	17	1.3	542	10	US-09-476-300-551	Sequence 551, App	c 611	17	1.3	626	13	US-10-027-632-291657	Sequence 291657, A
c 539	17	1.3	542	14	US-10-017-754-551	Sequence 551, App	c 612	17	1.3	626	13	US-10-027-632-291658	Sequence 291658, A
c 540	17	1.3	542	16	US-10-113-872-551	Sequence 551, App	c 613	17	1.3	626	17	US-10-027-632-291655	Sequence 291655, A
c 541	17	1.3	542	17	US-10-283-017-551	Sequence 551, App	c 614	17	1.3	626	17	US-10-027-632-291656	Sequence 291656, A
c 542	17	1.3	542	19	US-10-696-632-1831	Sequence 1831, Ap	c 615	17	1.3	626	17	US-10-027-632-291657	Sequence 291657, A
543	17	1.3	549	14	US-10-284-985-25	Sequence 25, Appl	c 616	17	1.3	626	17	US-10-027-632-291658	Sequence 291658, A
c 544	17	1.3	555	18	US-10-021-323-11014	Sequence 11014, A	617	17	1.3	634	18	US-10-357-930-48834	Sequence 48834, A
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546	17	1.3	560	18	US-10-021-323-2253	Sequence 2253, Ap	619	17	1.3	637	17	US-10-027-632-29234	Sequence 29234, A
c 547	17	1.3	569	16	US-10-029-386-6169	Sequence 6169, Ap	c 620	17	1.3	638	13	US-10-027-632-250234	Sequence 250234, A
c 548	17	1.3	572	13	US-10-027-632-322937	Sequence 322937, A	c 621	17	1.3	638	17	US-10-027-632-250234	Sequence 250234, A
c 549	17	1.3	572	13	US-10-027-632-322938	Sequence 322938, A	c 622	17	1.3	640	13	US-10-027-632-268155	Sequence 268155, A
c 550	17	1.3	572	13	US-10-027-632-322939	Sequence 322939, A	c 623	17	1.3	640	13	US-10-027-632-268156	Sequence 268156, A
c 551	17	1.3	572	17	US-10-027-632-322937	Sequence 322937, A	c 624	17	1.3	640	17	US-10-027-632-268155	Sequence 268155, A
c 552	17	1.3	572	17	US-10-027-632-322938	Sequence 322938, A	c 625	17	1.3	640	17	US-10-027-632-268156	Sequence 268156, A
c 553	17	1.3	572	17	US-10-027-632-322939	Sequence 322939, A	626	17	1.3	644	13	US-10-027-632-29872	Sequence 29872, A
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555	17	1.3	575	13	US-10-027-632-27282	Sequence 27282, A	c 628	17	1.3	645	18	US-10-767-701-160	Sequence 160, Appl
556	17	1.3	575	17	US-10-027-632-27281	Sequence 27281, A	c 629	17	1.3	647	14	US-10-284-985-26	Sequence 26, Appl
557	17	1.3	575	17	US-10-027-632-27282	Sequence 27282, A	c 630	17	1.3	654	11	US-09-969-034-4122	Sequence 4122, Ap
c 558	17	1.3	576	18	US-10-425-115-179055	Sequence 179055, A	c 631	17	1.3	655	9	US-09-764-846-31	Sequence 31, Appl
c 559	17	1.3	577	13	US-10-027-632-80724	Sequence 80724, A	632	17	1.3	655	14	US-10-091-483-31	Sequence 31, Appl
c 560	17	1.3	577	17	US-10-027-632-80724	Sequence 80724, A	633	17	1.3	656	13	US-10-027-632-191426	Sequence 191426, A
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563	17	1.3	585	17	US-10-027-632-200231	Sequence 200231, A	c 636	17	1.3	665	18	US-10-363-345A-12354	Sequence 12354, A
564	17	1.3	590	13	US-10-027-632-143044	Sequence 143044, A	c 637	17	1.3	665	19	US-10-363-483A-12353	Sequence 12353, A
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c 567	17	1.3	595	13	US-10-027-632-89765	Sequence 89765, A	c 640	17	1.3	667	17	US-10-027-632-48617	Sequence 48617, A
c 568	17	1.3	595	13	US-10-027-632-89766	Sequence 89766, A	c 641	17	1.3	670	18	US-10-357-930-47996	Sequence 47996, A
c 569	17	1.3	595	13	US-10-027-632-89767	Sequence 89767, A	c 642	17	1.3	699	18	US-10-437-963-22216	Sequence 22216, A
c 570	17	1.3	595	13	US-10-027-632-89768	Sequence 89768, A	c 643	17	1.3	707	18	US-10-425-115-16012	Sequence 16012, A
c 571	17	1.3	595	17	US-10-027-632-89765	Sequence 89765, A	c 644	17	1.3	707	18	US-10-425-115-16012	Sequence 16012, A
c 572	17	1.3	595	17	US-10-027-632-89766	Sequence 89766, A	645	17	1.3	709	17	US-10-388-934-285	Sequence 285, App
c 573	17	1.3	595	17	US-10-027-632-89767	Sequence 89767, A	646	17	1.3	712	13	US-10-027-632-13786	Sequence 13786, A
c 574	17	1.3	595	17	US-10-027-632-89768	Sequence 89768, A	647	17	1.3	712	13	US-10-027-632-13787	Sequence 13787, A
c 575	17	1.3	596	13	US-10-027-632-267507	Sequence 267507, A	648	17	1.3	712	17	US-10-027-632-13786	Sequence 13786, A
c 576	17	1.3	596	17	US-10-027-632-267507	Sequence 267507, A	649	17	1.3	712	17	US-10-027-632-13787	Sequence 13787, A
c 577	17	1.3	596	17	US-10-191-803-957	Sequence 957, App	c 650	17	1.3	716	17	US-10-437-963-60533	Sequence 60533, A
c 578	17	1.3	596	17	US-10-152-319A-922	Sequence 922, App	c 651	17	1.3	716	18	US-10-425-114-3741	Sequence 3741, Ap
c 579	17	1.3	598	17	US-10-424-599-24212	Sequence 24212, A	c 652	17	1.3	718	18	US-10-425-115-20459	Sequence 20459, A
c 580	17	1.3	598	18	US-10-437-963-65829	Sequence 65829, A	c 653	17	1.3	727	13	US-10-027-632-32847	Sequence 32847, A
c 581	17	1.3	598	18	US-10-363-345A-27273	Sequence 27273, A	c 654	17	1.3	727	17	US-10-027-632-32847	Sequence 32847, A
c 582	17	1.3	598	18	US-10-363-345A-27274	Sequence 27274, A	c 655	17	1.3	728	13	US-10-027-632-111128	Sequence 111128, A
583	17	1.3	598	19	US-10-363-483A-27273	Sequence 27274, A	656	17	1.3	728	17	US-10-027-632-111128	Sequence 111128, A
c 584	17	1.3	598	19	US-10-363-483A-27274	Sequence 27274, A	657	17	1.3	753	18	US-10-375-010-5	Sequence 5, Appl
c 585	17	1.3	599	13	US-10-027-632-243694	Sequence 243694, A	658	17	1.3	766	18	US-10-425-115-173673	Sequence 173673, A
c 586	17	1.3	599	17	US-10-027-632-243694	Sequence 243694, A	659	17	1.3	771	17	US-10-398-221-2195	Sequence 2195, Ap
587	17	1.3	600	18	US-10-021-323-15145	Sequence 15145, A	c 660	17	1.3	784	18	US-10-767-701-3084	Sequence 3084, Ap
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591	17	1.3	601	17	US-10-027-632-85562	Sequence 85562, A	c 664	17	1.3	784	17	US-10-027-632-8932	Sequence 8932, Ap
592	17	1.3	601	17	US-10-027-632-85563	Sequence 85563, A	c 665	17	1.3	784	17	US-10-027-632-8933	Sequence 8933, Ap
593	17	1.3	601	17	US-10-027-632-85564	Sequence 85564, A	c 666	17	1.3	784	17	US-10-027-632-8934	Sequence 8934, Ap
594	17	1.3	609	17	US-10-114-6748	Sequence 6748, Ap	667	17	1.3	789	17	US-10-027-632-503	Sequence 503, App
595	17	1.3	609	18	US-10-425-115-180603	Sequence 180603, A	668	17	1.3	831	18	US-10-767-701-8624	Sequence 8624, Ap

c 669	17	1.3	832	17	US-10-398-221-1542	Sequence 1542, Ap	c 742	17	1.3	1263	18	US-10-872-155-542	Sequence 542, App
c 670	17	1.3	836	17	US-10-220-891-54	Sequence 54, Appl	c 743	17	1.3	1276	13	US-10-027-632-123198	Sequence 123198,
c 671	17	1.3	836	17	US-10-479-081-85	Sequence 85, Appl	c 744	17	1.3	1276	17	US-10-027-632-123198	Sequence 123198,
c 672	17	1.3	837	17	US-10-424-599-53139	Sequence 53139, A	c 745	17	1.3	1280	17	US-10-424-599-111259	Sequence 111259,
c 673	17	1.3	845	13	US-10-027-632-162780	Sequence 162780,	c 746	17	1.3	1291	18	US-10-363-345A-27477	Sequence 27477, A
c 674	17	1.3	845	13	US-10-027-632-162781	Sequence 162781,	c 747	17	1.3	1291	18	US-10-363-345A-27478	Sequence 27478, A
c 675	17	1.3	845	13	US-10-027-632-162782	Sequence 162782,	c 748	17	1.3	1291	19	US-10-363-483A-27477	Sequence 27477, A
c 676	17	1.3	845	17	US-10-027-632-162780	Sequence 162780,	c 749	17	1.3	1291	19	US-10-363-483A-27478	Sequence 27478, A
c 677	17	1.3	845	17	US-10-027-632-162781	Sequence 162781,	c 750	17	1.3	1300	17	US-10-398-221-3299	Sequence 3299, Ap
c 678	17	1.3	845	17	US-10-027-632-162782	Sequence 162782,	c 751	17	1.3	1345	9	US-09-764-864-315	Sequence 315, App
c 679	17	1.3	852	13	US-10-027-632-9470	Sequence 9470, Ap	c 752	17	1.3	1356	17	US-10-282-122A-27914	Sequence 27914, A
c 680	17	1.3	852	13	US-10-027-632-9471	Sequence 9471, Ap	c 753	17	1.3	1367	18	US-10-723-860-3786	Sequence 3786, Ap
c 681	17	1.3	852	17	US-10-027-632-9470	Sequence 9470, Ap	c 754	17	1.3	1368	17	US-10-424-599-71998	Sequence 71998, A
c 682	17	1.3	852	17	US-10-027-632-9471	Sequence 9471, Ap	c 755	17	1.3	1424	17	US-10-424-599-91388	Sequence 91388, A
c 683	17	1.3	854	17	US-10-425-114-9385	Sequence 8385, Ap	c 756	17	1.3	1447	18	US-10-739-930-889	Sequence 889, App
c 684	17	1.3	856	13	US-10-027-632-127893	Sequence 127893,	c 757	17	1.3	1459	9	US-09-753-143-174	Sequence 174, App
c 685	17	1.3	856	13	US-10-027-632-127893	Sequence 127893,	c 758	17	1.3	1459	9	US-09-780-669-174	Sequence 174, App
c 686	17	1.3	857	13	US-10-027-632-101024	Sequence 101024,	c 759	17	1.3	1459	9	US-09-030-606-174	Sequence 174, App
c 687	17	1.3	857	17	US-10-027-632-101024	Sequence 101024,	c 760	17	1.3	1459	9	US-09-822-827-174	Sequence 174, App
c 688	17	1.3	860	17	US-10-424-599-115070	Sequence 115070,	c 761	17	1.3	1459	9	US-09-115-453-174	Sequence 174, App
c 689	17	1.3	877	17	US-10-425-114-5488	Sequence 5488, Ap	c 762	17	1.3	1459	9	US-09-232-880-174	Sequence 174, App
c 690	17	1.3	877	18	US-10-425-115-66121	Sequence 66121, A	c 763	17	1.3	1459	9	US-09-895-793-174	Sequence 174, App
c 691	17	1.3	878	18	US-10-425-115-173677	Sequence 173677, A	c 764	17	1.3	1459	13	US-09-898-814-174	Sequence 174, App
c 692	17	1.3	898	13	US-10-027-632-29740	Sequence 29740, A	c 765	17	1.3	1459	14	US-10-012-896-174	Sequence 174, App
c 693	17	1.3	898	17	US-10-027-632-29740	Sequence 29740, A	c 766	17	1.3	1459	16	US-10-144-678A-174	Sequence 174, App
c 694	17	1.3	899	9	US-09-938-842A-4488	Sequence 4488, Ap	c 767	17	1.3	1459	16	US-10-294-025-174	Sequence 174, App
c 695	17	1.3	899	11	US-09-938-842A-4488	Sequence 4488, Ap	c 768	17	1.3	1459	18	US-10-688-838-174	Sequence 174, App
c 696	17	1.3	900	13	US-10-001-879-18	Sequence 18, Appl	c 769	17	1.3	1463	13	US-10-005-057A-12	Sequence 12, Appl
c 697	17	1.3	917	17	US-10-425-114-1654	Sequence 1654, Ap	c 770	17	1.3	1463	17	US-10-675-072A-13	Sequence 13, Appl
c 698	17	1.3	937	18	US-10-357-930-22583	Sequence 22583, A	c 771	17	1.3	1504	9	US-09-938-842A-3727	Sequence 3727, Ap
c 699	17	1.3	937	18	US-10-357-930-22583	Sequence 22583, A	c 772	17	1.3	1504	11	US-09-938-842A-3727	Sequence 3727, Ap
c 700	17	1.3	940	18	US-10-363-345A-23321	Sequence 23321, A	c 773	17	1.3	1512	18	US-10-739-930-3581	Sequence 3581, Ap
c 701	17	1.3	940	18	US-10-363-345A-23322	Sequence 23322, A	c 774	17	1.3	1512	18	US-10-739-930-3581	Sequence 3581, Ap
c 702	17	1.3	940	19	US-10-363-483A-23321	Sequence 23321, A	c 775	17	1.3	1537	9	US-09-349-015-16	Sequence 16, Appl
c 703	17	1.3	940	19	US-10-363-483A-23322	Sequence 23322, A	c 776	17	1.3	1537	15	US-10-219-664-12	Sequence 12, Appl
c 704	17	1.3	962	18	US-10-425-115-66125	Sequence 66125, A	c 777	17	1.3	1559	17	US-10-466-720-18	Sequence 18, Appl
c 705	17	1.3	964	17	US-10-424-599-119830	Sequence 119830,	c 778	17	1.3	1559	17	US-10-466-720-18	Sequence 18, Appl
c 706	17	1.3	985	13	US-10-027-632-9326	Sequence 9326, Ap	c 779	17	1.3	1597	9	US-09-726-643-30	Sequence 30, Appl
c 707	17	1.3	985	17	US-10-027-632-9326	Sequence 9326, Ap	c 780	17	1.3	1597	13	US-10-042-141-30	Sequence 30, Appl
c 708	17	1.3	997	17	US-10-424-599-129494	Sequence 129494,	c 781	17	1.3	1597	19	US-10-919-272-30	Sequence 30, Appl
c 709	17	1.3	1008	17	US-10-369-100-53	Sequence 53, Appl	c 782	17	1.3	1615	18	US-10-425-115-66135	Sequence 66135, A
c 710	17	1.3	1008	17	US-10-369-100-130	Sequence 130, App	c 783	17	1.3	1634	18	US-10-739-930-3914	Sequence 3914, Ap
c 711	17	1.3	1008	17	US-10-369-100-131	Sequence 131, App	c 784	17	1.3	1668	18	US-10-282-122A-11028	Sequence 11028, A
c 712	17	1.3	1010	13	US-10-027-632-9990	Sequence 9990, Ap	c 785	17	1.3	1673	18	US-10-739-930-3422	Sequence 3422, Ap
c 713	17	1.3	1010	17	US-10-027-632-9990	Sequence 9990, Ap	c 786	17	1.3	1740	17	US-10-424-599-39491	Sequence 39491, A
c 714	17	1.3	1011	17	US-10-369-100-51	Sequence 51, Appl	c 787	17	1.3	1767	9	US-09-764-846-107	Sequence 107, App
c 715	17	1.3	1014	9	US-09-729-835-32	Sequence 32, Appl	c 788	17	1.3	1767	14	US-10-091-483-107	Sequence 107, App
c 716	17	1.3	1014	17	US-10-373-809-32	Sequence 32, Appl	c 789	17	1.3	1780	14	US-10-164-278-13	Sequence 13, Appl
c 717	17	1.3	1024	13	US-10-202-193-61	Sequence 61, Appl	c 790	17	1.3	1783	18	US-10-164-278-13	Sequence 13, Appl
c 718	17	1.3	1024	13	US-10-202-193-62	Sequence 62, Appl	c 791	17	1.3	1824	17	US-10-386-414-9	Sequence 9, Appl
c 719	17	1.3	1030	17	US-10-425-114-17292	Sequence 17292, A	c 792	17	1.3	1841	9	US-09-764-864-735	Sequence 735, App
c 720	17	1.3	1052	18	US-10-437-963-100391	Sequence 100391,	c 793	17	1.3	1848	13	US-10-027-632-201065	Sequence 201065,
c 721	17	1.3	1067	18	US-10-767-795-2376	Sequence 2376, Ap	c 794	17	1.3	1848	17	US-10-027-632-201065	Sequence 201065,
c 722	17	1.3	1086	13	US-10-027-632-116914	Sequence 116914,	c 795	17	1.3	1849	14	US-10-164-278-14	Sequence 14, Appl
c 723	17	1.3	1086	17	US-10-027-632-116914	Sequence 116914,	c 796	17	1.3	1861	18	US-10-471-450-46	Sequence 46, Appl
c 724	17	1.3	1109	18	US-10-437-963-7025	Sequence 7025, Ap	c 797	17	1.3	1872	17	US-10-398-221-847	Sequence 847, App
c 725	17	1.3	1112	13	US-10-027-632-119053	Sequence 119053,	c 798	17	1.3	1872	17	US-10-398-221-2762	Sequence 2762, Ap
c 726	17	1.3	1112	17	US-10-027-632-119053	Sequence 119053,	c 799	17	1.3	1872	17	US-10-282-122A-24198	Sequence 24198, A
c 727	17	1.3	1127	18	US-10-363-345A-28307	Sequence 28307, A	c 800	17	1.3	1884	17	US-10-425-114-19833	Sequence 19833, A
c 728	17	1.3	1127	18	US-10-363-345A-28308	Sequence 28308, A	c 801	17	1.3	1884	17	US-10-425-114-19833	Sequence 19833, A
c 729	17	1.3	1127	19	US-10-363-483A-28307	Sequence 28307, A	c 802	17	1.3	1886	17	US-10-264-049-98	Sequence 98, Appl
c 730	17	1.3	1127	19	US-10-363-483A-28308	Sequence 28308, A	c 803	17	1.3	1934	13	US-10-027-632-259050	Sequence 259050,
c 731	17	1.3	1127	19	US-10-363-483A-28308	Sequence 28308, A	c 804	17	1.3	1934	13	US-10-027-632-259051	Sequence 259051,
c 732	17	1.3	1155	18	US-10-363-345A-38681	Sequence 38681, A	c 805	17	1.3	1934	13	US-10-027-632-259052	Sequence 259052,
c 733	17	1.3	1155	18	US-10-363-345A-38682	Sequence 38682, A	c 806	17	1.3	1934	17	US-10-027-632-259050	Sequence 259050,
c 734	17	1.3	1155	19	US-10-363-483A-38682	Sequence 38682, A	c 807	17	1.3	1934	17	US-10-027-632-259051	Sequence 259051,
c 735	17	1.3	1175	9	US-09-938-842A-5221	Sequence 5221, Ap	c 808	17	1.3	1934	17	US-10-027-632-259052	Sequence 259052,
c 736	17	1.3	1175	11	US-09-938-842A-5221	Sequence 5221, Ap	c 809	17	1.3	1961	17	US-10-424-599-89406	Sequence 89406, A
c 737	17	1.3	1218	18	US-10-425-115-29128	Sequence 29128, A	c 810	17	1.3	1984	15	US-09-729-674-91	Sequence 91, Appl
c 738	17	1.3	1227	18	US-10-425-115-173675	Sequence 173675,	c 811	17	1.3	1992	9	US-10-913-553-91	Sequence 91, Appl
c 739	17	1.3	1239	17	US-10-425-114-25371	Sequence 25371, A	c 812	17	1.3	1992	18	US-10-913-553-91	Sequence 91, Appl
c 740	17	1.3	1263	9	US-09-841-132-542	Sequence 542, App	c 813	17	1.3	2000	9	US-09-938-842A-3550	Sequence 3550, Ap
c 741	17	1.3	1263	17	US-10-282-122A-18842	Sequence 18842, A	c 814	17	1.3	2000	9	US-09-938-842A-3550	Sequence 3550, Ap

815	17	1.3	2000	9	US-09-338-842A-3903	Sequence 3903, Ap	888	17	1.3	3633	13	US-10-044-090-123	Sequence 123, App
816	17	1.3	2000	9	US-09-338-842A-4412	Sequence 4412, Ap	889	17	1.3	3648	18	US-10-425-115-16045	Sequence 16045, A
817	17	1.3	2000	11	US-09-338-842A-2995	Sequence 2995, Ap	c 890	17	1.3	3743	18	US-10-437-963-49246	Sequence 49246, A
818	17	1.3	2000	11	US-09-338-842A-3550	Sequence 3550, Ap	891	17	1.3	3825	9	US-09-974-300-219	Sequence 219, App
819	17	1.3	2000	11	US-09-338-842A-3903	Sequence 3903, Ap	c 892	17	1.3	3837	11	US-09-984-429-302	Sequence 302, App
820	17	1.3	2000	11	US-09-338-842A-4412	Sequence 4412, Ap	893	17	1.3	3858	10	US-09-845-416-9	Sequence 9, Appli
821	17	1.3	2009	17	US-10-425-114-27990	Sequence 27990, A	c 894	17	1.3	3919	18	US-10-425-115-103401	Sequence 103401, A
822	17	1.3	2012	13	US-10-027-632-98654	Sequence 98654, A	895	17	1.3	3941	15	US-10-157-031-170	Sequence 170, App
823	17	1.3	2012	17	US-10-027-632-98654	Sequence 98654, A	896	17	1.3	3941	15	US-10-651-237-42	Sequence 42, Appl
824	17	1.3	2021	13	US-10-027-632-98014	Sequence 98014, A	897	17	1.3	3941	19	US-10-782-413-42	Sequence 42, Appl
825	17	1.3	2021	17	US-10-027-632-98015	Sequence 98015, A	898	17	1.3	3957	18	US-10-425-115-94204	Sequence 94204, A
826	17	1.3	2021	17	US-10-027-632-98015	Sequence 98015, A	899	17	1.3	3999	10	US-09-845-416-6	Sequence 6, Appli
827	17	1.3	2021	17	US-10-027-632-98015	Sequence 98015, A	900	17	1.3	4011	17	US-10-412-699B-1583	Sequence 1583, Ap
c 828	17	1.3	2033	17	US-10-425-114-27794	Sequence 27794, A	901	17	1.3	4079	17	US-10-305-720-1257	Sequence 1257, Ap
829	17	1.3	2080	18	US-10-425-115-107511	Sequence 107511, A	902	17	1.3	4105	9	US-09-931-157-1	Sequence 1, Appli
830	17	1.3	2113	9	US-09-338-803-22	Sequence 22, Appl	903	17	1.3	4105	15	US-10-225-567A-115	Sequence 115, App
c 831	17	1.3	2129	18	US-10-739-930-4622	Sequence 4622, Ap	904	17	1.3	4105	15	US-10-007-926A-229	Sequence 229, App
c 832	17	1.3	2143	14	US-10-164-278-3	Sequence 3, Appli	905	17	1.3	4105	15	US-10-101-510-370	Sequence 370, App
c 833	17	1.3	2160	18	US-10-717-597-151	Sequence 151, App	906	17	1.3	4105	17	US-10-372-683-46	Sequence 46, Appl
c 834	17	1.3	2167	18	US-10-730-034-7	Sequence 7, Appli	907	17	1.3	4105	18	US-10-723-860-894	Sequence 824, App
835	17	1.3	2169	10	US-09-845-416-4	Sequence 4, Appli	908	17	1.3	4182	10	US-09-845-416-2	Sequence 2, Appli
836	17	1.3	2196	18	US-10-425-115-89406	Sequence 89406, A	909	17	1.3	4202	18	US-10-723-860-5426	Sequence 5426, Ap
c 837	17	1.3	2204	9	US-09-842-552-97	Sequence 97, Appl	c 910	17	1.3	4230	17	US-10-398-221-3778	Sequence 3778, Ap
c 838	17	1.3	2224	14	US-10-284-985-6	Sequence 6, Appli	911	17	1.3	4385	18	US-10-473-485-12	Sequence 12, Appl
c 839	17	1.3	2224	18	US-10-684-422-269	Sequence 269, App	c 912	17	1.3	4415	15	US-10-311-485-1880	Sequence 1880, Ap
c 840	17	1.3	2229	17	US-10-468-125-19	Sequence 19, Appl	c 913	17	1.3	4415	15	US-10-240-485-156	Sequence 156, App
841	17	1.3	2235	17	US-10-425-114-20475	Sequence 20475, A	914	17	1.3	4415	18	US-10-370-715B-467	Sequence 467, App
842	17	1.3	2239	14	US-10-198-846-9807	Sequence 9807, Ap	915	17	1.3	4498	10	US-09-845-416-30	Sequence 30, Appl
843	17	1.3	2259	17	US-10-641-643-796	Sequence 796, App	c 916	17	1.3	4617	18	US-10-723-860-3682	Sequence 3682, Ap
844	17	1.3	2265	17	US-10-369-493-29930	Sequence 29930, A	917	17	1.3	4618	9	US-09-764-847-1491	Sequence 1491, Ap
c 845	17	1.3	2268	18	US-10-437-963-67942	Sequence 67942, A	918	17	1.3	4618	14	US-10-092-154-1491	Sequence 1491, Ap
c 846	17	1.3	2289	18	US-10-425-115-65663	Sequence 65663, A	919	17	1.3	4707	18	US-10-734-564-55	Sequence 55, Appl
847	17	1.3	2440	17	US-10-425-114-29973	Sequence 29973, A	920	17	1.3	4825	10	US-09-845-416-29	Sequence 29, Appl
848	17	1.3	2446	17	US-10-094-749-892	Sequence 892, App	921	17	1.3	4848	10	US-09-845-416-35	Sequence 35, Appl
849	17	1.3	2523	13	US-10-027-632-263627	Sequence 263627, A	922	17	1.3	4877	17	US-10-062-674-1824	Sequence 1824, Ap
850	17	1.3	2523	17	US-10-027-632-263627	Sequence 263627, A	923	17	1.3	4898	18	US-10-723-860-8096	Sequence 8096, Ap
c 851	17	1.3	2529	13	US-10-027-632-102760	Sequence 102760, A	924	17	1.3	4932	9	US-09-920-300A-1688	Sequence 1688, Ap
c 852	17	1.3	2539	17	US-10-027-632-102760	Sequence 102760, A	925	17	1.3	4932	13	US-10-033-528-1688	Sequence 1688, Ap
c 853	17	1.3	2591	17	US-10-094-749-811	Sequence 811, App	926	17	1.3	4932	16	US-10-099-926-1688	Sequence 1688, Ap
c 854	17	1.3	2595	9	US-09-919-497-12	Sequence 12, Appl	927	17	1.3	4933	17	US-10-172-118-1539	Sequence 1539, Ap
855	17	1.3	2595	16	US-10-204-753-30	Sequence 30, Appl	928	17	1.3	4933	17	US-10-342-887-1539	Sequence 1539, Ap
856	17	1.3	2639	17	US-10-425-114-29914	Sequence 29914, A	929	17	1.3	4933	18	US-10-723-860-4015	Sequence 4015, Ap
857	17	1.3	2659	17	US-10-424-599-83050	Sequence 83050, A	930	17	1.3	4949	18	US-10-723-860-7910	Sequence 7910, Ap
c 858	17	1.3	2660	17	US-10-264-049-630	Sequence 630, App	931	17	1.3	4966	10	US-09-845-416-28	Sequence 28, Appl
859	17	1.3	2667	13	US-10-424-599-91404	Sequence 91404, A	932	17	1.3	4990	10	US-09-845-416-36	Sequence 36, Appl
860	17	1.3	2697	13	US-10-027-632-111990	Sequence 111990, A	933	17	1.3	5060	10	US-09-845-416-36	Sequence 36, Appl
861	17	1.3	2697	17	US-10-027-632-111990	Sequence 111990, A	934	17	1.3	5079	16	US-10-240-965-192	Sequence 192, App
862	17	1.3	2699	17	US-10-424-599-91407	Sequence 91407, A	935	17	1.3	5127	14	US-10-239-676-132	Sequence 132, App
c 863	17	1.3	2708	10	US-09-820-649-37	Sequence 37, Appl	c 936	17	1.3	5127	18	US-10-425-115-98092	Sequence 98092, A
c 864	17	1.3	2708	16	US-10-160-162-37	Sequence 37, Appl	937	17	1.3	5149	10	US-09-845-416-27	Sequence 27, Appl
c 865	17	1.3	2708	19	US-10-936-773-37	Sequence 37, Appl	938	17	1.3	5217	17	US-10-240-425-1225	Sequence 1225, Ap
c 866	17	1.3	2716	18	US-10-425-115-29127	Sequence 29127, A	939	17	1.3	5244	17	US-10-257-166-95	Sequence 95, Appl
867	17	1.3	2727	15	US-10-037-270-218	Sequence 218, App	940	17	1.3	5276	15	US-10-311-455-124	Sequence 124, App
868	17	1.3	2727	17	US-10-117-722-218	Sequence 218, App	941	17	1.3	5287	15	US-10-311-455-1466	Sequence 1466, Ap
869	17	1.3	2866	18	US-10-425-115-71784	Sequence 71784, A	942	17	1.3	5303	15	US-10-311-455-843	Sequence 843, App
c 870	17	1.3	2898	17	US-10-386-414-7	Sequence 7, Appli	943	17	1.3	5313	15	US-10-311-455-736	Sequence 736, App
871	17	1.3	2903	17	US-10-425-114-24832	Sequence 24832, A	944	17	1.3	5317	15	US-10-311-455-582	Sequence 582, App
872	17	1.3	2952	17	US-10-094-749-1587	Sequence 1587, Ap	945	17	1.3	5339	17	US-10-149-736-40	Sequence 40, Appl
c 873	17	1.3	2954	14	US-10-164-278-2	Sequence 2, Appli	946	17	1.3	5339	19	US-10-964-536-40	Sequence 40, Appl
c 874	17	1.3	2980	17	US-10-425-114-32965	Sequence 32965, A	947	17	1.3	5365	15	US-10-311-455-20	Sequence 20, Appl
c 875	17	1.3	3031	9	US-09-841-132-87	Sequence 87, Appl	948	17	1.3	5365	17	US-10-221-613-6	Sequence 6, Appli
c 876	17	1.3	3031	14	US-10-872-155-87	Sequence 87, Appl	949	17	1.3	5439	15	US-10-311-455-1376	Sequence 1376, Ap
877	17	1.3	3081	18	US-10-014-799A-3	Sequence 3, Appli	950	17	1.3	5462	17	US-10-149-736-41	Sequence 41, Appl
c 878	17	1.3	3100	18	US-10-479-435-58	Sequence 58, Appl	951	17	1.3	5462	19	US-10-964-536-41	Sequence 41, Appl
c 879	17	1.3	3128	18	US-10-473-126-157	Sequence 157, App	952	17	1.3	5464	15	US-10-311-455-1889	Sequence 1889, Ap
880	17	1.3	3128	18	US-10-473-126-303	Sequence 303, App	953	17	1.3	5551	17	US-10-221-613-55	Sequence 55, Appl
c 881	17	1.3	3136	19	US-10-893-888-27	Sequence 27, Appl	954	17	1.3	5552	15	US-10-311-455-1231	Sequence 1231, Ap
c 882	17	1.3	3215	14	US-10-198-846-9945	Sequence 9945, Ap	955	17	1.3	5640	17	US-10-221-596B-21	Sequence 21, Appl
c 883	17	1.3	3361	17	US-10-104-047-964	Sequence 964, App	956	17	1.3	5659	15	US-10-172-086-31	Sequence 31, Appl
884	17	1.3	3531	10	US-09-845-416-10	Sequence 10, Appl	957	17	1.3	5659	15	US-10-311-455-347	Sequence 347, App
885	17	1.3	3548	17	US-10-425-114-31425	Sequence 31425, A	958	17	1.3	5659	15	US-10-240-485-39	Sequence 39, Appl
886	17	1.3	3560	18	US-10-425-115-183973	Sequence 183973, A	959	17	1.3	5659	18	US-10-311-507-13	Sequence 13, Appl
887	17	1.3	3599	17	US-10-424-599-53686	Sequence 53686, A	960	17	1.3	5659	18	US-10-480-846-31	Sequence 31, Appl

961 17 1.3 5735 9 US-09-728-952-44 Sequence 44, App1
962 17 1.3 5735 9 US-09-728-952-99 Sequence 99, App1
963 17 1.3 5759 15 US-10-311-455-1677 Sequence 1677, Ap
964 17 1.3 5768 15 US-10-311-455-2135 Sequence 2135, Ap
965 17 1.3 5807 15 US-10-311-455-1128 Sequence 1128, Ap
966 17 1.3 5815 17 US-10-257-166-105 Sequence 105, App
967 17 1.3 5823 15 US-10-240-453-256 Sequence 256, App
968 17 1.3 5890 15 US-10-311-455-1311 Sequence 1311, Ap
969 17 1.3 5971 15 US-10-311-455-356 Sequence 356, App
970 17 1.3 6014 17 US-10-221-613-367 Sequence 367, App
971 17 1.3 6014 17 US-10-221-613-367 Sequence 367, App
972 17 1.3 6014 17 US-10-221-613-368 Sequence 368, App
973 17 1.3 6024 15 US-10-311-455-1619 Sequence 1619, Ap
974 17 1.3 6042 15 US-10-311-455-1917 Sequence 1917, Ap
975 17 1.3 6049 15 US-10-311-455-346 Sequence 346, App
976 17 1.3 6061 14 US-10-239-676-40 Sequence 40, App1
977 17 1.3 6062 15 US-10-311-455-2051 Sequence 2051, Ap
978 17 1.3 6074 15 US-10-311-455-1037 Sequence 1037, Ap
979 17 1.3 6081 15 US-10-311-455-1401 Sequence 1401, Ap
980 17 1.3 6092 15 US-10-311-455-993 Sequence 993, App
981 17 1.3 6109 15 US-10-311-455-1704 Sequence 1704, Ap
982 17 1.3 6112 15 US-10-311-455-445 Sequence 445, App
983 17 1.3 6113 15 US-10-311-455-776 Sequence 776, App
984 17 1.3 6131 15 US-10-311-455-863 Sequence 863, App
985 17 1.3 6145 17 US-10-221-714A-269 Sequence 269, App
986 17 1.3 6171 15 US-10-311-455-1987 Sequence 1987, Ap
987 17 1.3 6182 15 US-10-311-455-983 Sequence 983, App
988 17 1.3 6197 15 US-10-311-455-1683 Sequence 1683, Ap
989 17 1.3 6204 15 US-10-311-455-1800 Sequence 1800, Ap
990 17 1.3 6246 15 US-10-172-086-27 Sequence 27, App1
991 17 1.3 6246 15 US-10-311-455-989 Sequence 989, App
992 17 1.3 6246 18 US-10-311-507-49 Sequence 49, App1
993 17 1.3 6246 18 US-10-480-846-27 Sequence 27, App1
994 17 1.3 6254 15 US-10-311-455-1593 Sequence 1593, Ap
995 17 1.3 6298 14 US-10-239-676-63 Sequence 63, App1
996 17 1.3 6298 15 US-10-240-453-67 Sequence 67, App1
997 17 1.3 6303 18 US-10-433-793-115 Sequence 115, App
998 17 1.3 6306 14 US-10-239-676-223 Sequence 223, App
999 17 1.3 6306 15 US-10-240-453-331 Sequence 331, App
c1000 17 1.3 6309 15 US-10-311-455-277 Sequence 277, App

ALIGNMENTS

RESULT 1
US-10-679-246-1
; Sequence 1, Application US/10679246
; Publication No. US20040163138A1
; GENERAL INFORMATION:
; APPLICANT: Reed, John C.
; APPLICANT: Matsuzawa, Shu-ichi
; TITLE OF INVENTION: Nucleic Acid Encoding Proteins Involved
; TITLE OF INVENTION: in Protein Degradation, Products and Methods Related Thereto
; FILE REFERENCE: 66821-235
; CURRENT APPLICATION NUMBER: US/10/679,246
; CURRENT FILING DATE: 2003-10-02
; PRIOR APPLICATION NUMBER: US 09/591,694
; PRIOR FILING DATE: 2000-06-09
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 1274
; TYPE: DNA
; ORGANISM: Homo sapien
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (274)...(1167)
US-10-679-246-1

Query Match 100.0%; Score 1274; DB 18; Length 1274;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1274; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTTCTTTAGTTGTTTATGGTCCATTTTCTATTTTAGCATTTTATTATTTCTATGTAGTCTAT 60
Db 1 TTTCTTTAGTTGTTTATGGTCCATTTTCTATTTTAGCATTTTATTATTTCTATGTAGTCTAT 60
QY 61 CCAAGACGATTAAGGGAGTTCCACATGTTTTCCGGAACATTTTGAAGAAGAGAGCTTATC 120
Db 61 CCAAGACGATTAAGGGAGTTCCACATGTTTTCCGGAACATTTTGAAGAAGAGAGCTTATC 120
QY 121 CAGTGTACAGATCCTAATAAAGTGACATTCAGTGTAAATTTTATTTTATTTTATATCTTTT 180
Db 121 CAGTGTACAGATCCTAATAAAGTGACATTCAGTGTAAATTTTATTTTATTTTATATCTTTT 180
QY 181 TTAATCTTATTTTCT 240
Db 181 TTAATCTTATTTTCT 240
QY 241 TATGCGATGTAACATTTATTTATAAGTAAGTCAATGTTTATTTTATTTTCTCTCTCTCT 300
Db 241 TATGCGATGTAACATTTATTTATAAGTAAGTCAATGTTTATTTTATTTTCTCTCTCTCT 300
QY 301 CCTTATGTTATTTTATTTTATGAAATGAGCGTCTGAGTCTGCTAGCATTAACCTACCGGTACC 360
Db 301 CCTTATGTTATTTTATTTTATGAAATGAGCGTCTGAGTCTGCTAGCATTAACCTACCGGTACC 360
QY 361 TCGAAGTGTCCACCATCCAGAGGGTGCCTGCCCTGAGTGGGCAACATGCAATCCAAACAT 420
Db 361 TCGAAGTGTCCACCATCCAGAGGGTGCCTGCCCTGAGTGGGCAACATGCAATCCAAACAT 420
QY 421 GACTTGGGGAGTCTTTTGGAGTGTCCAGTCTGCTTTGAGTGTCCAGTCTGCTTTGAGTGTCC 480
Db 421 GACTTGGGGAGTCTTTTGGAGTGTCCAGTCTGCTTTGAGTGTCCAGTCTGCTTTGAGTGTCC 480
QY 481 CAATGTCTCAGATGGGCACTTTGTTTGTAGCAACTCTGCGCCCAAAAGCTCACATGTTGTCCA 540
Db 481 CAATGTCTCAGATGGGCACTTTGTTTGTAGCAACTCTGCGCCCAAAAGCTCACATGTTGTCCA 540
QY 541 ACTTCCCGGGGGCCCTTTGGGATCCAACTTGGGATCCAACTTGGGATCCAACTTGGGATCCAA 600
Db 541 ACTTCCCGGGGGCCCTTTGGGATCCAACTTGGGATCCAACTTGGGATCCAACTTGGGATCCAA 600
QY 601 GTACTTTTCCCTGTAAATATGCGTCTTCTGATGTAAATTAACCTCTGCCACACACAGAA 660
Db 601 GTACTTTTCCCTGTAAATATGCGTCTTCTGATGTAAATTAACCTCTGCCACACACAGAA 660
QY 661 AAAGCAGACCATGAAGAGCTCTGTGAGTTTAGGCGCTTATTCCTGTCGCGTCCCTGGTGT 720
Db 661 AAAGCAGACCATGAAGAGCTCTGTGAGTTTAGGCGCTTATTCCTGTCGCGTCCCTGGTGT 720
QY 721 TCCTGTAAATGGCAAGGCTCTCTGGATGCTGTAATGCCCATCTCATGTCATCAGCATAG 780
Db 721 TCCTGTAAATGGCAAGGCTCTCTGGATGCTGTAATGCCCATCTCATGTCATCAGCATAG 780
QY 781 TCCATTACAAACCTCAGGAGGAGATAGTTTTTCTTGTACAGACATTAATCTTCTCT 840
Db 781 TCCATTACAAACCTCAGGAGGAGATAGTTTTTCTTGTCTCAGACATTAATCTTCTCT 840
QY 841 GGTGCTGTTGACTGGGTGATGATGAGTCTGTTTGGCTTTTCACTTCATGTTAGTCTT 900
Db 841 GGTGCTGTTGACTGGGTGATGATGAGTCTGTTTGGCTTTTCACTTCATGTTAGTCTT 900
QY 901 GAGAAACAGGAAAAATACGATGGTCAACGAGATTTCTTGGCAATCGTACAGCTGATAGA 960
Db 901 GAGAAACAGGAAAAATACGATGGTCAACGAGATTTCTTGGCAATCGTACAGCTGATAGA 960
QY 961 ACACGCAAGCAAGCTGAAATTTTCTTACCGACTTGGCTTAAATGCTCATAGGCGACGA 1020
Db 961 ACACGCAAGCAAGCTGAAATTTTCTTACCGACTTGGCTTAAATGCTCATAGGCGACGA 1020
QY 1021 TTAGCTTTGGGAAGCGACTCTCTCGATCTATTCATGAAGGAATTTGCAACAGCCATTAAT 1080
Db 1021 TTAGCTTTGGGAAGCGACTCTCTCGATCTATTCATGAAGGAATTTGCAACAGCCATTAAT 1080

QY 1081 AGCGACTGTCTAGTCTTTGACACACAGCANTGACAGCTTTTTCAGAGAAATGCAATTTA 1140
Db 1081 AGCGACTGTCTAGTCTTTGACACACAGCANTGACAGCTTTTTCAGAGAAATGCAATTTA 1140
QY 1141 GGCAATCAATGTAATTTTCCATGCTGTCGAAATGGCAATCAAAACATTTTCTGGCCAGTGT 1200
Db 1141 GGCAATCAATGTAATTTTCCATGCTGTCGAAATGGCAATCAAAACATTTTCTGGCCAGTGT 1200
QY 1201 TTAAACCTTCAGTTTTCACAGAAATTAAGGACCCATCTGCTGCGCAACCTTAAACCTCTTT 1260
Db 1201 TTAAACCTTCAGTTTTCACAGAAATTAAGGACCCATCTGCTGCGCAACCTTAAACCTCTTT 1260
QY 1261 CGGTAGGTGGAAGC 1274
Db 1261 CGGTAGGTGGAAGC 1274

RESULT 2

US-10-357-930-22959
; Sequence 22959, Application US/10357930
; Publication No. US20040259086A1
; GENERAL INFORMATION:
; APPLICANT: Schlegel, Robert
; APPLICANT: Endege, Wilson
; APPLICANT: Monahan, John
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
; TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY OF
; TITLE OF INVENTION: HUMAN PROSTATE CANCER
; FILE REFERENCE: MRI-007BCN
; CURRENT APPLICATION NUMBER: US/10/357,930
; CURRENT FILING DATE: 2003-02-04
; PRIOR APPLICATION NUMBER: 09/785,276
; PRIOR FILING DATE: 2003-02-16
; PRIOR APPLICATION NUMBER: 60/183,319
; PRIOR FILING DATE: 2000-02-17
; PRIOR APPLICATION NUMBER: 60/189,862
; PRIOR FILING DATE: 2000-03-16
; PRIOR APPLICATION NUMBER: 60/207,454
; PRIOR FILING DATE: 2000-05-25
; PRIOR APPLICATION NUMBER: 60/211,314
; PRIOR FILING DATE: 2000-06-09
; PRIOR APPLICATION NUMBER: 60/219,007
; PRIOR FILING DATE: 2000-07-18
; PRIOR APPLICATION NUMBER: 60/255,281
; PRIOR FILING DATE: 2000-12-13
; NUMBER OF SEQ ID NOS: 62232
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 22959
; LENGTH: 2924
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 1, 57, 2923, 2924
; OTHER INFORMATION: n = A,T,C or G
US-10-357-930-22959

Query Match 100.0%; Score 1274; DB 18; Length 2924;
Best Local Similarity 100.0%; Pred No. 0;
Matches 1274; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TTTCTTTAGTCTGTTTATGCTCCATTTTCTATTTTATTTAGCATTATTTATTTCTATGCTAT 60
Db 480 TTTCTTTAGTCTGTTTATGCTCCATTTTCTATTTTATTTAGCATTATTTATTTCTATGCTAT 539
QY 61 CCAAGACGATTAAGGAGTTCACATGTTTCCGGAACATTTTGAAGAGAGCTTATC 120
Db 540 CCAAGACGATTAAGGAGTTCACATGTTTCCGGAACATTTTGAAGAGAGCTTATC 599
QY 121 CAGTGTACAGATCCTTAATAAGTGACATTCAGTGTAAATTTTATTTTATATCTTTT 180
Db 600 CAGTGTACAGATCCTTAATAAGTGACATTCAGTGTAAATTTTATTTTATATCTTTT 659

QY 181 TTAATCTTATTTTCTCTCTCTTTGCTCAGTAAATTTTGTATGAAACTTTTAAAGGACT 240
Db 660 TTAATCTTATTTTCTCTCTCTTTGCTCAGTAAATTTTGTATGAAACTTTTAAAGGACT 719
QY 241 TATGGCATGTAACATTTATTTATAAGTAAGTCATGTTTATATTTTCTCTCTCTCTCT 300
Db 720 TATGGCATGTAACATTTATTTATAAGTAAGTCATGTTTATATTTTCTCTCTCTCTCT 779
QY 301 CTTTATGTTATTTTATTTTACAGAAATGAGCCCTCAGACTGTCTACAGCATTTACTACCGGTACC 360
Db 780 CTTTATGTTATTTTATTTTACAGAAATGAGCCCTCAGACTGTCTACAGCATTTACTACCGGTACC 839
QY 361 TCGAAGTGTCCACCATCCAGAGGGTCCCTGCTGACTGCGCACAACTGATGATCAACAT 420
Db 840 TCGAAGTGTCCACCATCCAGAGGGTCCCTGCTGACTGCGCACAACTGATGATCAACAT 899
QY 421 GACTTGGCGAGTCTTTTTCAGTGTCCAGTCTGCTTTGAGCTATGTGTTCACGCCCATCTTT 480
Db 900 GACTTGGCGAGTCTTTTTCAGTGTCCAGTCTGCTTTGAGCTATGTGTTCACGCCCATCTTT 959
QY 481 CAATGTACAGTGGCCATCTTCTTTGTAGCAACTGTGCGCCCAAAGCTCAGATGTTGTCCA 540
Db 960 CAATGTACAGTGGCCATCTTCTTTGTAGCAACTGTGCGCCCAAAGCTCAGATGTTGTCCA 1019
QY 541 ACTTGGCGGGGCCCTTTGGGATCCATTCGCAACTTGGCTATGAGAAAGTGGCTAATTTCA 600
Db 1020 ACTTGGCGGGGCCCTTTGGGATCCATTCGCAACTTGGCTATGAGAAAGTGGCTAATTTCA 1079
QY 601 GTACTTTTCCCTGTAAATATATCGCTTCTGATGTGAATTAACCTGCGCACACACAGAA 660
Db 1080 GTACTTTTCCCTGTAAATATATCGCTTCTGATGTGAATTAACCTGCGCACACACAGAA 1139
QY 661 AAAGCAGACCATGAAGAGCTCTGTGAGTTTAGGCCCTTATTCCTGTCGCGCCCTGCTGTCT 720
Db 1140 AAAGCAGACCATGAAGAGCTCTGTGAGTTTAGGCCCTTATTCCTGTCGCGCCCTGCTGTCT 1199
QY 721 TCCTGTAATGGCAAGGCTCTCTGATGCTGTAATGCCCCATCTGATGATGATGATGATGAT 780
Db 1200 TCCTGTAATGGCAAGGCTCTCTGATGCTGTAATGCCCCATCTGATGATGATGATGATGAT 1259
QY 781 TCCATTACAACTTACAGGAGAGATATAGTTTTTCTGCTACAGACATTAATCTTCTCT 840
Db 1260 TCCATTACAACTTACAGGAGAGATATAGTTTTTCTGCTACAGACATTAATCTTCTCT 1319
QY 841 GGTGCTGTTGACTGGGTGATGATGAGTCTCTGTTTGGCTTTTCACTTCACTTGTAGTCTTA 900
Db 1320 GGTGCTGTTGACTGGGTGATGATGAGTCTCTGTTTGGCTTTTCACTTCACTTGTAGTCTTA 1379
QY 901 GAGAAACAGGAAAAATACGATGGTCCAGAGAGTCTTCGCAATCGTACAGCTGATAGGA 960
Db 1380 GAGAAACAGGAAAAATACGATGGTCCAGAGAGTCTTCGCAATCGTACAGCTGATAGGA 1439
QY 961 ACACCGAAGCAGCTGAAATTTTCTTACCGACTTGAGCTAAATGGTCAATGGCCAGCA 1020
Db 1440 ACACCGAAGCAGCTGAAATTTTCTTACCGACTTGAGCTAAATGGTCAATGGCCAGCA 1499
QY 1021 TTGACTTTGGGAAGCGACTCTCTCGATCTATTTCATGAAGGAATTTGCAACAGCCATTTAAT 1080
Db 1500 TTGACTTTGGGAAGCGACTCTCTCGATCTATTTCATGAAGGAATTTGCAACAGCCATTTAAT 1559
QY 1081 AGCGATGCTTAGTCTTTGACACCGAGATGACAGCTTTTTCAGAGAAATGGCAATTTTA 1140
Db 1560 AGCGATGCTTAGTCTTTGACACCGAGATGACAGCTTTTTCAGAGAAATGGCAATTTTA 1619
QY 1141 GGCATCAATGTAACATTTTCCATGTTGAAATGGCAATCAACATTTTCTGCGCCAGTGT 1200
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QY 1201 TTAAACCTTCAGTTTTCACAGAAATTAAGGACCCATCTGCTGCGCAACCTTAAACCTTTT 1260
Db 1680 TTAAACCTTCAGTTTTCACAGAAATTAAGGACCCATCTGCTGCGCAACCTTAAACCTTTT 1739
QY 1261 CGGTAGGTGGAAGC 1274

Mon Apr 25 11:06:37 2005

1740 CCGTAGGTGAAGC 1753

RESULT 3

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US-10-357-930-25457
; Sequence 25457, Application US/10357930
; Publication No. US20040259086A1
; GENERAL INFORMATION:
; APPLICANT: Schlegel, Robert
; APPLICANT: Endege, Wilson
; APPLICANT: Monahan, John
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
; TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY OF
; TITLE OF INVENTION: HUMAN PROSTATE CANCER
; FILE REFERENCE: MRI-007BCN
; CURRENT APPLICATION NUMBER: US/10/357,930
; CURRENT FILING DATE: 2003-02-04
; PRIOR APPLICATION NUMBER: 09/785,276
; PRIOR FILING DATE: 2003-02-16
; PRIOR APPLICATION NUMBER: 60/183,319
; PRIOR FILING DATE: 2000-02-17
; PRIOR APPLICATION NUMBER: 60/189,862
; PRIOR FILING DATE: 2000-03-16
; PRIOR APPLICATION NUMBER: 60/207,454
; PRIOR FILING DATE: 2000-05-25
; PRIOR APPLICATION NUMBER: 60/211,314
; PRIOR FILING DATE: 2000-06-09
; PRIOR APPLICATION NUMBER: 60/219,007
; PRIOR FILING DATE: 2000-07-18
; PRIOR APPLICATION NUMBER: 60/255,281
; PRIOR FILING DATE: 2000-12-13
; NUMBER OF SEQ ID NOS: 62232
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 25457
; LENGTH: 2924
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 1, 57, 2923, 2924
; OTHER INFORMATION: n = A,T,C or G
US-10-357-930-25457

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Query Match	100.0%;	Score 1274;	DB 18;	Length 2924;
Best Local Similarity	100.0%;	Pred. No. 0;		
Matches 1274;	Conservative	0;	Mismatches 0;	Indels 0;
Gaps	0;			
QY	1	TTTTCTTTAGTTGTTTATCGTCCATTTTCTATTTTAGCATTTATTTATTTCTATGTAGTCTAT	60	
DB	480	TTTTCTTTAGTTGTTTATCGTCCATTTTCTATTTTAGCATTTATTTATTTCTATGTAGTCTAT	539	
QY	61	CCAAAGACGATTAAAGGAGTTCCACATGTTTTCCGGAA CATTTTGGAAAAGAGAGCTTATC	120	
DB	540	CCAAAGACGATTAAAGGAGTTCCACATGTTTTCCGGAA CATTTTGGAAAAGAGAGCTTATC	599	
QY	121	CAGGTACAGATCCTAATAAAGTGCACATTCAGTGTAAATTTATTTTTTTTAAATATCTTTT	180	
DB	600	CAGGTACAGATCCTAATAAAGTGCACATTCAGTGTAAATTTATTTTTTTTAAATATCTTTT	659	
QY	181	TTAAATCCATTTTTTCTTCTCTTTTGCTCAGTAAATTTTGTATGAAACTTTTAAAGGACT	240	
DB	660	TTAAATCCATTTTTTCTTCTCTTTTGCTCAGTAAATTTTGTATGAAACTTTTAAAGGACT	719	
QY	241	TATGGCATGTAAACATTTATTAAGTAAGTCATGGTTATAAATTTATTTTTCTCTCGCT	300	
DB	720	TATGGCATGTAAACATTTATTAAGTAAGTCATGGTTATAAATTTATTTTTCTCTCGCT	779	
QY	301	CCCTATGTATTTATTTTTCAGAAATGAGCCCGTCAGACTGCTACAGCATTACTACCGGTACC	360	
DB	780	CCCTATGTATTTATTTTTCAGAAATGAGCCCGTCAGACTGCTACAGCATTACTACCGGTACC	839	
QY	361	TCGAAAGTGTCACCAATCCAGAGGGTGCTGCCCTGACGTGGCACAAGCTGCACACAT	420	

840	Db	TCGAAGTGTCCACATCCCAGAGGGTCTGCGCTGACATGGGCACAACTGCATTCCAACAAT	899
421	QY	GACTTGGCGAGTCTTTTTCAGTGTCCAGTCTCGCTTTCGACTATGTGTGTACGGCCCAATCTTT	480
900	Db	GACTTGGCGAGTCTTTTTCAGTGTCCAGTCTCGCTTTCGACTATGTGTGTACGGCCCAATCTTT	959
481	QY	CAATGTCCAGAGTGGCCATCTTTTTCAGTGTCCAGTCTCGCTTTCGACTATGTGTGTACGGCCCAATCTTT	540
960	Db	CAATGTCCAGAGTGGCCATCTTTTTCAGTGTCCAGTCTCGCTTTCGACTATGTGTGTGTACGGCCCAATCTTT	1019
541	QY	ACTTGGCGGGCCCTTTGGGATCCATTCGCACTTGGCTATGGAGAAAGTGGCTAATTC	600
1020	Db	ACTTGGCGGGCCCTTTGGGATCCATTCGCACTTGGCTATGGAGAAAGTGGCTAATTC	1079
601	QY	GTACTTTTCCCTGTAAATATGCGTCTTCTGGATGTGAAATAACTCTGCCACACACAGAA	660
1080	Db	GTACTTTTCCCTGTAAATATGCGTCTTCTGGATGTGAAATAACTCTGCCACACACAGAA	1139
661	QY	AAAGCAGACATGAAGAGCTCTGTGAGTTTGTAGGCTTATTCGTGCTGCTGCTGCTGCTGCT	720
1140	Db	AAAGCAGACATGAAGAGCTCTGTGAGTTTGTAGGCTTATTCGTGCTGCTGCTGCTGCTGCT	1199
721	QY	TCCGTAAATGCGAAGCTCTCTGGATGCTGTAATGCCCATCTGATGCATCAGCATAAG	780
1200	Db	TCCGTAAATGCGAAGCTCTCTGGATGCTGTAATGCCCATCTGATGCATCAGCATAAG	1259
781	QY	TCCATTACAACCTTACAGGAGAGGATATAGTTTTTCTTGCTACAGACATTAATCTTCTCT	840
1260	Db	TCCATTACAACCTTACAGGAGAGGATATAGTTTTTCTTGCTACAGACATTAATCTTCTCT	1319
841	QY	GGTCTGTTGACTGGGTGATGATGCGAGTCTGCTGTTTGGCTTTCACATTCATGTTAGTCTTA	900
1320	Db	GGTCTGTTGACTGGGTGATGATGCGAGTCTGCTGTTTGGCTTTCACATTCATGTTAGTCTTA	1379
901	QY	GAGAAACAGGAAAAATACGATGTTCCAGCAGCTTCTTCGCAATCGTACAGCTGATAGGA	960
1380	Db	GAGAAACAGGAAAAATACGATGTTCCAGCAGCTTCTTCGCAATCGTACAGCTGATAGGA	1439
961	QY	ACACGCAAGCAGCTGAAAAATTTTGGCTTACCGACTTGGCTTTCAGCTGATAGGCAAGGA	1020
1440	Db	ACACGCAAGCAGCTGAAAAATTTTGGCTTACCGACTTGGCTTTCAGCTGATAGGCAAGGA	1499
1021	QY	TTGACTTTGGGAAGCGACTCTCTCGATCTATTTCATGAAGGAATTCGACAGCCATTAATGAAT	1080
1500	Db	TTGACTTTGGGAAGCGACTCTCTCGATCTATTTCATGAAGGAATTCGACAGCCATTAATGAAT	1559
1081	QY	AGCGACTGCTTAGTCTTTTGACAACAGCAATTCGACAGCTTTTTCGAGAAAAATGCAATTTTA	1140
1560	Db	AGCGACTGCTTAGTCTTTTGACAACAGCAATTCGACAGCTTTTTCGAGAAAAATGCAATTTTA	1619
1141	QY	GGCATCAATGTAACTATTTCATGTTGAAATGGCAATCAAAATTTTCTGGCCAGTGT	1200
1620	Db	GGCATCAATGTAACTATTTCATGTTGAAATGGCAATCAAAATTTTCTGGCCAGTGT	1679
1201	QY	TTAAAACTTCAGTTTTCAGAAAAATAAGGCCATCCATCTGTCTGCCAACCTTAAACCTCTTT	1260
1680	Db	TTAAAACTTCAGTTTTCAGAAAAATAAGGCCATCCATCTGTCTGCCAACCTTAAACCTCTTT	1739
1261	QY	CGGTAGGTGGAAGC	1274
1740	Db	CGGTAGGTGGAAGC	1753

RESULT 4

```

RESUL 4
US-10-357-930-28822
; Sequence 28822, Application US/10357930
; Publication No. US20040259086A1
; GENERAL INFORMATION:
; APPLICANT: Schlegel, Robert
; APPLICANT: Endege, Wilson
; APPLICANT: Monahan, John
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR

```

;; TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY OF
;; FILE REFERENCE: MRI-007BCN
;; CURRENT APPLICATION NUMBER: US/10/357,930
;; CURRENT FILING DATE: 2003-02-04
;; PRIOR APPLICATION NUMBER: 09/785,276
;; PRIOR FILING DATE: 2003-02-16
;; PRIOR APPLICATION NUMBER: 60/183,319
;; PRIOR FILING DATE: 2000-02-17
;; PRIOR APPLICATION NUMBER: 60/189,862
;; PRIOR FILING DATE: 2000-03-16
;; PRIOR APPLICATION NUMBER: 60/207,454
;; PRIOR FILING DATE: 2000-05-25
;; PRIOR APPLICATION NUMBER: 60/211,314
;; PRIOR FILING DATE: 2000-06-09
;; PRIOR APPLICATION NUMBER: 60/219,007
;; PRIOR FILING DATE: 2000-07-18
;; PRIOR APPLICATION NUMBER: 60/255,281
;; PRIOR FILING DATE: 2000-12-13
;; NUMBER OF SEQ ID NOS: 62232
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO 28822
;; LENGTH: 2924
;; TYPE: DNA
;; ORGANISM: Homo sapiens
;; FEATURE:
;; NAME/KEY: misc feature
;; LOCATION: 1, 57, 2923, 2924
;; OTHER INFORMATION: n = A,T,C or G
US-10-357-930-28822

Query Match 100.0%; Score 1274; DB 18; Length 2924;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1274; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTTCTTTAGTCTTTATGCTGCAATTTCTTATTTTACGATTTATTTCTATGCTAGTCTAT 60
DB |||||||
QY 61 CCAAAGCAGATTAAAGGAGTTCACATGTTTTCGGGAACATTTTGAAGAGAGAGCTTATC 120
DB |||||||
QY 121 CAGTGACAGATCTTAATAAGTGCACTTCAGTGTAATTTTATTTTATTTTATATCTTTT 180
DB |||||||
QY 600 CAGTGACAGATCTTAATAAGTGCACTTCAGTGTAATTTTATTTTATTTTATATCTTTT 659
QY 181 TTAATCCTATTTTCTTCTCTTTGCTCAGTAAATTTTGTATGAACCTTAAAGGACT 240
DB |||||||
QY 660 TTAATCCTATTTTCTTCTCTTTTGTCTCAGTAAATTTTGTATGAACCTTAAAGGACT 719
QY 241 TATGCGATGTAAACATTTATTTATAAGTAAGTCATGTTTATTAATTTTCTCTGCGCT 300
DB |||||||
QY 720 TATGCGATGTAAACATTTATTTATAAGTAAGTCATGTTTATTAATTTTCTCTGCGCT 779
QY 301 CTTTATGATTTATTTTACAGAAATGAGCCGTCAGACTGTACAGCAATTTACCTACCGGTACC 360
DB |||||||
QY 780 CTTTATGATTTATTTTACAGAAATGAGCCGTCAGACTGTACAGCAATTTACCTACCGGTACC 839
QY 361 TCGAAGTGTCCACCATCCAGAGGGTCTGCGCTGACTGGCAGCAACTGCATCCCAACAT 420
DB |||||||
QY 840 TCGAAGTGTCCACCATCCAGAGGGTCTGCGCTGACTGGCAGCAACTGCATCCCAACAT 899
QY 421 GACTTGGCGAGTCTTTTTCAGTGTCAGTCTGCTTTGACTATGTGTACCGCCCATCTTT 480
DB |||||||
QY 900 GACTTGGCGAGTCTTTTTCAGTGTCAGTCTGCTTTGACTATGTGTACCGCCCATCTTT 959
QY 481 CAATGTACAGATGGCCATCTTTGTTGTAGCAACTGTGCGCCCAAGCTCAATGTTGTCCA 540
DB |||||||
QY 960 CAATGTACAGATGGCCATCTTTGTTGTAGCAACTGTGCGCCCAAGCTCAATGTTGTCCA 1019
QY 541 ACTTGCGGGGGCCCTTTGGATGCCATTTGCCAATTTGGCTATGAGAGAAAGTGCGTAATCA 600
DB |||||||

DB 1020 ACTTGC CGGGGCCCTTTGGATCCATTGCAACTTGGCTATGAGAGAAAGTGGCTAATCA 1079
QY 601 GTACTTTTCCCTGTAAATATATGCTCTTCTGGATGTAAATTAATCTCTGCCACACAGAA 660
DB |||||||
DB 1080 GTACTTTTCCCTGTAAATATATGCTCTTCTGGATGTAAATTAATCTCTGCCACACAGAA 1139
QY 661 AAAGCAGACCATGAAGAGCTCTGTGAGTTTAGGCCCTTATTTCTGTGCGGCCCTGGTCT 720
DB |||||||
DB 1140 AAAGCAGACCATGAAGAGCTCTGTGAGTTTAGGCCCTTATTTCTGTGCGGCCCTGGTCT 1199
QY 721 TCTGTAAATGCAAGGCTCTCTGGATGCTGTAATGCCCATCTGATGATCAGCATAAG 780
DB |||||||
DB 1200 TCTGTAAATGCAAGGCTCTCTGGATGCTGTAATGCCCATCTGATGATCAGCATAAG 1259
QY 781 TCCATTACAAACCTCAGGGAGAGATATAGTTTTTTCTTGTCTACAGACATTAATCTTCCT 840
DB |||||||
DB 1260 TCCATTACAAACCTCAGGGAGAGATATAGTTTTTTCTTGTCTACAGACATTAATCTTCCT 1319
QY 841 GGTGCTGTTGACTGGGTGATGATGCTGCTGTTTGGCTTTTCACTTCATGTTAGTCTTA 900
DB |||||||
DB 1320 GGTGCTGTTGACTGGGTGATGATGCTGCTGTTTGGCTTTTCACTTCATGTTAGTCTTA 1379
QY 901 GAGAAACAGGAAAAATACGATGCTCACAGCAGCTTCTTCGCAATCGTACAGCTGATAGGA 960
DB |||||||
DB 1380 GAGAAACAGGAAAAATACGATGCTCACAGCAGCTTCTTCGCAATCGTACAGCTGATAGGA 1439
QY 961 ACACGCAAGCAAGCTGAAAAATTTTGTCTTACCGACTTGAGCTAAATGCTCATAGCGACGA 1020
DB |||||||
DB 1440 ACACGCAAGCAAGCTGAAAAATTTTGTCTTACCGACTTGAGCTAAATGCTCATAGCGACGA 1499
QY 1021 TTGACTTGGGAAGGACTCTCTGATCTATTCTATGAAGAAATGCAACAGCCATTAATGAAT 1080
DB |||||||
DB 1500 TTGACTTGGGAAGGACTCTCTGATCTATTCTATGAAGAAATGCAACAGCCATTAATGAAT 1559
QY 1081 AGCGACTGCTAGTCTTTTGCACACAGCATTGCAAGCTTTTTCAGAGAAATGCGCAATTTA 1140
DB |||||||
DB 1560 AGCGACTGCTAGTCTTTTGCACACAGCATTGCAAGCTTTTTCAGAGAAATGCGCAATTTA 1619
QY 1141 GGCATCAATGTAATTTTCCATGTTTGAATGCAATCAAAACATTTTCTGGCCAGTGT 1200
DB |||||||
DB 1620 GGCATCAATGTAATTTTCCATGTTTGAATGCAATCAAAACATTTTCTGGCCAGTGT 1679
QY 1201 TTAAACCTTCAGTTTTCAGAGAAATTAAGCACCCTATCTCTGTGCGCAACCTAAACCTCTTT 1260
DB |||||||
DB 1680 TTAAACCTTCAGTTTTCAGAGAAATTAAGCACCCTATCTCTGTGCGCAACCTAAACCTCTTT 1739
QY 1261 CGGTAGTGGAGC 1274
DB |||||||
DB 1740 CGGTAGTGGAGC 1753

RESULT 5
US-09-764-891-8070
; Sequence 8070, Application US/09764891
; Publication No. US20030077808A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PC006
; CURRENT APPLICATION NUMBER: US/09/764,891
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 10231
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 8070
; LENGTH: 6107
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-764-891-8070

Query Match 100.0%; Score 1274; DB 10; Length 6107;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1274; Conservative 0; Mismatches 0; Indels 0; Gaps 0;


```
QY 1 TTTCTTTAGTGTGTTATGGTCAATTTCTATTTTATGCAATTTATTTCTATGTAAGTCTAT 60
Db |||
3164 TTTCTTTAGTGTGTTATGGTCAATTTCTATTTTATGCAATTTATTTCTATGTAAGTCTAT 3223
QY 61 CCAAGAGAGATTAAAGGAGTTCCACATGTTTCCGGAACATTTTGAAAGAGAGAGCTTATC 120
Db |||
3224 CCAAGAGAGATTAAAGGAGTTCCACATGTTTCCGGAACATTTTGAAAGAGAGAGCTTATC 3283
QY 121 CAGTGTACAGATCCTAATAAAGTCACATTCAGTGTAAATTTTATTTTATTAATATCTTTT 180
Db |||
3284 CAGTGTACAGATCCTAATAAAGTCACATTCAGTGTAAATTTTATTTTATTAATATCTTTT 3343
QY 181 TTAATCCTATTTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 240
Db |||
3344 TTAATCCTATTTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 3403
QY 241 TATGTCATGTAACCAATTTATTAAGTAAGTCATGGTTATATTTATTTTCTCTCTGCT 300
Db |||
3404 TATGTCATGTAACCAATTTATTAAGTAAGTCATGGTTATATTTATTTTCTCTCTGCT 3463
QY 301 CTTTATGTTATTTATTCAGAAATGAGCGGTACAGTGTACAGCAATTTACCTACCGGTACC 360
Db |||
3464 CTTTATGTTATTTATTCAGAAATGAGCGGTACAGTGTACAGCAATTTACCTACCGGTACC 3523
QY 361 TCGAAGTGTCCACCATCCAGAGGGTGCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 420
Db |||
3524 TCGAAGTGTCCACCATCCAGAGGGTGCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3583
QY 421 GACTTGGCGAGTCTTTTTCAGTGTCCAGTGTCTGCTTGTGACTATGTTTACCGCCCATCTT 480
Db |||
3584 GACTTGGCGAGTCTTTTTCAGTGTCCAGTGTCTGCTTGTGACTATGTTTACCGCCCATCTT 3643
QY 481 CAATGTCAGAGTGGCAATCTTGTGTTAGCAACTGTGCGCCCAAGCTCAATGTTGTCCA 540
Db |||
3644 CAATGTCAGAGTGGCAATCTTGTGTTAGCAACTGTGCGCCCAAGCTCAATGTTGTCCA 3703
QY 541 ACTTGGCGGGCCCTTGGATGCCATTCGCACTTGGCTATGAGAAAGTGGCTAATTTCA 600
Db |||
3704 ACTTGGCGGGCCCTTGGATGCCATTCGCACTTGGCTATGAGAAAGTGGCTAATTTCA 3763
QY 601 GTACTTTTCCCTGTAAATATGCGTCTCTGGAATGTAATAACTCTGCAACACACAGAA 660
Db |||
3764 GTACTTTTCCCTGTAAATATGCGTCTCTGGAATGTAATAACTCTGCAACACACAGAA 3823
QY 661 AAGAGAGACATGAAGAGCTCTGTGAGTTTAGGCTTATTCCTGTCGCGTGGCTGTGCT 720
Db |||
3824 AAGAGAGACATGAAGAGCTCTGTGAGTTTAGGCTTATTCCTGTCGCGTGGCTGTGCT 3883
QY 721 TCTGTAAATGGCAAGGCTCTCTGGAATGCTGTAATGCCCATCTGATGCAATGAGCAATAAG 780
Db |||
3884 TCTGTAAATGGCAAGGCTCTCTGGAATGCTGTAATGCCCATCTGATGCAATGAGCAATAAG 3943
QY 781 TCCATTACAAACCTACAGGAGAGGATATAGTTTTTCTGCTACAGACATTAATCTTCCT 840
Db |||
3944 TCCATTACAAACCTACAGGAGAGGATATAGTTTTTCTGCTACAGACATTAATCTTCCT 4003
QY 841 GGTGCTGTTGACTGGGTGATGATGAGTCTGTGTTTTTGGCTTTTCACTTCATGTTAGTCTTA 900
Db |||
4004 GGTGCTGTTGACTGGGTGATGATGAGTCTGTGTTTTTGGCTTTTCACTTCATGTTAGTCTTA 4063
QY 901 GAGAAAACAGAAAATACAGATGTCACAGAGTCTCTTCCGAATCGTACAGCTGTAGGA 960
Db |||
4064 GAGAAAACAGAAAATACAGATGTCACAGAGTCTCTTCCGAATCGTACAGCTGTAGGA 4123
QY 961 ACACGCAAGCAAGCTGAAAATTTTGTCTTACCGACTTGAGCTTAATGGTCATAGGACGCA 1020
Db |||
4124 ACACGCAAGCAAGCTGAAAATTTTGTCTTACCGACTTGAGCTTAATGGTCATAGGACGCA 4183
QY 1021 TTGACTTGGGAAGGACTCTCTCATCTTATTCATGCAAGGATTCGAACAGCCATTAATGAAT 1080
Db |||
4184 TTGACTTGGGAAGGACTCTCTCATCTTATTCATGCAAGGATTCGAACAGCCATTAATGAAT 4243
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QY 1081 AGCGACTGTCTAGTCTTTTGACACACAGCATTTGCACAGCTTTTTCAGAAAATGGCAATTTA 1140
Db |||
4244 AGCGACTGTCTAGTCTTTTGACACACAGCATTTGCACAGCTTTTTCAGAAAATGGCAATTTA 4303
QY 1141 GGCATCAATGTAACATTTTCCATGTTGAAATGGCAATCAAAATTTTCTGGCCAGTGT 1200
Db |||
4304 GGCATCAATGTAACATTTTCCATGTTGAAATGGCAATCAAAATTTTCTGGCCAGTGT 4363
QY 1201 TTAACACTTCAGTTCACAGAAAATAAGGCAACCATCTGTCTGCAACCTAAAACTCTTTT 1260
Db |||
4364 TTAACACTTCAGTTCACAGAAAATAAGGCAACCATCTGTCTGCAACCTAAAACTCTTTT 4423
QY 1261 CGGTAGTGGGAAGC 1274
Db |||
4424 CGGTAGTGGGAAGC 4437

RESULT 6
US-10-108-260A-269
; Sequence 269, Application US/10108260A
; Publication No. US20040005560A1
; GENERAL INFORMATION:
; APPLICANT: HELIX RESEARCH INSTITUTE
; TITLE OF INVENTION: NO. US20040005560A1el full length cDNA
; FILE REFERENCE: H1-A0106
; CURRENT APPLICATION NUMBER: US/10/108,260A
; CURRENT FILING DATE: 2002-03-27
; NUMBER OF SEQ ID NOS: 5458
; SOFTWARE: PatentIn ver. 2.1
; SEQ ID NO 269
; LENGTH: 2829
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-108-260A-269

Query Match 96.0%; Score 1223; DB 17; Length 2829;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1273; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TTTCTTTAGTGTGTTATGGTCCATTTTCTATTTTATGCAATTTATTTCTATGTAAGTCTAT 60
Db |||
1134 TTTCTTTAGTGTGTTATGGTCCATTTTCTATTTTATGCAATTTATTTCTATGTAAGTCTAT 1193
QY 61 CCAAGAGAGATTAAAGGAGTTCCACATGTTTCCGGAACATTTTGAAAGAGAGAGCTTATC 120
Db |||
1194 CCAAGAGAGATTAAAGGAGTTCCACATGTTTCCGGAACATTTTGAAAGAGAGAGCTTATC 1253
QY 121 CAGTGTACAGATCCTAATAAAGTCACATTCAGTGTAAATTTTATTTTATTAATATCTTTT 180
Db |||
1254 CAGTGTACAGATCCTAATAAAGTCACATTCAGTGTAAATTTTATTTTATTAATATCTTTT 1313
QY 181 TTAATCCTATTTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 240
Db |||
1314 TTAATCCTATTTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1373
QY 241 TATGTCATGTAACCAATTTATTAAGTAAGTCATGGTTATATTTTCTCTCTGCTCT 300
Db |||
1374 TATGTCATGTAACCAATTTATTAAGTAAGTCATGGTTATATTTTCTCTCTGCTCT 1433
QY 301 CTTTATGTTATTTTATTCAGAAATGAGCGGTACAGTGTCTGCTGCTGCTGCTGCTGCTGCT 360
Db |||
1434 CTTTATGTTATTTATTTTCAGAAATGAGCGGTACAGTGTCTGCTGCTGCTGCTGCTGCTGCT 1493
QY 361 TCGAAGTGTCCACCATCCAGAGGGTGCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 420
Db |||
1494 TCGAAGTGTCCACCATCCAGAGGGTGCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1553
QY 421 GACTTGGCGAGTCTTTTTCAGTGTCCAGTGTCTGCTTGTGACTATGTTTACCGCCCATCTT 480
Db |||
1554 GACTTGGCGAGTCTTTTTCAGTGTCCAGTGTCTGCTTGTGACTATGTTTACCGCCCATCTT 1613
QY 481 CAATGTCAGAGTGGCAATCTTGTGTTAGCAACTGTGCGCCCAAGCTCAATGTTGTCCA 540
Db |||
```


Db 1614 CAAATGTCAGAGTGGCCATCTTTGTTGTAGCAACTGTGCCAAAGCTCACATGTTGTCCA 1673
Qy 541 ACTTGGCGGGGCCCTTTGGATCCATTCGAACTTCGGCTATGAGAAAGTGGCTAATCA 600
Db 1674 ACTTGGCGGGGCCCTTTGGATCCATTCGAACTTCGGCTATGAGAAAGTGGCTAATCA 1733
Qy 601 GTACTTTTCCCTGTAATAATGCTCTCTGGATGTGAATAACTCTGCCACACAGAA 660
Db 1734 GTACTTTTCCCTGTAATAATGCTCTCTGGATGTGAATAACTCTGCCACACAGAA 1793
Qy 661 AAAGCAGACCATGAAGAGCTCTGTAGTTTAGGCCCTTATTCCTGTCCGTGCCCTGGTCT 720
Db 1794 AAAGCAGACCATGAAGAGCTCTGTAGTTTAGGCCCTTATTCCTGTCCGTGCCCTGGTCT 1853
Qy 721 TCTGTAAATGGCAAGGCTCTCTGGATGTGAATAAGCCCATCTGATGATCAGCATAAG 780
Db 1854 TCTGTAAATGGCAAGGCTCTCTGGATGTGAATAAGCCCATCTGATGATCAGCATAAG 1913
Qy 781 TCATTACACCCCTCAGGAGAGGATATAGTTTCTTGTGCTACACACATTAATCTTCCT 840
Db 1914 TCATTACACCCCTCAGGAGAGGATATAGTTTCTTGTGCTACACACATTAATCTTCCT 1973
Qy 841 GGTGCTGTTGACTGGGTGATGATGAGTCTCTGTTTGGCTTTTACCTTCACTTGTAGTCTTA 900
Db 1974 GGTGCTGTTGACTGGGTGATGATGAGTCTCTGTTTGGCTTTTACCTTCACTTGTAGTCTTA 2033
Qy 901 GAGAAACAGGAAATAACGATGTCACAGAGTCTTTCGCAATCGTACAGCTGATAGGA 960
Db 2034 GAGAAACAGGAAATAACGATGTCACAGAGTCTTTCGCAATCGTACAGCTGATAGGA 2093
Qy 961 ACACGCAACGAGCTGAAATTTTGTCTACGACTTGGCTTAAGTGTATGAGCGACGA 1020
Db 2094 ACACGCAACGAGCTGAAATTTTGTCTACGACTTGGCTTAAGTGTATGAGCGACGA 2153
Qy 1021 TTGACTTTGGAAGCGACTCTCGATCTATTTCATGAAGGAATGCAACAGCCATTATGAAT 1080
Db 2154 TTGACTTTGGAAGCGACTCTCGATCTATTTCATGAAGGAATGCAACAGCCATTATGAAT 2213
Qy 1081 AGCGACTGTCTAGTCTTTGACACACGAGCATTTGACAGCTTTTTCGAGAAATGGCAATTTA 1140
Db 2214 AGCGACTGTCTAGTCTTTGACACACGAGCATTTGACAGCTTTTTCGAGAAATGGCAATTTA 2273
Qy 1141 GCATCAATGTAACATTTTCCATGTTTGAATGGAATCAACATTTTTCGCGCAGTGT 1200
Db 2274 GCATCAATGTAACATTTTCCATGTTTGAATGGAATCAACATTTTTCGCGCAGTGT 2333
Qy 1201 TTAATACTTCAGTTTTCACAGAAATAAGGACCCATCTCTGTCGCAACCTTAAATCTTTT 1260
Db 2334 TTAATACTTCAGTTTTCACAGAAATAAGGACCCATCTCTGTCGCAACCTTAAATCTTTT 2393
Qy 1261 CGGTAGGTGGAAGC 1274
Db 2394 CGGTAGGTGGAAGC 2407

RESULT 7

US-10-641-643-588
; Sequence 588, Application US/10641643
; Publication No. US20040077003A1

GENERAL INFORMATION:

APPLICANT: Cocks, Benjamin G.

Susan G. Stuart

Jeffrey J. Seilhamer

TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL

GENE EXPRESSION

NUMBER OF SEQUENCES: 1508

CORRESPONDENCE ADDRESS:

ADDRESSEE: INCYTE PHARMACEUTICALS, INC.

STREET: 3174 PORTER DRIVE

CITY: PALO ALTO

STATE: CALIFORNIA

COUNTRY: USA

ZIP: 94304

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
CURRENT APPLICATION DATA: US/10/641,643
APPLICATION NUMBER: 14-Aug-2003
FILING DATE: 14-Aug-2003
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: <Unknown>
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Zeller, Karen J.
REGISTRATION NUMBER: 37,071
REFERENCE/DOCKET NUMBER: PA-0001 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 855-0555
TELEFAX: (650) 845-4166
INFORMATION FOR SEQ ID NO: 588:
SEQUENCE CHARACTERISTICS:
LENGTH: 2440 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: SPLNFET01
CLONE: 29244
SEQUENCE DESCRIPTION: SEQ ID NO: 588 :
US-10-641-643-588

Query Match 81.7%; Score 1041; DB 17; Length 2440;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1041; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 234 AAGGACTTATGCGATGTAACATTTATTAAGTAAGTCATGGTTATATTTTCT 293
Db 467 AAGGACTTATGCGATGTAACATTTATTAAGTAAGTCATGGTTATATTTTCT 526
Qy 294 CCGTCTCTCTATGTTATTTTTCAGAAATGAGCGTCAGCTGCTACAGCATTACCTAC 353
Db 527 CCGTCTCTCTATGTTATTTTTCAGAAATGAGCGTCAGCTGCTACAGCATTACCTAC 586
Qy 354 CGGTACCTCGAAGTGTCCACCATCCAGAGGTGCTGCCCTGACTGGCACAACCTGCATC 413
Db 587 CGGTACCTCGAAGTGTCCACCATCCAGAGGTGCTGCCCTGACTGGCACAACCTGCATC 646
Qy 414 CAACATGACTTGGCGAGTCTTTTGTAGTGTCCAGTCTGCTTTGACTATGTGTACCGCC 473
Db 647 CAACATGACTTGGCGAGTCTTTTGTAGTGTCCAGTCTGCTTTGACTATGTGTACCGCC 706
Qy 474 CATTCTTCAATGTCAGAGTGGCCATCTTGTGTTGTAGCAACTGTGCCCAAGCTCACATG 533
Db 707 CATTCTTCAATGTCAGAGTGGCCATCTTGTGTTGTAGCAACTGTGCCCAAGCTCACATG 766
Qy 534 TTGTCCAACTTGGCGGGGCCCTTTGGGATCCATTCCCACTTTGGCTATGGAGAAAGTGGC 593
Db 767 TTGTCCAACTTGGCGGGGCCCTTTGGGATCCATTCCCACTTTGGCTATGGAGAAAGTGGC 826
Qy 594 TAAATTCAGTACTTTTCCCTGTAAATATGCGTCTTCTGAGATGGAATAACTCTGCCACA 653
Db 827 TAAATTCAGTACTTTTCCCTGTAAATATGCGTCTTCTGAGATGGAATAACTCTGCCACA 886
Qy 654 CACAGAAAAAGCAGACCATGAAGAGCTCTGTGAGTTTAGGCTTATTCCTGTCCGTGCC 713
Db 887 CACAGAAAAAGCAGACCATGAAGAGCTCTGTGAGTTTAGGCTTATTCCTGTCCGTGCC 946
Qy 714 TGGTCTTCTCTGTAATGGCAAGGCTCTCTGATGCTGTAAATGCCCATCTGATGATCA 773
Db 947 TGGTCTTCTCTGTAATGGCAAGGCTCTCTGATGCTGTAAATGCCCATCTGATGATCA 1006
Qy 774 GCATAAGTCCATTACAACCTTACAGGAGAGATAGTTTTTCTTGTGTACAGATTAA 833

Db	1007	GCATAAGTCCATTACAAACCCCTACAGGGAGAGGATATAGTTTTTTCTTGCTACAGACATTAA	1066
Qy	834	TCCTCCGTGCTGTTGACTGGGTGATGATGCAGTCTCTGTTTTGGCTTTTCACATTCACTGT	893
Db	1067	TCCTCCGTGCTGTTGACTGGGTGATGATGCAGTCTCTGTTTTGGCTTTTCACATTCACTGT	1126
Qy	894	AGTCTTTAGAAACACAGAAAAATACAGATGTCACAGCAGTTCCTTCGCAATCGTACAGCT	953
Db	1127	AGTCTTTAGAAACACAGAAAAATACAGATGTCACAGCAGTTCCTTCGCAATCGTACAGCT	1186
Qy	954	GATAGGAACACGGAAGCAAGCTGAAATTTTTGCTTACCGACTTTGACTAAATGGTCATAG	1013
Db	1187	GATAGGAACACGCAAGCAAGCTGAAATTTTTGCTTACCGACTTTGACTAAATGGTCATAG	1246
Qy	1014	CGCAGCATTGACTTTGGGAAGCGACTCTCGATCTATTTCATGAAGGAATTCGAACGCCAT	1073
Db	1247	CGCAGCATTGACTTTGGGAAGCGACTCTCGATCTATTTCATGAAGGAATTCGAACGCCAT	1306
Qy	1074	TATGAATAGCGACTGTCTAGTCTTTGACACGACGATTGCACAGCTTTTTCGAGAAATGG	1133
Db	1307	TATGAATAGCGACTGTCTAGTCTTTGACACGACGATTGCACAGCTTTTTCGAGAAATGG	1366
Qy	1134	CAATTTAGGCATCAATCTAACTATTTCATGTTGAAATGGCAATCAAAACATTTTCTGG	1193
Db	1367	CAATTTAGGCATCAATCTAACTATTTCATGTTGAAATGGCAATCAAAACATTTTCTGG	1426
Qy	1194	CCAGTGTTTAAACTCTCAGTTTTCACAGAAATTAAGGCACCCCATCTGTCTGCCAACCTAAA	1253
Db	1427	CCAGTGTTTAAACTCTCAGTTTTCACAGAAATTAAGGCACCCCATCTGTCTGCCAACCTAAA	1486
Qy	1254	ACTCTTTTCGGTAGTGGGAAGC	1274
Db	1487	ACTCTTTTCGGTAGTGGGAAGC	1507

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RESULT 8
US-09-925-297-84
; Sequence 84, Application US/09925297
; Patent No. US20020081659A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PA105
; CURRENT APPLICATION NUMBER: US/09/925,297
; CURRENT FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/05989
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 60/124,270
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 928
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 84
; LENGTH: 1535
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-297-84

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Qy	1099	GACACAGAGATTG	CACAGCTTTTT	GCAGAAAAAT	TGGCAATTT	TAGGCATCAAT	TGTAACCTATT	1155
Db	216	GACACAGACGATT	TGCACAGCTTTTT	TGCAGAAAAAT	TGGCAATTT	TAGGCATCAAT	TGTAACCTATT	275
Qy	1159	TCGATGTGTTGAAT	AGGCGCAATCA	AAACATTTTT	CTGGCCAGTGTTT	TAAACCTTCAGTTT	TCAC	1218
Db	276	TCGATGTGTTGAAT	AGGCGCAATCA	AAACATTTTT	CTGGCCAGTGTTT	TAAACCTTCAGTTT	TCAC	335
Qy	1219	AGAAAAATAGGCAC	CCCATCTGTCTG	CCCAACCTAAAA	ACTCTTT	CGGTAGTGGGAAGC	1274	
Db	336	AGAAAAATAGGCAC	CCCATCTGTCTG	CCCAACCTAAAA	ACTCTTT	CGGTAGTGGGAAGC	391	

RESULT 9
US-10-357-930-38440/c
; Sequence 38440, Application US/10357930
; Publication No. US20040259086A1
; GENERAL INFORMATION:
; APPLICANT: Schlegel, Robert
; APPLICANT: Endege, Wilson
; APPLICANT: Monahan, John
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
; TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY OF
; TITLE OF INVENTION: HUMAN PROSTATE CANCER
; FILE REFERENCE: MRI-007BCN
; CURRENT APPLICATION NUMBER: US/10/357,930
; CURRENT FILING DATE: 2003-02-04
; PRIOR APPLICATION NUMBER: 09/785,276
; PRIOR FILING DATE: 2003-02-16
; PRIOR APPLICATION NUMBER: 60/183,319
; PRIOR FILING DATE: 2000-02-17
; PRIOR APPLICATION NUMBER: 60/189,862
; PRIOR FILING DATE: 2000-03-16
; PRIOR APPLICATION NUMBER: 60/207,454
; PRIOR FILING DATE: 2000-05-25
; PRIOR APPLICATION NUMBER: 60/211,314
; PRIOR FILING DATE: 2000-06-09
; PRIOR APPLICATION NUMBER: 60/219,007
; PRIOR FILING DATE: 2000-07-18
; PRIOR APPLICATION NUMBER: 60/255,281
; PRIOR FILING DATE: 2000-12-13
; NUMBER OF SEQ ID NOS: 62232
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 38440
; LENGTH: 405
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-357-930-38440

RESULT 10
US-10-357-930-8510/c
; Sequence 8510, Application US/10357930
; Publication No. US2004025908A1
; GENERAL INFORMATION:
; APPLICANT: Schlegel, Robert
; APPLICANT: Endege, Wilson

```
; APPLICANT: Monahan, John
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
; TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY OF
; TITLE OF INVENTION: HUMAN PROSTATE CANCER
; FILE REFERENCE: MRI-007BCN
; CURRENT APPLICATION NUMBER: US/10/357,930
; CURRENT FILING DATE: 2003-02-04
; PRIOR APPLICATION NUMBER: 09/785,276
; PRIOR FILING DATE: 2003-02-16
; PRIOR APPLICATION NUMBER: 60/183,319
; PRIOR FILING DATE: 2000-02-17
; PRIOR APPLICATION NUMBER: 60/189,862
; PRIOR FILING DATE: 2000-03-16
; PRIOR APPLICATION NUMBER: 60/207,454
; PRIOR FILING DATE: 2000-05-25
; PRIOR APPLICATION NUMBER: 60/211,314
; PRIOR FILING DATE: 2000-06-09
; PRIOR APPLICATION NUMBER: 60/219,007
; PRIOR FILING DATE: 2000-07-18
; PRIOR APPLICATION NUMBER: 60/255,281
; PRIOR FILING DATE: 2000-12-13
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8510
; LENGTH: 277
; TYPE: DNA
; ORGANISM: Homo sapiens
; NAME/KEY: misc feature
; LOCATION: 213-214, 216, 218, 220, 224, 225, 233, 260, 265, 269
; OTHER INFORMATION: n = A,T,C or G
US-10-357-930-8510

Query Match      12.1%; Score 154; DB 18; Length 277;
Best Local Similarity 100.0%; Pred. No. 2.2e-70;
Matches 154; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 182 TAATCTATTTTCTCTCTTTTGGTCAGTAAATTTTGTATGAAACTTTAAAGACTT 241
Db 212 TAATCTATTTTCTCTCTTTTGGTCAGTAAATTTTGTATGAAACTTTAAAGACTT 153

QY 242 ATGGCATGTAACATTTATTAAGTAAATGATGTTATATTTTCTCTCTCTCTC 301
Db 152 ATGGCATGTAACATTTATTAAGTAAATGATGTTATATTTTCTCTCTCTCTC 93

QY 302 CTTATGATTTATTTTCAGAAATGAGCGGCAGAC 335
Db 92 CTTATGATTTATTTTCAGAAATGAGCGGCAGAC 59

RESULT 11
US-10-357-930-43808/c
; Sequence 43808, Application US/10357930
; Publication No. US20040259086A1
; GENERAL INFORMATION:
; APPLICANT: Schlegel, Robert
; APPLICANT: Endege, Wilson
; APPLICANT: Monahan, John
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
; TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY OF
; TITLE OF INVENTION: HUMAN PROSTATE CANCER
; FILE REFERENCE: MRI-007BCN
; CURRENT APPLICATION NUMBER: US/10/357,930
; CURRENT FILING DATE: 2003-02-04
; PRIOR APPLICATION NUMBER: 09/785,276
; PRIOR FILING DATE: 2003-02-16
; PRIOR APPLICATION NUMBER: 60/183,319
; PRIOR FILING DATE: 2000-02-17
; PRIOR APPLICATION NUMBER: 60/207,454
; PRIOR FILING DATE: 2000-03-16
; PRIOR APPLICATION NUMBER: 60/211,314
; PRIOR FILING DATE: 2000-05-25
; PRIOR APPLICATION NUMBER: 60/219,007
; PRIOR FILING DATE: 2000-07-18
; PRIOR APPLICATION NUMBER: 60/255,281
; PRIOR FILING DATE: 2000-12-13
; NUMBER OF SEQ ID NOS: 62232
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 43808
; LENGTH: 473
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-357-930-43808

Query Match      10.0%; Score 128; DB 18; Length 473;
Best Local Similarity 100.0%; Pred. No. 1.3e-56;
Matches 128; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 969 GCAAGCTGAAATTTTGTCTACCGACTTACGCTAAATGCTATAGCGCGACTTGTG 1028
Db 473 GCAAGCTGAAATTTTGTCTACCGACTTACGCTAAATGCTATAGCGCGACTTGTG 414
```

```
; PRIOR FILING DATE: 2000-06-09
; PRIOR APPLICATION NUMBER: 60/219,007
; PRIOR FILING DATE: 2000-07-18
; PRIOR APPLICATION NUMBER: 60/255,281
; PRIOR FILING DATE: 2000-12-13
; NUMBER OF SEQ ID NOS: 62232
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 43808
; LENGTH: 417
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-357-930-43808

Query Match      10.9%; Score 139; DB 18; Length 417;
Best Local Similarity 100.0%; Pred. No. 2e-62;
Matches 139; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1136 ATTTAGGCATCAATGTTAACTATTTCATGTTGTTGAATGGCAATCAAACTTTCTGGCC 1195
Db 413 ATTTAGGCATCAATGTTAACTATTTCATGTTGTTGAATGGCAATCAAACTTTCTGGCC 354

QY 1196 AGTGTTTAAACTTCAGTTTTCACAGAAAATAAGGCACCCATCTGTGCAACCTAAAC 1255
Db 353 AGTGTTTAAACTTCAGTTTTCACAGAAAATAAGGCACCCATCTGTGCAACCTAAAC 294

QY 1256 TCTTTCCGTTAGTGAAGC 1274
Db 293 TCTTTCCGTTAGTGAAGC 275

RESULT 12
US-10-357-930-48480/c
; Sequence 48480, Application US/10357930
; Publication No. US20040259086A1
; GENERAL INFORMATION:
; APPLICANT: Schlegel, Robert
; APPLICANT: Endege, Wilson
; APPLICANT: Monahan, John
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
; TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY OF
; TITLE OF INVENTION: HUMAN PROSTATE CANCER
; FILE REFERENCE: MRI-007BCN
; CURRENT APPLICATION NUMBER: US/10/357,930
; CURRENT FILING DATE: 2003-02-04
; PRIOR APPLICATION NUMBER: 09/785,276
; PRIOR FILING DATE: 2003-02-16
; PRIOR APPLICATION NUMBER: 60/183,319
; PRIOR FILING DATE: 2000-02-17
; PRIOR APPLICATION NUMBER: 60/189,862
; PRIOR FILING DATE: 2000-03-16
; PRIOR APPLICATION NUMBER: 60/207,454
; PRIOR FILING DATE: 2000-05-25
; PRIOR APPLICATION NUMBER: 60/211,314
; PRIOR FILING DATE: 2000-06-09
; PRIOR APPLICATION NUMBER: 60/219,007
; PRIOR FILING DATE: 2000-07-18
; PRIOR APPLICATION NUMBER: 60/255,281
; PRIOR FILING DATE: 2000-12-13
; NUMBER OF SEQ ID NOS: 62232
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 48480
; LENGTH: 473
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-357-930-48480

Query Match      10.0%; Score 128; DB 18; Length 473;
Best Local Similarity 100.0%; Pred. No. 1.3e-56;
Matches 128; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 969 GCAAGCTGAAATTTTGTCTACCGACTTACGCTAAATGCTATAGCGCGACTTGTG 1028
Db 473 GCAAGCTGAAATTTTGTCTACCGACTTACGCTAAATGCTATAGCGCGACTTGTG 414
```

RESULT 14
US-10-357-930-13819/c
; Sequence 13819, Application US/10357930
; Publication No. US20040259086A1
; GENERAL INFORMATION:
; APPLICANT: Schlengel, Robert
; APPLICANT: Endege, Wilson
; APPLICANT: Monahan, John
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
; TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY OF
; TITLE OF INVENTION: HUMAN PROSTATE CANCER
; FILE REFERENCE: MRI-007BCN
; CURRENT APPLICATION NUMBER: US/10/357,930
; CURRENT FILING DATE: 2003-02-04
; PRIOR APPLICATION NUMBER: 09/785,276
; PRIOR FILING DATE: 2003-02-16
; PRIOR APPLICATION NUMBER: 60/183,319
; PRIOR FILING DATE: 2000-02-17

; PRIOR APPLICATION NUMBER: 60/189,862
; PRIOR FILING DATE: 2000-03-16
; PRIOR APPLICATION NUMBER: 60/207,454
; PRIOR FILING DATE: 2000-05-25
; PRIOR APPLICATION NUMBER: 60/211,314
; PRIOR FILING DATE: 2000-06-09
; PRIOR APPLICATION NUMBER: 60/219,007
; PRIOR FILING DATE: 2000-07-18
; PRIOR APPLICATION NUMBER: 60/255,281
; PRIOR FILING DATE: 2000-12-13
; NUMBER OF SEQ ID NOS: 62232
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13819
; LENGTH: 411
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-357-930-13819

Query Match 9.3%; Score 118; DB 18; Length 411;
Best Local Similarity 100.0%; Pred. No. 2.6e-51;
Matches 118; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1157 TTTCATGTTGAAATGGAATCAAAACATTTCTGCGCCAGTGTTTTAAACTTCAGTTTC 1216
DB 364 TTTCATGTTGAAATGGAATCAAAACATTTCTGCGCCAGTGTTTTAAACTTCAGTTTC 305

QY 1217 ACAGAAATAAGGACCCCATCTCTGTCGCCAACCTAAACTTTTCGGTAGGTGGAAGC 1274
DB 304 ACAGAAATAAGGACCCCATCTCTGTCGCCAACCTAAACTTTTCGGTAGGTGGAAGC 247

RESULT 15
US-10-357-930-34958/c
; Sequence 34958, Application US/10357930
; Publication No. US20040259086A1
; GENERAL INFORMATION:
; APPLICANT: Schlegel, Robert
; APPLICANT: Endege, Wilson
; APPLICANT: Monahan, John
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
; TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY OF
; TITLE OF INVENTION: HUMAN PROSTATE CANCER
; FILE REFERENCE: MRI-007BCN
; CURRENT APPLICATION NUMBER: US/10/357,930
; CURRENT FILING DATE: 2003-02-04
; PRIOR APPLICATION NUMBER: 60/189,862
; PRIOR FILING DATE: 2003-02-16
; PRIOR APPLICATION NUMBER: 60/207,454
; PRIOR FILING DATE: 2000-05-25
; PRIOR APPLICATION NUMBER: 60/211,314
; PRIOR FILING DATE: 2000-06-09
; PRIOR APPLICATION NUMBER: 60/219,007
; PRIOR FILING DATE: 2000-07-18
; PRIOR APPLICATION NUMBER: 60/255,281
; NUMBER OF SEQ ID NOS: 62232
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 34958
; LENGTH: 441
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-357-930-34958

Query Match 9.3%; Score 118; DB 18; Length 441;
Best Local Similarity 100.0%; Pred. No. 2.6e-51;
Matches 118; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1157 TTTCATGTTGAAATGGAATCAAAACATTTCTGCGCCAGTGTTTTAAACTTCAGTTTC 1216

DB 399 TTTCATGTTGTTGAAATGGAATCAAAACATTTTCTGCGCCAGTGTTTTAAACTTCAGTTTC 340
QY 1217 ACAGAAATAAGGACCCCATCTCTGTCGCCAACCTAAACTTTTCGGTAGGTGGAAGC 1274
DB 339 ACAGAAATAAGGACCCCATCTCTGTCGCCAACCTAAACTTTTTCGGTAGGTGGAAGC 282

RESULT 16
US-10-357-930-4650/c
; Sequence 4650, Application US/10357930
; Publication No. US20040259086A1
; GENERAL INFORMATION:
; APPLICANT: Schlegel, Robert
; APPLICANT: Endege, Wilson
; APPLICANT: Monahan, John
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
; TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY OF
; TITLE OF INVENTION: HUMAN PROSTATE CANCER
; FILE REFERENCE: MRI-007BCN
; CURRENT APPLICATION NUMBER: US/10/357,930
; CURRENT FILING DATE: 2003-02-04
; PRIOR APPLICATION NUMBER: 60/189,862
; PRIOR FILING DATE: 2003-02-16
; PRIOR APPLICATION NUMBER: 60/207,454
; PRIOR FILING DATE: 2000-05-25
; PRIOR APPLICATION NUMBER: 60/211,314
; PRIOR FILING DATE: 2000-06-09
; PRIOR APPLICATION NUMBER: 60/219,007
; PRIOR FILING DATE: 2000-07-18
; PRIOR APPLICATION NUMBER: 60/255,281
; NUMBER OF SEQ ID NOS: 62232
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4650
; LENGTH: 438
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 106, 367, 418
; OTHER INFORMATION: n = A,T,C or G
US-10-357-930-4650

Query Match 6.7%; Score 85; DB 18; Length 438;
Best Local Similarity 100.0%; Pred. No. 8e-34;
Matches 85; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1190 CTGGCCAGTGTTTTAAACTTCAGTTTTCACAGAAATAAGGACCCCATCTCTGTCGCCAAC 1249
DB 366 CTGGCCAGTGTTTTAAACTTCAGTTTTCACAGAAATAAGGACCCCATCTCTGTCGCCAAC 307

QY 1250 TAAACTCTTTCGGTAGGTGGAAGC 1274
DB 306 TAAACTCTTTCGGTAGGTGGAAGC 282

RESULT 17
US-09-960-352-10011
; Sequence 10011, Application US/09960352
; Patent No. US20020137139A1
; GENERAL INFORMATION:
; APPLICANT: Warren, Wesley C.
; APPLICANT: Byatt, John C.
; APPLICANT: Mathialagan, Nagappan
; TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND
; FILE REFERENCE: 16511.006/37-21(10298)C
; CURRENT APPLICATION NUMBER: US/09/960,352

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QY 965 GCAAGCAAGCTGAAAAATTTTGGCTTACCGACTTGAGCTTAATGCTCATAGCG 1016
|||||
Db 426 GCAAGCAAGCTGAAAAATTTTGGCTTACCGACTTGAGCTTAATGCTCATAGCG 375

RESULT 19
US-10-425-115-63145
; Sequence 63145, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 63145
; LENGTH: 188
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(188)
; OTHER INFORMATION: unsure at all n locations
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_157588C.1
US-10-425-115-63145

Query Match 3.6%; Score 46; DB 18; Length 188;
Best Local Similarity 100.0%; Pred. No. 3.4e-13;
Matches 46; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 446 CAGTCTGCTTGCACTATGTTTACGCGCCATCTTCAATGTCAGAG 491
|||||
Db 143 CAGTCTGCTTGCACTATGTTTACGCGCCATCTTCAATGTCAGAG 188

RESULT 20
US-09-764-891-1549
; Sequence 1549, Application US/09764891
; Publication No. US20030077808A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: FC006
; CURRENT APPLICATION NUMBER: US/09/764,891
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 10231
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1549
; LENGTH: 222
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-764-891-1549

Query Match 2.6%; Score 33; DB 10; Length 222;
Best Local Similarity 100.0%; Pred. No. 2.7e-06;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 318 AGAAATGAGCGGTCAGACTGCTACAGCATTACC 350
|||||
Db 190 AGAAATGAGCGGTCAGACTGCTACAGCATTACC 222

RESULT 21
US-10-719-900-612660
; Sequence 612660, Application US/10719900
; Publication No. US20050026164A1

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; CURRENT FILING DATE: 2001-09-24
; NUMBER OF SEQ ID NOS: 15112
; SEQ ID NO 10011
; LENGTH: 360
; TYPE: DNA
; ORGANISM: Bos taurus
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (312)
; OTHER INFORMATION: unsure at all n locations
; OTHER INFORMATION: Clone ID: 43-LIB3058-032-Q1-K1-C4
US-09-960-352-10011

Query Match          4.9%; Score 62; DB 9; Length 360;
Best Local Similarity 100.0%; Pred. No. 1.2e-21;
Matches 62; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1120 TTTCGAGAAATGGCAATTTAGGCATCAATGTAACTATTTCCTATGTGTTGAAATGGCAAT 1179
Db       211 TTTCGAGAAATGGCAATTTAGGCATCAATGTAACTATTTCCTATGTGTTGAAATGGCAAT 270
QY      1180 CA 1181
Db       271 CA 272

RESULT 18
US-10-357-930-18669/c
; Sequence 18669, Application US/10357930
; Publication No. US20040259086A1
; GENERAL INFORMATION:
; APPLICANT: Schlegel, Robert
; APPLICANT: Endege, Wilson
; APPLICANT: Monahan, John
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
; TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY OF
; TITLE OF INVENTION: HUMAN PROSTATE CANCER
; FILE REFERENCE: MRI-007BCN
; CURRENT APPLICATION NUMBER: US/10/357,930
; CURRENT FILING DATE: 2003-02-04
; PRIOR APPLICATION NUMBER: 09/785,276
; PRIOR FILING DATE: 2003-02-16
; PRIOR APPLICATION NUMBER: 60/183,319
; PRIOR FILING DATE: 2000-02-17
; PRIOR APPLICATION NUMBER: 60/189,862
; PRIOR FILING DATE: 2000-03-16
; PRIOR APPLICATION NUMBER: 60/207,454
; PRIOR FILING DATE: 2000-05-25
; PRIOR APPLICATION NUMBER: 60/211,314
; PRIOR FILING DATE: 2000-06-09
; PRIOR APPLICATION NUMBER: 60/219,007
; PRIOR FILING DATE: 2000-07-18
; PRIOR APPLICATION NUMBER: 60/255,281
; PRIOR FILING DATE: 2000-12-13
; NUMBER OF SEQ ID NOS: 62232
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 18669
; LENGTH: 426.
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 43, 44, 46, 51, 54, 63, 73, 74, 79, 91, 93, 115, 116, 121,
; LOCATION: 150, 156, 157, 168, 175, 181, 184, 186, 190, 193, 200, 202,
; LOCATION: 205, 208, 213, 231, 239, 240, 252, 253, 254, 261, 302, 309,
; LOCATION: 358, 366, 374
; OTHER INFORMATION: n = A,T,C or G
US-10-357-930-18669

Query Match          4.1%; Score 52; DB 18; Length 426;
Best Local Similarity 100.0%; Pred. No. 2.4e-16;
Matches 52; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; PRIOR FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002-11-20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 612660
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
; US-10-719-900-612660

Query Match          2.0%; Score 25; DB 19; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.039;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1141 GGCATCAATGTAAGTATTTCCATGT 1165
      |||||
Db 1 GGCATCAATGTAAGTATTTCCATGT 25

RESULT 22
US-10-490-581-10/c
; Sequence 10, Application US/10490581
; Publication No. US20050070015A1
; GENERAL INFORMATION:
; APPLICANT: Nakamura, Yusuke
; APPLICANT: Furukawa, Yoichi
; APPLICANT: Japan as represented by
; APPLICANT: The President of the University of Tokyo
; APPLICANT: Oncotherapy Science, Inc.
; TITLE OF INVENTION: Methods of Regulating Growth and Death of Cancer Cells
; FILE REFERENCE: 082368-000400US
; CURRENT APPLICATION NUMBER: US/10/490,581
; CURRENT FILING DATE: 2004-03-18
; PRIOR APPLICATION NUMBER: JP 2001-290248
; PRIOR FILING DATE: 2001-09-21
; PRIOR APPLICATION NUMBER: WO PCT/JP02/08416
; PRIOR FILING DATE: 2002-08-21
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 10
; LENGTH: 33
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: artificially
; OTHER INFORMATION: synthesized sequence
US-10-490-581-10

Query Match          1.9%; Score 24; DB 19; Length 33;
Best Local Similarity 100.0%; Pred. No. 0.13;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1142 GGCATCAATGTAAGTATTTCCATGT 1165
      |||||
Db 33 GGCATCAATGTAAGTATTTCCATGT 10

RESULT 23
US-09-728-445-159
; Sequence 159, Application US/09728445
; Patent No. US20020102543A1
; GENERAL INFORMATION:
; APPLICANT: Friedrich, Glenn
; APPLICANT: Zambrowicz, Brian
; APPLICANT: Sands, Arthur T.
; TITLE OF INVENTION: No. US20020102543A1el Mutated Mammalian Cells and
; Animals

; GENERAL INFORMATION:
; FILE REFERENCE: LEX-0102-USA
; CURRENT APPLICATION NUMBER: US/09/728,445
; CURRENT FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/168,358
; PRIOR FILING DATE: 1999-12-01
; NUMBER OF SEQ ID NOS: 891
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 159
; LENGTH: 226
; TYPE: DNA
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(226)
; OTHER INFORMATION: n = A,T,C or G
US-09-728-445-159

Query Match          1.8%; Score 23; DB 9; Length 226;
Best Local Similarity 100.0%; Pred. No. 0.53;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 364 AAGTGTCCACCATCCGAGGGT 386
      |||||
Db 175 AAGTGTCCACCATCCGAGGGT 197

RESULT 24
US-10-424-599-69723
; Sequence 69723, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 69723
; LENGTH: 2466
; TYPE: DNA
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_33973C.1
US-10-424-599-69723

Query Match          1.7%; Score 22; DB 17; Length 2466;
Best Local Similarity 100.0%; Pred. No. 2.2;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 836 TTCCTGGTCTGTTGACTGGT 857
      |||||
Db 596 TTCCTGGTCTGTTGACTGGT 617

RESULT 25
US-10-490-581-5
; Sequence 5, Application US/10490581
; Publication No. US20050070015A1
; GENERAL INFORMATION:
; APPLICANT: Nakamura, Yusuke
; APPLICANT: Furukawa, Yoichi
; APPLICANT: Japan as represented by
; APPLICANT: The President of the University of Tokyo
; APPLICANT: Oncotherapy Science, Inc.
; TITLE OF INVENTION: Methods of Regulating Growth and Death of Cancer Cells
; FILE REFERENCE: 082368-000400US
; CURRENT APPLICATION NUMBER: US/10/490,581
; CURRENT FILING DATE: 2004-03-18
; PRIOR APPLICATION NUMBER: JP 2001-290248
```

```
; PRIOR FILING DATE: 2001-09-21
; PRIOR APPLICATION NUMBER: WO PCT/JP02/08416
; PRIOR FILING DATE: 2002-08-21
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: artificially
; OTHER INFORMATION: synthesized sequence
US-10-490-581-5

Query Match          1.6%; Score 21; DB 19; Length 21;
Best Local Similarity 100.0%; Pred. No. 5;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 412 TCCACAATGACTTGGCGAGT 432
Db 1 TCCACAATGACTTGGCGAGT 21

RESULT 26
US-10-490-581-6/c
; Sequence 6, Application US/10490581
; Publication No. US20050070015A1
; GENERAL INFORMATION:
; APPLICANT: Nakamura, Yusuke
; APPLICANT: Furukawa, Yoichi
; APPLICANT: Japan as represented by
; APPLICANT: The President of the University of Tokyo
; APPLICANT: Oncotherapy Science, Inc.
; TITLE OF INVENTION: Methods of Regulating Growth and Death of Cancer Cells
; FILE REFERENCE: 082368-000400US
; CURRENT APPLICATION NUMBER: US/10/490,581
; CURRENT FILING DATE: 2004-03-18
; PRIOR APPLICATION NUMBER: JP 2001-290248
; PRIOR FILING DATE: 2001-09-21
; PRIOR APPLICATION NUMBER: WO PCT/JP02/08416
; PRIOR FILING DATE: 2002-08-21
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: artificially
; OTHER INFORMATION: synthesized sequence
US-10-490-581-6

Query Match          1.6%; Score 21; DB 19; Length 21;
Best Local Similarity 100.0%; Pred. No. 5;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 644 CTCTGCCACACACAGAAAAG 664
Db 21 CTCTGCCACACACAGAAAAG 1

RESULT 27
US-10-719-900-37747
; Sequence 37747, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002-11-20

; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 257078
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-257078

Query Match          1.6%; Score 21; DB 19; Length 25;
Best Local Similarity 100.0%; Pred. No. 5.1;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 859 ATGATGCAGTCTCTGTTTGGC 879
Db 1 ATGATGCAGTCTCTGTTTGGC 21

RESULT 29
US-09-918-995-15609
; Sequence 15609, Application US/09918995
; Publication No. US20030073623A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
; FILE REFERENCE: 20411-756
; CURRENT APPLICATION NUMBER: US/09/918,995
; CURRENT FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: US/09/235,076
; PRIOR FILING DATE: 1999-01-20
; NUMBER OF SEQ ID NOS: 38054
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 15609
; LENGTH: 442
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)-(442)
; OTHER INFORMATION: n = A,T,C or G
US-09-918-995-15609

Query Match          1.6%; Score 21; DB 10; Length 442;
Best Local Similarity 100.0%; Pred. No. 6.4;
```


Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 165 TTTTAAATATCTTTTAAAT 185
Db 307 TTTTAAATATCTTTTAAAT 327

RESULT 30
US-10-425-115-119327
; Sequence 119327, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 119327
; LENGTH: 442
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(442)
; OTHER INFORMATION: unsure at all n locations
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_4030C.1
US-10-425-115-119327

Query Match 1.6%; Score 21; DB 18; Length 442;
Best Local Similarity 100.0%; Pred. No. 6.4;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 152 AGTGAATTTTATTTTAA 172
Db 151 AGTGAATTTTATTTTAA 171

RESULT 31
US-09-918-995-15341
; Sequence 15341, Application US/09918995
; Publication No. US20030073623A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
; TITLE OF INVENTION: FROM VARIOUS CDNA LIBRARIES
; FILE REFERENCE: 20411-756
; CURRENT APPLICATION NUMBER: US/09/918,995
; CURRENT FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: US/09/235,076
; PRIOR FILING DATE: 1999-01-20
; NUMBER OF SEQ ID NOS: 38054
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 15341
; LENGTH: 477
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(477)
; OTHER INFORMATION: n = A,T,C or G
US-09-918-995-15341

Query Match 1.6%; Score 21; DB 10; Length 477;
Best Local Similarity 100.0%; Pred. No. 6.5;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 165 TTTTAAATATCTTTTAAAT 185

Db 355 TTTTAAATATCTTTTAAAT 375

RESULT 32
US-10-627-757-10
; Sequence 10, Application US/10627757
; Publication No. US20040091914A1
; GENERAL INFORMATION:
; APPLICANT: KOUCHI YASUHIRO
; APPLICANT: MASASGO AKINORI
; APPLICANT: TAKAHATI TAKAYUKI
; TITLE OF INVENTION: GENE ASSAY METHOD FOR PREDICTING GLAUCOMA ONSET RISK
; FILE REFERENCE: Q76319
; CURRENT APPLICATION NUMBER: US/10/627,757
; CURRENT FILING DATE: 2003-07-28
; PRIOR APPLICATION NUMBER: JP P2002-226612
; PRIOR FILING DATE: 2002-08-02
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 10
; LENGTH: 1094
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-627-757-10

Query Match 1.6%; Score 21; DB 17; Length 1094;
Best Local Similarity 100.0%; Pred. No. 6.9;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 165 TTTTAAATATCTTTTAAAT 185
Db 478 TTTTAAATATCTTTTAAAT 498

RESULT 33
US-10-627-757-9
; Sequence 9, Application US/10627757
; Publication No. US20040091914A1
; GENERAL INFORMATION:
; APPLICANT: KOUCHI YASUHIRO
; APPLICANT: MASASGO AKINORI
; APPLICANT: TAKAHATI TAKAYUKI
; TITLE OF INVENTION: GENE ASSAY METHOD FOR PREDICTING GLAUCOMA ONSET RISK
; FILE REFERENCE: Q76319
; CURRENT APPLICATION NUMBER: US/10/627,757
; CURRENT FILING DATE: 2003-07-28
; PRIOR APPLICATION NUMBER: JP P2002-226612
; PRIOR FILING DATE: 2002-08-02
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 9
; LENGTH: 1150
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-627-757-9

Query Match 1.6%; Score 21; DB 17; Length 1150;
Best Local Similarity 100.0%; Pred. No. 7;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 165 TTTTAAATATCTTTTAAAT 185
Db 1006 TTTTAAATATCTTTTAAAT 1026

RESULT 34
US-10-091-281-2
; Sequence 2, Application US/10091281
; Publication No. US20030190617A1
; GENERAL INFORMATION:
; APPLICANT: RAYMOND, VINCENT
; APPLICANT: SI, ERWIN

APPLICANT: MORISETTE, JEAN
; TITLE OF INVENTION: OPTINEURIN NUCLEIC ACID MOLECULES AND USES THEREOF
; FILE REFERENCE: 13587.338
; CURRENT APPLICATION NUMBER: US/10/091,281
; CURRENT FILING DATE: 2002-03-06
; NUMBER OF SEQ ID NOS: 463
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 46951
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: allele
; LOCATION: 391
; OTHER INFORMATION: single nucleotide polymorphism (SNP)
; NAME/KEY: allele
; LOCATION: 691
; OTHER INFORMATION: single nucleotide polymorphism (SNP)
; NAME/KEY: allele
; LOCATION: 709
; OTHER INFORMATION: single nucleotide polymorphism (SNP)
; NAME/KEY: allele
; LOCATION: 887
; OTHER INFORMATION: single nucleotide polymorphism (SNP)
; NAME/KEY: allele
; LOCATION: 834
; OTHER INFORMATION: single nucleotide polymorphism (SNP)
; NAME/KEY: allele
; LOCATION: 987
; OTHER INFORMATION: single nucleotide polymorphism (SNP)
; NAME/KEY: allele
; LOCATION: 1112
; OTHER INFORMATION: single nucleotide polymorphism (SNP)
; NAME/KEY: allele
; LOCATION: 1505
; OTHER INFORMATION: insertion of additional c residue
; NAME/KEY: allele
; LOCATION: 1606
; OTHER INFORMATION: single nucleotide polymorphism (SNP)
; NAME/KEY: allele
; LOCATION: 2405
; OTHER INFORMATION: single nucleotide polymorphism (SNP)
; NAME/KEY: allele
; LOCATION: 2606
; OTHER INFORMATION: single nucleotide polymorphism (SNP)
; NAME/KEY: allele
; LOCATION: 3113
; OTHER INFORMATION: single nucleotide polymorphism (SNP)
; NAME/KEY: allele
; LOCATION: 3555
; OTHER INFORMATION: insertion of additional t residue
; NAME/KEY: allele
; LOCATION: 3625
; OTHER INFORMATION: single nucleotide polymorphism (SNP)
; NAME/KEY: allele
; LOCATION: 3629
; OTHER INFORMATION: single nucleotide polymorphism (SNP)
; NAME/KEY: allele
; LOCATION: 3882
; OTHER INFORMATION: insertion of additional t residue
; NAME/KEY: allele
; LOCATION: 3988
; OTHER INFORMATION: single nucleotide polymorphism (SNP)
; NAME/KEY: allele
; LOCATION: 4452
; OTHER INFORMATION: single nucleotide polymorphism (SNP)
; NAME/KEY: repeat region
; LOCATION: 598..878
; OTHER INFORMATION: repeat element
; NAME/KEY: repeat_region
; LOCATION: 938..957
; OTHER INFORMATION: Short repeat element
; NAME/KEY: repeat_region

LOCATION: 1002..1329
; OTHER INFORMATION: ALU repeat element
; NAME/KEY: repeat region
; LOCATION: 2288..2587
; OTHER INFORMATION: ALU repeat element
; NAME/KEY: misc feature
; LOCATION: 5054
; OTHER INFORMATION: putative transcription start site
US-10-091-281-2
Query Match 1.6%; Score 21; DB 16; Length 46951;
Best Local Similarity 100.0%; Pred. No. 9.5; Mismatches 0; Indels 0; Gaps 0;
Matches 21; Conservative 0;
QY 165 TTTTAAATATCTTTTAAAT 185
|||||
Db 30767 TTTTAAATATCTTTTAAAT 30787
|||||
RESULT 35
US-10-679-246-42
; Sequence 42, Application US/10679246
; Publication No. US20040163138A1
; GENERAL INFORMATION:
; APPLICANT: Reed, John C.
; TITLE OF INVENTION: Nucleic Acid Encoding Proteins Involved
; TITLE OF INVENTION: in Protein Degradation, Products and Methods Related Thereto
; FILE REFERENCE: 6821-235
; CURRENT APPLICATION NUMBER: US/10/679,246
; CURRENT FILING DATE: 2003-10-02
; PRIOR APPLICATION NUMBER: US 09/591,694
; PRIOR FILING DATE: 2000-06-09
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 42
; LENGTH: 28
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Primer
US-10-679-246-42
Query Match 1.6%; Score 20; DB 18; Length 28;
Best Local Similarity 100.0%; Pred. No. 17; Mismatches 0; Indels 0; Gaps 0;
Matches 20; Conservative 0;
QY 236 GGACTTATGGCATGTAACA 255
|||||
Db 9 GGACTTATGGCATGTAACA 28
|||||
RESULT 36
US-10-305-720-397
; Sequence 397, Application US/10305720
; Publication No. US20040010136A1
; GENERAL INFORMATION:
; APPLICANT: Au-Young, Janice K.; Seilhamer, Jeffrey J.
; TITLE OF INVENTION: Composition for the Detection of Signaling Pathway Gene Expression
; FILE REFERENCE: PA-0002-1 CON
; CURRENT APPLICATION NUMBER: US/10/305,720
; CURRENT FILING DATE: 2002-11-26
; PRIOR APPLICATION NUMBER: 09/016,434
; PRIOR FILING DATE: 1998-01-30
; NUMBER OF SEQ ID NOS: 1490
; SOFTWARE: PERL Program
; SEQ ID NO 397
; LENGTH: 257
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. US20040010136A1 2113436

US-10-305-720-397

Query Match 1.6%; Score 20; DB 17; Length 257;
Best Local Similarity 100.0%; Pred. No. 21;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 850 GACTGGGTGATGATGCAGTC 869
|||||
Db 222 GACTGGGTGATGATGCAGTC 241

RESULT 37

US-10-242-535A-55073
; Sequence 55073, Application US/10242535A
; Publication No. US20040013663A1
; GENERAL INFORMATION:
; APPLICANT: ChondroGene Inc.
; APPLICANT: Liew, C.C.

; TITLE OF INVENTION: Compositions and Methods Relating to Osteoarthritis
; FILE REFERENCE: 4231/2005
; CURRENT APPLICATION NUMBER: US/10/242,535A
; CURRENT FILING DATE: 2002-09-12
; PRIOR APPLICATION NUMBER: US 10/085,783
; PRIOR FILING DATE: 2002-02-28
; PRIOR APPLICATION NUMBER: US 60/305,340
; PRIOR FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: US 60/275,017
; PRIOR FILING DATE: 2001-03-12
; PRIOR APPLICATION NUMBER: US 60/271,955
; PRIOR FILING DATE: 2001-02-28
; NUMBER OF SEQ ID NOS: 58994
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 55073
; LENGTH: 335
; TYPE: DNA
; ORGANISM: Human

; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (6)..(6)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (9)..(9)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (20)..(20)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (65)..(65)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (318)..(319)
; OTHER INFORMATION: n is a, c, g, or t
US-10-242-535A-55073

Query Match 1.6%; Score 20; DB 17; Length 335;
Best Local Similarity 100.0%; Pred. No. 21;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 155 GTAATTTTATTTTAAATA 174
|||||
Db 43 GTAATTTTATTTTAAATA 62

RESULT 38

US-10-085-783A-55073
; Sequence 55073, Application US/10085783A
; Publication No. US20040037841A1
; GENERAL INFORMATION:
; APPLICANT: ChondroGene Inc.

; APPLICANT: Liew, C.C.
; TITLE OF INVENTION: Compositions and Methods Relating to Osteoarthritis
; FILE REFERENCE: 4231/2002
; CURRENT APPLICATION NUMBER: US/10/085,783A
; CURRENT FILING DATE: 2002-02-28
; PRIOR APPLICATION NUMBER: US 60/305,340
; PRIOR FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: US 60/275,017
; PRIOR FILING DATE: 2001-03-12
; PRIOR APPLICATION NUMBER: US 60/271,955
; PRIOR FILING DATE: 2001-02-28
; NUMBER OF SEQ ID NOS: 58994
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 55073
; LENGTH: 335
; TYPE: DNA
; ORGANISM: Human

; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (6)..(6)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (9)..(9)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (20)..(20)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (65)..(65)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (318)..(319)
; OTHER INFORMATION: n is a, c, g, or t
US-10-085-783A-55073

Query Match 1.6%; Score 20; DB 17; Length 335;
Best Local Similarity 100.0%; Pred. No. 21;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 155 GTAATTTTATTTTAAATA 174
|||||
Db 43 GTAATTTTATTTTAAATA 62

RESULT 39

US-10-027-632-317039/c
; Sequence 317039, Application US/10027632
; Publication No. US20020198371A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09

```

; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 317039
; LENGTH: 497
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-317039

Query Match
Best Local Similarity 100.0%; Score 20; DB 13; Length 497;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 231 TAAAGGACTTATGGCATGT 250
Db 159 TAAAGGACTTATGGCATGT 140

RESULT 40
US-10-027-632-317040/c
; Sequence 317040, Application US/10027632
; Publication No. US20020198371A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; PRIOR FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/195,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: Fast-Seq for Windows Version 4.0
; SEQ ID NO 317040
; LENGTH: 497
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-317040

Query Match
Best Local Similarity 100.0%; Score 20; DB 13; Length 497;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 231 TAAAGGACTTATGGCATGT 250
Db 159 TAAAGGACTTATGGCATGT 140

RESULT 41
US-10-027-632-317039/c
; Sequence 317039, Application US/10027632
; Publication No. US20030204075A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; PRIOR FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
```

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; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 317039
; LENGTH: 497
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-317039

Query Match
Best Local Similarity 100.0%; Score 20; DB 17; Length 497;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 231 TAAAGGACTTATGGCATGT 250
Db 159 TAAAGGACTTATGGCATGT 140

RESULT 42
US-10-027-632-317040/c
; Sequence 317040, Application US/10027632
; Publication No. US20030204075A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; PRIOR FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 317040
; LENGTH: 497
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-317040

Query Match
Best Local Similarity 100.0%; Score 20; DB 17; Length 497;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 231 TAAAGGACTTATGGCATGT 250
Db 159 TAAAGGACTTATGGCATGT 140

RESULT 43
US-10-027-632-88621/c
; Sequence 88621, Application US/10027632
```

; Publication No. US20020198371A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; TITLE OF INVENTION: Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 88621
; LENGTH: 498
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-88621

Query Match 1.6%; Score 20; DB 13; Length 498;
Best Local Similarity 100.0%; Pred. No. 22;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 231 TAAAGGACTTATGGCATGT 250
Db 159 TAAAGGACTTATGGCATGT 140

RESULT 44
US-10-027-632-88622/c
; Sequence 88622, Application US/10027632
; Publication No. US20020198371A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; TITLE OF INVENTION: Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 88622
; LENGTH: 498
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-88622

Query Match 1.6%; Score 20; DB 13; Length 498;

Best Local Similarity 100.0%; Pred. No. 22;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 231 TAAAGGACTTATGGCATGT 250
Db 159 TAAAGGACTTATGGCATGT 140

RESULT 45
US-10-027-632-88621/c
; Sequence 88621, Application US/10027632
; Publication No. US20030204075A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; TITLE OF INVENTION: Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 88621
; LENGTH: 498
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-88621

Query Match 1.6%; Score 20; DB 17; Length 498;
Best Local Similarity 100.0%; Pred. No. 22;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 231 TAAAGGACTTATGGCATGT 250
Db 159 TAAAGGACTTATGGCATGT 140

RESULT 46
US-10-027-632-88622/c
; Sequence 88622, Application US/10027632
; Publication No. US20030204075A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; TITLE OF INVENTION: Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28

; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 88622
; LENGTH: 498
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-88622

Query Match 1.6%; Score 20; DB 17; Length 498;
Best Local Similarity 100.0%; Pred. No. 22;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 231 TAAAGGACTTATGCGATCT 250
DB 159 TAAAGGACTTATGCGATCT 140

RESULT 47

US-10-027-632-91273/c
; Sequence 91273, Application US/10027632
; Publication No. US20020198371A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 91273
; LENGTH: 507
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-91273

Query Match 1.6%; Score 20; DB 13; Length 507;
Best Local Similarity 100.0%; Pred. No. 22;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 154 TGTAAATTTTATTTTAAAT 173
DB 407 TGTAAATTTTATTTTAAAT 388

RESULT 48

US-10-027-632-317676/c
; Sequence 317676, Application US/10027632
; Publication No. US20020198371A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006

; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 317676
; LENGTH: 507
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-317676

Query Match 1.6%; Score 20; DB 13; Length 507;
Best Local Similarity 100.0%; Pred. No. 22;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 154 TGTAAATTTTATTTTAAAT 173
DB 407 TGTAAATTTTATTTTAAAT 388

RESULT 49

US-10-027-632-91273/c
; Sequence 91273, Application US/10027632
; Publication No. US20030204075A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 91273
; LENGTH: 507
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-91273

Query Match 1.6%; Score 20; DB 17; Length 507;
Best Local Similarity 100.0%; Pred. No. 22;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 154 TGTAAATTTTATTTTAAAT 173
DB 407 TGTAAATTTTATTTTAAAT 388

RESULT 50

US-10-027-632-317676/c
; Sequence 317676, Application US/10027632
; Publication No. US20030204075A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 317676
; LENGTH: 507
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-317676

Query Match 1.6%; Score 20; DB 17; Length 507;
Best Local Similarity 100.0%; Pred. No. 22;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 154 TGTAAATTTTATTTTAAAT 173
|||
Db 407 TGTAAATTTTATTTTAAAT 388

Search completed: April 25, 2005, 06:36:57
Job time : 2403 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 25, 2005, 03:56:57 ; Search time 80 Seconds
(without alignments)
1440.682 Million cell updates/sec

Title: US-10-679-246-2

Perfect score: 1611

Sequence: 1 MWIIIFLLPPYVFIEMSRQ.....IAQLFAENGLGINTVISM 298

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_16Dec04:*
1: Geneseqp1980s:*
2: Geneseqp1990s:*
3: Geneseqp2000s:*
4: Geneseqp2001s:*
5: Geneseqp2002s:*
6: Geneseqp2003as:*
7: Geneseqp2003bs:*
8: Geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1611	100.0	298	4	AAB35157 Human Sia
2	1603	99.5	298	7	ADM04027 Human pro
3	1537	95.4	313	8	ADS34491 POSH prot
4	1532	95.1	282	8	ADS34492 POSH prot
5	1528	94.8	282	5	ABB84454 Murine mm
6	1528	94.8	282	5	ABB57146 Mouse isc
7	1522	94.5	282	5	ABB84452 Murine hss
8	1498	93.0	282	5	ABB84455 Murine hss
9	1489	92.4	282	2	AAW18520 Tumour su
10	1198	74.4	324	5	ABB84447 Human Sai
11	1198	74.4	324	5	ABB84453 Human hss
12	1198	74.4	324	6	ABR47593 Breast ca
13	1190	73.9	324	8	ADR14123 Human NF-
14	1190	73.9	324	5	ADP54831 Human PRO
15	1190	73.9	325	5	ABB84456 Murine mm
16	1190	73.9	325	5	ABB57147 Mouse isc
17	1153.5	71.6	314	4	ABB64778 Drosophi
18	1153.5	71.6	314	5	ABB84451 Siah-rela
19	1037.5	64.4	339	5	ABB84450 Siah-rela
20	530	32.9	310	4	ABB67709 Drosophi
21	447	27.7	284	3	AAG33121 Zea mays
22	447	27.7	313	3	AAV67582 Maize SIN
23	447	27.7	313	3	AAG33120 Zea mays
24	439	27.3	315	5	ABB84458 Siah-rela
25	434.5	27.0	297	3	AAG20022 Arabidops

26	434.5	27.0	297	3	AAG54067 Arabidops
27	434.5	27.0	308	3	AAG54066 Arabidops
28	434.5	27.0	308	3	AAG20021 Arabidops
29	432.5	26.8	290	3	AAG20023 Arabidops
30	432.5	26.8	290	3	AAG54068 Arabidops
31	432	26.8	89	3	AAB54091 Human pan
32	429	26.6	322	3	AAG31375 Arabidops
33	429	26.6	327	3	AAG31374 Arabidops
34	429	26.6	327	5	ABB84449 Siah-rela
35	423	26.3	321	3	AAG13847 Arabidops
36	423	26.3	326	3	AAG13846 Arabidops
37	423	26.3	361	3	AAG13845 Arabidops
38	422	26.2	305	3	AAG30769 Arabidops
39	422	26.2	305	5	ABB84448 Siah-rela
40	421	26.1	281	3	AAG30770 Arabidops
41	421	26.1	347	3	AAG35743 Zea mays
42	421	26.1	349	3	AAG35742 Zea mays
43	421	26.1	373	3	AAG35741 Zea mays
44	419	26.0	321	3	AAG53803 Arabidops
45	419	26.0	326	3	AAG53802 Arabidops

ALIGNMENTS

RESULT 1
AAB35157
ID AAB35157 standard; protein; 298 AA.

AC AAB35157;

XX 09-APR-2001 (first entry)

XX Human Siah-1alpha SEQ ID NO: 2.

Human; protein degradation; siah-mediated degradation protein; SMDF;
SCF-complex protein; SCP; siah-1alpha; siah-1 interacting protein; SIP;
Skp1-associated F-box protein; SAF-1; SAF-2; SAD; cancer; cell division;
Skp1-associated destruction-box protein; inflammatory disease.

OS Homo sapiens.

XX WO200077207-A2.

PN 21-DEC-2000.

XX 09-JUN-2000; 2000WO-US015873.

XX 11-JUN-1999; 99US-00330517.

XX (BURN-) BURNHAM INST.

XX Reed JC, Matsuzawa S;

XX WPI; 2001-071273/08.

XX N-PSDB; AAG67281.

Siah-Mediated Degradation Protein, useful for drug screening, for
therapeutic applications and for functional genomics.

Claim 15; Page 97; 121pp; English.

The present invention provides the protein and coding sequences of
several siah-mediated degradation proteins and SCF-complex proteins.
These are designated Siah-1alpha, Siah-1 interacting protein (SIP), which
encodes two proteins due to alternative splicing (SIP-L and SIP-S), Skp1-
associated F-box protein-lalpha and beta and -2 (SAF-lalpha, SAF-lbeta
and SAF-2) and Skp1-associated destruction-box protein (SAD). The
proteins and their coding sequences are useful in the diagnosis and
treatment of cancers, disorders where too little cell division occurs
such as bone marrow aplasia, immunodeficiencies and inflammatory
diseases including sepsis, fibrosis, arthritis and graft versus host
disease

are useful as pharmaceutical agents. The present sequence represents a protein sequence of the invention.

Query Match 99.5%; Score 1603; DB 7; Length 298;
Best Local Similarity 99.7%; Pred. No. 4.8e-149;
Matches 297; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MVIIFLLPPVYFISEMSRQTATLPTGTSKPPSQRPALPTGTTASNDLASLFECPVC 60
DB 1 MVIIFLLPPVYFISEMSRQTATLPTGTSKPPSQRPALPTGTTASNDLASLFECPVC 60
QY 61 FDYVLPPILOQSGHLVCSNCRPKLTCCPTCRGLSGIRNLAMEKVANSVLPCKYASSG 120
DB 61 FDYVLPPILOQSGHLVCSNCRPKLTCCPTCRGLSGIRNLAMEKVANSVLPCKYASSG 120
QY 121 CEITLPHTKADHEELCEFRPYSCPGASCCKWQSLDAMPHLMHQHKSITTLQGEDIV 180
DB 121 CEITLPHTKADHEELCEFRPYSCPGASCCKWQSLDAMPHLMHQHKSITTLQGEDIV 180
QY 181 FLATDINLPGAVDWMQSCFGFHFMLVLEKQKYDGHQOQFAIVQLIGTRKQAFAYR 240
DB 181 FLATDINLPGAVDWMQSCFGFHFMLVLEKQKYDGHQOQFAIVQLIGTRKQAFAYR 240
QY 241 LELNGHRRRLTWEATPRSIHEGIATAMNSDCLVFDTSIAQLFAENGNGINVTISM 298
DB 241 LELNGHRRRLTWEATPRSIHEGIATAMNSDCLVFDTSIAQLFAENGNGINVTISM 298

RESULT 3
ADS34491
ID ADS34491 standard; protein; 313 AA.
AC ADS34491;
XX
DT 02-DEC-2004 (first entry)
XX
DE POSH protein associated protein #55.
XX
KW cytostatic; nootropic; neuroprotective; antiparkinsonian; anticonvulsant;
KW antiviral; neuroleptic; central nervous system; POSH polypeptide;
KW POSH-associated protein; POSH-AP; HERPULI; Ubiquitin ligase;
KW antiviral agent; anti-apoptotic agent; anti-cancer agent;
KW secretory pathway trafficking inhibitor;
KW neurological disorder progression disorder; Alzheimer's disease;
KW Parkinson's disease; Huntington's disease; schizophrenia;
KW Niemann-Pick's disease.
XX
OS Homo sapiens.
XX
PN WO2004078130-A2.
XX
PD 16-SEP-2004.
XX
PF 02-MAR-2004; 2004WO-US006308.
XX
PR 03-MAR-2003; 2003US-0451437P.
PR 05-MAR-2003; 2003US-0452284P.
PR 19-MAR-2003; 2003US-0455760P.
PR 20-MAR-2003; 2003US-0456640P.
PR 03-APR-2003; 2003US-0460526P.
PR 04-APR-2003; 2003US-0460792P.
PR 21-APR-2003; 2003US-0464285P.
PR 09-MAY-2003; 2003US-0469462P.
PR 15-MAY-2003; 2003US-0471378P.
PR 20-MAY-2003; 2003US-0472327P.
PR 30-MAY-2003; 2003US-0474706P.
PR 03-JUN-2003; 2003US-0475825P.
PR 17-JUN-2003; 2003US-0479317P.
PR 19-JUN-2003; 2003US-0480215P.
PR 19-JUN-2003; 2003US-0480376P.
PR 08-AUG-2003; 2003US-0493860P.

Query Match 100.0%; Score 1611; DB 4; Length 298;
Best Local Similarity 100.0%; Pred. No. 7.8e-150;
Matches 298; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MVIIFLLPPVYFISEMSRQTATLPTGTSKPPSQRPALPTGTTASNDLASLFECPVC 60
DB 1 MVIIFLLPPVYFISEMSRQTATLPTGTSKPPSQRPALPTGTTASNDLASLFECPVC 60
QY 61 FDYVLPPILOQSGHLVCSNCRPKLTCCPTCRGLSGIRNLAMEKVANSVLPCKYASSG 120
DB 61 FDYVLPPILOQSGHLVCSNCRPKLTCCPTCRGLSGIRNLAMEKVANSVLPCKYASSG 120
QY 121 CEITLPHTKADHEELCEFRPYSCPGASCCKWQSLDAMPHLMHQHKSITTLQGEDIV 180
DB 121 CEITLPHTKADHEELCEFRPYSCPGASCCKWQSLDAMPHLMHQHKSITTLQGEDIV 180
QY 181 FLATDINLPGAVDWMQSCFGFHFMLVLEKQKYDGHQOQFAIVQLIGTRKQAFAYR 240
DB 181 FLATDINLPGAVDWMQSCFGFHFMLVLEKQKYDGHQOQFAIVQLIGTRKQAFAYR 240
QY 241 LELNGHRRRLTWEATPRSIHEGIATAMNSDCLVFDTSIAQLFAENGNGINVTISM 298
DB 241 LELNGHRRRLTWEATPRSIHEGIATAMNSDCLVFDTSIAQLFAENGNGINVTISM 298

RESULT 2
ADM04027
ID ADM04027 standard; protein; 298 AA.
AC ADM04027;
XX
DT 20-MAY-2004 (first entry)
XX
DE Human protein of the invention SEQ ID NO:2712.
XX
KW human; gene therapy; diagnostic marker; pharmaceutical.
XX
OS Homo sapiens.
XX
PN EP1347046-A1.
XX
PD 24-SEP-2003.
XX
PF 12-APR-2002; 2002EP-00008400.
XX
PR 22-MAR-2002; 2002JP-00137785.
XX
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
XX
PI Isogai T, Sugiyama T, Otsuki T, Wakamatsu A, Sato H, Ishii S;
PI Yamamoto J, Isono Y, Hio Y, Otsuka K, Nagai K, Irie R, Tamechika I;
PI Seki N, Yoshikawa T, Otsuka M, Nagahari K, Masuho Y;
XX
XX WPI; 2003-723558/69.
DR N-PSDB; ADM01584.
XX
XX New polynucleotides and polypeptides are useful in gene therapy, for
PT developing a diagnostic marker or medicines for regulating their
PT expression and activity, or as a target of gene therapy.
XX
XX Claim 1; SEQ ID NO 2712; 305pp; English.
XX
XX The invention relates to a novel human polynucleotide and the encoded
CC polypeptide. A polynucleotide of the invention may have a use in gene
CC therapy. An oligonucleotide of the invention ADM06202-ADM06773 is useful
CC as a primer for synthesizing the polynucleotide or as a probe for
CC detecting the polynucleotide. The polynucleotides ADM01316-ADM03758 are
CC useful in gene therapy, for developing a diagnostic marker or medicines
CC for regulating their expression and activity, or as a target of gene
CC therapy. The proteins ADM03759-ADM06201 encoded by the polynucleotides

PR 28-AUG-2003; 2003US-0498634P.
 PR 16-SEP-2003; 2003US-0503931P.
 PR 10-NOV-2003; 2003WO-US035712.
 PR 05-FEB-2004; 2004WO-US003600.
 PR 02-MAR-2004; 2004US-0549896P.
 XX
 PA (PROT-) PROTEOLOGICS INC.
 XX
 XX Taglicht DN, Alroy I, Reiss Y, Yaar L, Ben-Avraham D, Tuvia S;
 PI Greener T;
 XX WPI; 2004-662346/64.
 XX
 XX Isolated, purified or recombinant complex, useful for identifying an
 PT antiviral, anti-apoptotic or anti-cancer, comprising POSH polypeptide and
 PT POSH-associated protein (POSH-AP).
 XX
 XX Disclosure; SEQ ID NO 255; 374pp; English.
 PS
 XX The invention relates to an isolated, purified or recombinant complex (I)
 CC comprising a POSH polypeptide and a POSH-associated protein (POSH-AP) (a)
 CC or HERPUDI and a ubiquitin ligase (b). Methods using (I), (a) or (b) are
 CC useful for identifying an agent that modulates an activity of a POSH
 CC polypeptide or POSH-AP, for identifying an antiviral agent, an anti-
 CC apoptotic agent, an anti-cancer agent, an agent that inhibits trafficking
 CC of a protein through the secretory pathway, an agent that inhibits the
 CC progression of a neurological disorder, an agent that modulates a POSH
 CC function, an agent that modulates a HERPUDI function. The methods can be
 CC used for treating a viral infection, for inhibiting an activity of a POSH
 CC -AP in a cell, for treating a POSH-associated disease in a subject. The
 CC POSH-associated disease is viral infection, POSH-associated cancer or
 CC POSH-associated neurological disorder. The methods are useful for
 CC treating or preventing POSH-associated neurological disorder in a subject
 CC e.g. Alzheimer's disease, Parkinson's disease, Huntington's disease,
 CC schizophrenia, Niemann-Pick's disease. This sequence corresponds to a
 CC protein of the invention.
 XX
 XX Sequence 313 AA;
 SQ
 Query Match 95.4%; Score 1537; DB 8; Length 313;
 Best Local Similarity 100.0%; Pred. No. 1.6e-142; Mismatches 0; Gaps 0;
 Matches 283; Conservative 0; Indels 0;
 QY 16 EMSQTATALPTGTSKCPSPQRPVLTGTTASNNDLASLFECPCFVYVLPPILOCSGH 75
 DB 31 EMSQTATALPTGTSKCPSPQRPVLTGTTASNNDLASLFECPCFVYVLPPILOCSGH 90
 QY 76 LVCSNCRPKLTCCPTCRGLSIRNLAMEKVANSVLPCKYASSGCEITLPHTEKADHDEE 135
 DB 91 LVCSNCRPKLTCCPTCRGLSIRNLAMEKVANSVLPCKYASSGCEITLPHTEKADHDEE 150
 QY 136 LCEFRPYSCPCGACCKWQSLDVMVPHLMHQHSITTLQGEDIVFLATDINLPADVWV 195
 DB 151 LCEFRPYSCPCGACCKWQSLDVMVPHLMHQHSITTLQGEDIVFLATDINLPADVWV 210
 QY 196 MMQSCFGFHMVLVEKQEKYDGHQFQFAIVOLIGTRKQAFNAYRLNGLHRRRLTWEAT 255
 DB 211 MMQSCFGFHMVLVEKQEKYDGHQFQFAIVOLIGTRKQAFNAYRLNGLHRRRLTWEAT 270
 QY 256 PRSIEHGIATAMNSDCLVDFTSIAQLFENGLNINVTISM 298
 DB 271 PRSIEHGIATAMNSDCLVDFTSIAQLFENGLNINVTISM 313
 RESULT 4
 ADS34492
 ID ADS34492 standard; protein; 282 AA.
 XX
 AC ADS34492;
 XX
 DT 02-DEC-2004 (first entry)
 XX
 DE POSH protein associated protein #56.

XX cytostatic; neurotropic; neuroprotective; antiparkinsonian; anticonvulsant;
 KW antiviral; neuroleptic; central nervous system; POSH polypeptide;
 KW POSH-associated protein; POSH-AP; HERPUDI; Ubiquitin ligase;
 KW antiviral agent; anti-apoptotic agent; anti-cancer agent;
 KW secretory pathway trafficking inhibitor;
 KW neurological disorder progression disorder; Alzheimer's disease;
 KW Parkinson's disease; Huntington's disease; schizophrenia;
 KW Niemann-Pick's disease.
 XX
 OS Homo sapiens.
 XX
 XX WO2004078130-A2.
 XX
 PD 16-SEP-2004.
 XX
 XX 02-MAR-2004; 2004WO-US006308.
 XX
 PR 03-MAR-2003; 2003US-0451437P.
 PR 05-MAR-2003; 2003US-0452284P.
 PR 19-MAR-2003; 2003US-0455760P.
 PR 20-MAR-2003; 2003US-0456640P.
 PR 03-APR-2003; 2003US-0460526P.
 PR 04-APR-2003; 2003US-0460792P.
 PR 21-APR-2003; 2003US-0464285P.
 PR 09-MAY-2003; 2003US-0469462P.
 PR 15-MAY-2003; 2003US-0471378P.
 PR 20-MAY-2003; 2003US-0472327P.
 PR 30-MAY-2003; 2003US-0474706P.
 PR 03-JUN-2003; 2003US-0475825P.
 PR 17-JUN-2003; 2003US-0479317P.
 PR 19-JUN-2003; 2003US-0480215P.
 PR 19-JUN-2003; 2003US-0480376P.
 PR 08-AUG-2003; 2003US-0493860P.
 PR 28-AUG-2003; 2003US-0498634P.
 PR 16-SEP-2003; 2003US-0503931P.
 PR 10-NOV-2003; 2003WO-US035712.
 PR 05-FEB-2004; 2004WO-US003600.
 PR 02-MAR-2004; 2004US-0549896P.
 XX
 XX (PROT-) PROTEOLOGICS INC.
 PA
 XX Taglicht DN, Alroy I, Reiss Y, Yaar L, Ben-Avraham D, Tuvia S;
 PI Greener T;
 XX WPI; 2004-662346/64.
 XX
 XX Isolated, purified or recombinant complex, useful for identifying an
 PT antiviral, anti-apoptotic or anti-cancer, comprising POSH polypeptide and
 PT POSH-associated protein (POSH-AP).
 XX
 XX Disclosure; SEQ ID NO 256; 374pp; English.
 PS
 XX The invention relates to an isolated, purified or recombinant complex (I)
 CC comprising a POSH polypeptide and a POSH-associated protein (POSH-AP) (a)
 CC or HERPUDI and a ubiquitin ligase (b). Methods using (I), (a) or (b) are
 CC useful for identifying an agent that modulates an activity of a POSH
 CC polypeptide or POSH-AP, for identifying an antiviral agent, an anti-
 CC apoptotic agent, an anti-cancer agent, an agent that inhibits trafficking
 CC of a protein through the secretory pathway, an agent that inhibits the
 CC progression of a neurological disorder, an agent that modulates a POSH
 CC function, an agent that modulates a HERPUDI function. The methods can be
 CC used for treating a viral infection, for inhibiting an activity of a POSH
 CC -AP in a cell, for treating a POSH-associated disease in a subject. The
 CC POSH-associated disease is viral infection, POSH-associated cancer or
 CC POSH-associated neurological disorder. The methods are useful for
 CC treating or preventing POSH-associated neurological disorder in a subject
 CC e.g. Alzheimer's disease, Parkinson's disease, Huntington's disease,
 CC schizophrenia, Niemann-Pick's disease. This sequence corresponds to a
 CC protein of the invention.
 XX
 XX Sequence 282 AA;
 SQ

Query Match 95.1%; Score 1532; DB 8; Length 282;
Best Local Similarity 100.0%; Pred. No. 4.4e-142;
Matches 282; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 17 MSRTATATLPTGTSKCPSPQSRVPALTTASNNDLASLFECPCFDYVLPPILOQSGHL 76
DB 1 MSRTATATLPTGTSKCPSPQSRVPALTTASNNDLASLFECPCFDYVLPPILOQSGHL 60

QY 77 VCSNCRPKLTCCPTCRGPIGSRINLAMEKVANSVLPCKYASSGCEITLPHTEKADHEEL 136
DB 61 VCSNCRPKLTCCPTCRGPIGSRINLAMEKVANSVLPCKYASSGCEITLPHTEKADHEEL 120

QY 137 CEFRPYSCPCGASCKWQSGSLDAMVPHLMHOKHSITTLQGEDIVFLATDINLPGAVDWM 196
DB 121 CEFRPYSCPCGASCKWQSGSLDAMVPHLMHOKHSITTLQGEDIVFLATDINLPGAVDWM 180

QY 197 MQSCFGFHFMLVLEKQEKYDGHQOFFAIVQLIGTRKQAFNAYRLELNGHRRRLTWEATP 256
DB 181 MQSCFGFHFMLVLEKQEKYDGHQOFFAIVQLIGTRKQAFNAYRLELNGHRRRLTWEATP 240

QY 257 RSIHEGIATAMNSDCLVFDTSIAQLFAENGNGINVTISMC 298
DB 241 RSIHEGIATAMNSDCLVFDTSIAQLFAENGNGINVTISMC 282

RESULT 5
ABB84454
ID ABB84454 standard; peptide; 282 AA.

AC ABB84454;

DT 08-NOV-2002 (first entry)

DE Murine mmSiah1A protein.

KW mmSiah1A; seven in absentia homologue; ubiquitination pathway; cancer;
KW infertility; inflammation; Siah; cytostatic; antiinflammatory;
KW neuroprotective; immunosuppressive; apoptosis; NF kappa B signaling;
KW neurological disorder; protein co-ordinate data.

OS Mus musculus.
XX WO200262838-A1.
XX 15-AUG-2002.
XX 06-FEB-2002; 2002WO-AU000118.
XX 06-FEB-2001; 2001AU-00002908.
XX (MACC-) MACCALLUM CANCER INST PETER.
XX (SVIN-) ST VINCENTS INST MEDICAL RES.
XX Bowtell DDL, House CM, Parker MW, Polekhina G;
XX WPI; 2002-657521/70.
XX New binding domain of a seven in absentia homolog protein, useful for
PT identifying agonists or antagonists of the domain, for treating or
PT preventing e.g. cancer, inflammation, infertility or other related
PT conditions, or apoptosis.
XX Disclosure; Fig 2; 153pp; English.

XX This invention describes a novel binding domain or a portion of the
CC binding domain of a seven in absentia homologue (Siah) protein. Siah is
CC an important protein in the ubiquitination pathway and the binding domain
CC is capable of binding substrates, co-factors and interactors of the Siah
CC protein. The products of the invention have antiinflammatory, cytostatic,
CC neuroprotective and immunosuppressive activity. The binding domain is
CC useful for identifying agonists and antagonists to the domain. The
CC antagonist, agonist or ligand of the binding domain of Siah may be used
CC for treating or preventing cancer e.g. breast cancer, inflammation,

CC infertility or other related conditions, a disease relating to abnormal
CC protein degradation, a pathological immune response, a disease relating
CC to apoptosis, a disease relating to NF kappa B signaling, or a
CC neurological disorder. This sequence represents a Siah-related protein,
CC mmSiah1A described in the disclosure of the invention. Note: This
CC sequence contains 3-D protein co-ordinate data

XX Sequence 282 AA;

Query Match 94.8%; Score 1528; DB 5; Length 282;
Best Local Similarity 99.6%; Pred. No. 1.1e-141;
Matches 281; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 17 MSRTATATLPTGTSKCPSPQSRVPALTTASNNDLASLFECPCFDYVLPPILOQSGHL 76
DB 1 MSRTATATLPTGTSKCPSPQSRVPALTTASNNDLASLFECPCFDYVLPPILOQSGHL 60

QY 77 VCSNCRPKLTCCPTCRGPIGSRINLAMEKVANSVLPCKYASSGCEITLPHTEKADHEEL 136
DB 61 VCSNCRPKLTCCPTCRGPIGSRINLAMEKVANSVLPCKYASSGCEITLPHTEKADHEEL 120

QY 137 CEFRPYSCPCGASCKWQSGSLDAMVPHLMHOKHSITTLQGEDIVFLATDINLPGAVDWM 196
DB 121 CEFRPYSCPCGASCKWQSGSLDAMVPHLMHOKHSITTLQGEDIVFLATDINLPGAVDWM 180

QY 197 MQSCFGFHFMLVLEKQEKYDGHQOFFAIVQLIGTRKQAFNAYRLELNGHRRRLTWEATP 256
DB 181 MQSCFGFHFMLVLEKQEKYDGHQOFFAIVQLIGTRKQAFNAYRLELNGHRRRLTWEATP 240

QY 257 RSIHEGIATAMNSDCLVFDTSIAQLFAENGNGINVTISMC 298
DB 241 RSIHEGIATAMNSDCLVFDTSIAQLFAENGNGINVTISMC 282

RESULT 6
ABB57146
ID ABB57146 standard; protein; 282 AA.

AC ABB57146;

DT 07-MAR-2002 (first entry)

DE Mouse ischaemic condition related protein sequence SEQ ID NO:355.

KW Mouse; ischaemia; compressive ischaemia; occlusive ischaemia;
KW vasospastic ischaemia; ischaemic condition; ischaemic disease.

OS Mus musculus.
XX WO200188188-A2.
XX 22-NOV-2001.
XX 18-MAY-2001; 2001WO-JP0004192.
XX 18-MAY-2000; 2000JP-00145977.
XX (UYNI-) UNIV NIHON SCHOOL JURIDICAL PERSON.
XX Ishikawa K, Asai S, Takahashi Y, Nagata T, Ishii Y;
XX WPI; 2002-034733/04.
XX N-PSDB; ABI99429.

XX Examining the ischemic condition (e.g. occlusive ischemia) by measuring
PT expression levels of particular genes defined in the specification or by
PT determining the expression profile of a gene group comprising these
PT genes.
XX Claim 2; Page 958-959; 2690pp; English.
XX The present invention describes a method for examining ischaemic
CC conditions, comprising measuring the expression levels of particular

CC genes (I) in a test sample or determining the expression profile of a
 CC gene group in the sample comprising genes selected from (I). The method
 CC is useful for examining the ischaemic condition (e.g. compressive
 CC ischaemia, occlusive ischaemia or vasospastic ischaemia) by measuring the
 CC expression levels of particular genes (ABI99912 to ABI99914, encoding the
 CC protein sequences in ABB57020 to ABB57374) or by determining the
 CC expression profile of a gene group comprising these genes. The expression
 CC levels or expression profiles produced by these genes are used as an
 CC indicator when screening for ischaemic condition-improving drugs or
 CC therapeutics for ischaemic diseases. ABI99913 and ABI99914 represent PCR
 CC primers for a mouse ischaemic condition related sequence, which are used
 CC in the exemplification of the present invention
 XX
 SQ Sequence 282 AA;

Query Match 94.8%; Score 1528; DB 5; Length 282;
 Best Local Similarity 99.6%; Pred. No. 1.1e-141;
 Matches 281; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 17 MSRTATATPTGTSKCPSPQSRVPALGTGTASNNDLASLFECPVCFDYVLPPILOCSGHL 76
 Db 1 MSRTATATPTGTSKCPSPQSRVPALGTGTASNNDLASLFECPVCFDYVLPPILOCSGHL 60
 QY 77 VCSNCRPKLTCCPTCRGLGSIIRNLAMEKVANSVLPCKYASSGCEITLPHTEKADHEEL 136
 Db 61 VCSNCRPKLTCCPTCRGLGSIIRNLAMEKVANSVLPCKYASSGCEITLPHTEKADHEEL 120
 QY 137 CEFRPYSCPCPGASCCKWQSLDAVMPHLMHQHKSITTLQGEDIVFLATDINLPGAVDWM 196
 Db 121 CEFRPYSCPCPGASCCKWQSLDAVMPHLMHQHKSITTLQGEDIVFLATDINLPGAVDWM 180
 QY 197 MOSCFGHFMVLVEKQEKYDGHQOFPFAIVQLIGTRKQAFNFAVRLNGHRRRLTWEATP 256
 Db 181 MOSCFGHFMVLVEKQEKYDGHQOFPFAIVQLIGTRKQAFNFAVRLNGHRRRLTWEATP 240
 QY 257 RSIEGIATAIMNSDCLVFTDSIAQLFAENGNGINVTISM 298
 Db 241 RSIEGIATAIMNSDCLVFTDSIAQLFAENGNGINVTISM 282

RESULT 7
 ABB84452
 ID ABB84452 standard; peptide; 282 AA.
 XX
 AC ABB84452;
 XX
 DT 08-NOV-2002 (first entry)
 XX
 DE Human hsSiah1 protein.
 XX
 KW hsSiah1; seven in absentia homologue; ubiquitination pathway; cancer;
 KW infertility; inflammation; Siah; cytostatic; antiinflammatory;
 KW neuroprotective; immunosuppressive; apoptosis; NF kappa B signaling;
 KW neurological disorder; protein co-ordinate data.

XX Homo sapiens.
 XX WO200262838-A1.
 XX
 XX 15-AUG-2002.
 XX
 XX 06-FEB-2002; 2002WO-AU000118.
 XX
 XX 06-FEB-2001; 2001AU-00002908.
 XX
 XX (MACC-) MACCALLUM CANCER INST PETER.
 XX (SVIN-) ST VINCENTS INST MEDICAL RES.
 XX
 XX Bowtell DDL, House CW, Parker MW, Polekhina G;
 XX WPI; 2002-657521/70.

XX New binding domain of a seven in absentia homolog protein, useful for

PT identifying agonists or antagonists of the domain, for treating or
 PT preventing e.g. cancer, inflammation, infertility or other related
 PT conditions, or apoptosis.
 XX
 XX Disclosure; Fig 2; 153pp; English.
 XX
 XX This invention describes a novel binding domain or a portion of the
 CC binding domain of a seven in absentia homologue (Siah) protein. Siah is
 CC an important protein in the ubiquitination pathway and the binding domain
 CC is capable of binding substrates, co-factors and interactors of the Siah
 CC protein. The products of the invention have antiinflammatory, cytostatic,
 CC neuroprotective and immunosuppressive activity. The binding domain is
 CC useful for identifying agonists and antagonists to the domain. The
 CC antagonist, agonist or ligand of the binding domain of Siah may be used
 CC for treating or preventing cancer e.g. breast cancer, inflammation,
 CC infertility or other related conditions, a disease relating to abnormal
 CC protein degradation, a pathological immune response, a disease relating
 CC to apoptosis, a disease relating to NF kappa B signaling, or a
 CC neurological disorder. This sequence represents a Siah-related protein,
 CC hsSiah described in the disclosure of the invention. Note: This sequence
 CC contains 3-D protein co-ordinate data
 XX
 SQ Sequence 282 AA;

Query Match 94.5%; Score 1522; DB 5; Length 282;
 Best Local Similarity 98.9%; Pred. No. 4.2e-141;
 Matches 279; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
 QY 17 MSRTATATPTGTSKCPSPQSRVPALGTGTASNNDLASLFECPVCFDYVLPPILOCSGHL 76
 Db 1 MSRTATATPTGTSKCPSPQSRVPALGTGTASNNDLASLFECPVCFDYVLPPILOCSGHL 60
 QY 77 VCSNCRPKLTCCPTCRGLGSIIRNLAMEKVANSVLPCKYASSGCEITLPHTEKADHEEL 136
 Db 61 VCSNCRPKLTCCPTCRGLGSIIRNLAMEKVANSVLPCKYASSGCEITLPHTEKADHEEL 120
 QY 137 CEFRPYSCPCPGASCCKWQSLDAVMPHLMHQHKSITTLQGEDIVFLATDINLPGAVDWM 196
 Db 121 CEFRPYSCPCPGASCCKWQSLDAVMPHLMHQHKSITTLQGEDIVFLATDINLPGAVDWM 180
 QY 197 MOSCFGHFMVLVEKQEKYDGHQOFPFAIVQLIGTRKQAFNFAVRLNGHRRRLTWEATP 256
 Db 181 MOSCFGHFMVLVEKQEKYDGHQOFPFAIVQLIGTRKQAFNFAVRLNGHRRRLTWEATP 240
 QY 257 RSIEGIATAIMNSDCLVFTDSIAQLFAENGNGINVTISM 298
 Db 241 RSIEGIATAIMNSDCLVFTDSIAQLFAENGNGINVTISM 282

RESULT 8
 ABB84455
 ID ABB84455 standard; peptide; 282 AA.
 XX
 AC ABB84455;
 XX
 DT 08-NOV-2002 (first entry)
 XX
 DE Murine mmSiah1B protein.
 XX
 KW mmSiah1B; seven in absentia homologue; ubiquitination pathway; cancer;
 KW infertility; inflammation; Siah; cytostatic; antiinflammatory;
 KW neuroprotective; immunosuppressive; apoptosis; NF kappa B signaling;
 KW neurological disorder; protein co-ordinate data.

XX Mus musculus.
 XX WO200262838-A1.
 XX
 XX 15-AUG-2002.
 XX
 XX 06-FEB-2002; 2002WO-AU000118.
 XX
 XX 06-FEB-2001; 2001AU-00002908.

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133 HEELCEFRPYSCEP

QV 133 HEELCEFRYPSCPGASCKWQSLDAMPHLMHOKHSITTLQGEDIVFLATDINLPGAV 19

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Db 157 HEDICEYRPSYPCPCGASCKWQSGLEAVMSHLMAHKSITITLQGEDIVFLATDINLPGAV 216
Qy 193 DVMVMQSCFGHFHMLVLEKQEKYDGHQOFFFAIVQLIGTRKQAEFPAYRLELNGHRRRLTW 252
Db 217 DVMVMQSCFGHFHMLVLEKQEKYEGHQOFFFAIVLLIGTRKQAEFPAYRLELNGHRRRLTW 276
Qy 253 EATPRSIEHGIATATMNSDCLVFDTSIAQLFAENGNGINVTISMC 298
Db 277 EATPRSIIHDGVAAAIMNSDCLVFDTAIAHLFADNGNLGINVTI1STC 322

RESULT 12
ABR47593
ID ABR47593 standard; protein; 324 AA.
XX
AC ABR47593;
XX
DT 12-JUN-2003 (first entry)
XX
DE Breast cancer associated protein sequence SEQ ID NO:425.
XX
KW Human; breast cancer; cytostatic; gene therapy.
XX
OS Homo sapiens.
XX
PN WO2003004989-A2.
XX
PD 16-JAN-2003.
XX
PF 21-JUN-2002; 2002WO-US019669.
XX
PR 21-JUN-2001; 2001US-0299887P.
XX
PR 27-JUN-2001; 2001US-0301572P.
XX
PR 18-JUL-2001; 2001US-0306501P.
XX
PR 25-SEP-2001; 2001US-0325002P.
XX
PR 05-MAR-2002; 2002US-0362585P.
XX
PR 14-MAY-2002; 2002US-0380391P.
XX
PA (MILL-) MILLENIUM PHARM INC.
XX
PI Lillie J, Gannavarapu M, Glatt K, Hoersh S, Kamatkar S;
PI Mertens M, Monahan JE, Myer V, Wang Y, Xu Y, Zhao X, Meyers RE;
PI Bast RC, Hortobagyi GN, Puzstai L, Mexic F, Sahin A, Mills GB;
XX
XX WPI; 2003-210381/20.
XX
XX N-PSDB; ACC50292.
XX
XX Breast cancer diagnosis or treatment by comparing the level of expression
XX of a marker in a patient sample with that in the control non-breast
XX cancer sample.
XX
XX Claim 1; SEQ ID NO 425; 128pp; English.
XX
XX The present invention describes a method for assessing whether a patient
XX is afflicted with breast cancer. The method comprises comparing the level
XX of expression of a marker (gene/polypeptide see ACC50076 to ACC50334 and
XX ABR47386 to ABR47632) in a patient sample and the normal level of
XX expression of the marker in a control non-breast cancer sample, where a
XX significant increase in the level of expression of the marker in the
XX patient sample and the normal level is an indication that the patient is
XX afflicted with breast cancer. The breast cancer associated sequences from
XX the present invention have cytostatic activities and can be used in gene
XX therapy. The method is useful for diagnosing and treating breast cancer.
XX N.B. The sequence data for this patent did not form part of the printed
XX specification, but was obtained in electronic format directly from WIPO
XX at ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 324 AA;
XX
XX Query Match 74.4%; Score 1198; DB 6; Length 324;
XX Best Local Similarity 77.3%; Pred. No. 4e-109;
XX Matches 221; Conservative 27; Mismatches 30; Indels 8; Gaps 2;
```

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Qy 21 TATALPTGTSKCPPSQRPALVTG-----TTASNNDLASLFECPVCFDYVLPILQOQS 73
Db 37 TISAAGFGSSAVPAAAVISGPGGGGAGPVSPOHBELTSLFECPVCFDYVLPILQOQA 96
Qy 74 GHLVCSNCRPKLTCCPTCRGPL-GSIRNLAMEKVANSVLPCKYASSGCEITLPHTEKAD 132
Db 97 GHLVCNQCRQKLSCCPTCRGALTPIRNLAMEKVASAVLPCKYATTGCSUTLHHTKEPE 156
Qy 133 HEELCEFRPYSCPCGASCKWQSGLDVAMPHLMHQHKSITITLQGEDIVFLATDINLPGAV 192
Db 157 HEDICEYRPSYPCPCGASCKWQSGLEAVMSHLMAHKSITITLQGEDIVFLATDINLPGAV 216
Qy 193 DVMVMQSCFGHFHMLVLEKQEKYDGHQOFFFAIVQLIGTRKQAEFPAYRLELNGHRRRLTW 252
Db 217 DVMVMQSCFGHFHMLVLEKQEKYEGHQOFFFAIVLLIGTRKQAEFPAYRLELNGHRRRLTW 276
Qy 253 EATPRSIEHGIATATMNSDCLVFDTSIAQLFAENGNGINVTISMC 298
Db 277 EATPRSIIHDGVAAAIMNSDCLVFDTAIAHLFADNGNLGINVTI1STC 322

RESULT 13
ADRI4123
ID ADRI4123 standard; protein; 324 AA.
XX
AC ADRI4123;
XX
DT 21-OCT-2004 (first entry)
XX
DE Human NF-kappaB pathway-associated protein SeqID124.
XX
KW NF-kappaB pathway; antiinflammatory; cytostatic; hepatotropic; virucide;
KW antiarthritic; antirheumatic; gastrointestinal-Gen; antiasthmatic;
KW antiarteriosclerotic; immunomodulator; cerebroprotective; vasotropic;
KW immunosuppressive; vulnary; gene therapy; immune disorder;
KW inflammatory disorder; NF-kappaB regulation; cancer; aberrant apoptosis;
KW hepatic disorder; Hodgkin's lymphoma; haematopoietic tumour;
KW hyper-IgM syndrome; hypohidrotic ectodermal dysplasia;
KW X-linked anhidrotic ectodermal dysplasia; immunodeficiency;
KW viral infection; HIV-1; HTLV-1; hepatitis B; hepatitis C; EBV; influenza;
KW rheumatoid arthritis; host cell survival; evasion of immune response;
KW atherosclerosis; cachexia; inflammatory bowel disease; colitis; asthma;
KW autoimmune disorder; hyper immune activity;
KW aberrant acute phase response; hypercongenital condition; birth defect;
KW necrotic lesion; wound; organ transplant rejection;
KW aberrant signal transduction; proliferating disorder; cancer;
KW HIV propagation; human.
XX
XX Homo sapiens.
XX
XX WO2004065577-A2.
XX
XX 05-AUG-2004.
XX
XX 13-JAN-2004; 2004WO-US0000799.
XX
XX 14-MAY-2003; 2003US-0440068P.
XX
XX 12-MAY-2003; 2003US-0469757P.
XX
XX (BRIM ) BRISTOL-MYERS SQUIBB CO.
XX
XX Nadler SG, Neubauer MG, Feder JN, Carman J;
XX
XX WPI; 2004-562168/54.
XX
XX N-PSDB; ADRI4122.
XX
XX New isolated polynucleotides and polypeptides associated with NF-kappaB
XX pathway, useful for diagnosing, treating, or preventing disorders or
XX diseases associated with NF-kappaB pathway.
XX
XX Claim 6; SEQ ID NO 124; 237pp; English.
```


Db 217 DWVMQSCFHHFVLEKQEKYEQHQFFAIVLLIGTRKQAFNFAYLELNGNRRLLTW 276
QY 253 EATPRSIHEGIATAMNSDCLVFDTSIAQLFAENGLGINVTISM 298
Db 277 EATPRSIHDGVAAMNSDCLVFDTAIAHLFADNGLNGLINVTISTC 322

RESULT 15
ABB84456
ID ABB84456 standard; peptide; 325 AA.
XX AC ABB84456;
XX DT 08-NOV-2002 (first entry)
XX DE Murine mmsiah2 protein.
XX KW mmsiah2; seven in absentia homologue; ubiquitination pathway; cancer;
KW infertility; inflammation; Siah; cytostatic; antiinflammatory;
KW neuroprotective; immunosuppressive; apoptosis; NF kappa B signaling;
KW neurological disorder; protein co-ordinate data.

XX OS Mus musculus.
XX PN WO200262838-A1.
XX PD 15-AUG-2002.
XX PF 06-FEB-2002; 2002WO-AU000118.
XX PR 06-FEB-2001; 2001AU-00002908.
XX PA (MACC-) MACCALLUM CANCER INST PETER.
XX PA (SVIN-) ST VINCENTS INST MEDICAL RES.

XX PI Bowtell DDL, House CM, Parker MW, Polekhina G;
XX WPI; 2002-657521/70.
XX New binding domain of a seven in absentia homolog protein, useful for
PT identifying agonists or antagonists of the domain, for treating or
PT preventing e.g. cancer, inflammation, infertility or other related
PT conditions, or apoptosis.
XX Disclosure; Fig 2; 153pp; English.

XX This invention describes a novel binding domain or a portion of the
CC binding domain of a seven in absentia homologue (Siah) protein. Siah is
CC an important protein in the ubiquitination pathway and the binding domain
CC is capable of binding substrates, co-factors and interactors of the Siah
CC protein. The products of the invention have antiinflammatory, cytostatic,
CC neuroprotective and immunosuppressive activity. The binding domain is
CC useful for identifying agonists and antagonists to the domain. The
CC antagonist, agonist or ligand of the binding domain of Siah may be used
CC for treating or preventing cancer e.g. breast cancer, inflammation,
CC infertility or other related conditions, a disease relating to abnormal
CC protein degradation, a pathological immune response, a disease relating
CC to apoptosis, a disease relating to NF kappa B signaling, or a
CC neurological disorder. This sequence represents a Siah-related protein,
CC mmsiah2 described in the disclosure of the invention. Note: This sequence
CC contains 3-D protein co-ordinate data

XX SQ Sequence 325 AA;

Query Match 73.9%; Score 1190; DB 5; Length 325;
Best Local Similarity 76.9%; Pred. No. 2.5e-108;
Matches 220; Conservative 27; Mismatches 31; Indels 8; Gaps 3;

QY 21 TATLFTGTSKCPSPQSRV---PALTG---TTASNNDLASLFECPCVCFDVLPPILQCOCS 73
Db 38 TISAGFGSSAPAAAVISGPGAGGADPVSQPHHELTSLFECPCVCFDVLPPILQCOA 97

QY 74 GHLVCSNCRPKLTCCPTCRGEL-GSIRNLAMEKVANSVLFPCKYASSGCEITLPHTEKAD 132
Db 98 GHLVCSNCRPKLTCCPTCRGEL-GSIRNLAMEKVANSVLFPCKYASSGCEITLPHTEKAD 157
QY 133 HEELCEPRPYSCPCPGASCKWQSGSLDAVMPHLMHQHKSITTLQGEDIVFLATDINLPGAV 192
Db 158 HEDICEYRFPYSCPCPGASCKWQSGSLDAVMPHLMHQHKSITTLQGEDIVFLATDINLPGAV 217
QY 193 DWVMQSCFHHFVLEKQEKYEQHQFFAIVLLIGTRKQAFNFAYLELNGNRRLLTW 252
Db 218 DWVMQSCFHHFVLEKQEKYEQHQFFAIVLLIGTRKQAFNFAYLELNGNRRLLTW 277
QY 253 EATPRSIHEGIATAMNSDCLVFDTSIAQLFAENGLGINVTISM 298
Db 278 EATPRSIHDGVAAMNSDCLVFDTAIAHLFADNGLNGLINVTISTC 323

Search completed: April 25, 2005, 06:37:16
Job time : 86 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 25, 2005, 05:30:15 ; Search time 24 Seconds
(without alignments)
1194.691 Million cell updates/sec

Title: US-10-679-246-2
Perfect score: 1611
Sequence: 1 MWIIIFLLPPYVIFSEMSRQ.....IAQLFAENGNGINVTISMC 298

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR 79.*

1: pir1.*

2: pir2.*

3: pir3.*

4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1528	94.8	282	2	148763
2	1498	93.0	282	2	335754
3	1190	73.9	325	2	148765
4	1153.5	71.6	314	2	346195
5	1149	71.3	314	2	441544
6	1037.5	64.4	339	2	T37470
7	439	27.3	315	2	T50562
8	434.5	27.0	308	2	T46026
9	429	26.6	327	2	T09027
10	422	26.2	305	2	E84848
11	419	26.0	315	2	T47971
12	417	25.9	315	2	T50561
13	385.5	23.9	336	2	T50560
14	232.5	14.4	303	2	C96692
15	215.5	13.4	313	2	B96692
16	182.5	11.3	366	2	A96692
17	120.5	7.5	458	2	A29361
18	109	6.8	113	2	T01657
19	107.5	6.7	468	2	T48615
20	106	6.6	522	2	S71821
21	105	6.5	89	2	T03072
22	104	6.5	574	2	S28275
23	104	6.5	974	2	E88549
24	103.5	6.4	897	2	T37813
25	101	6.3	587	2	T24103
26	100	6.2	374	2	T32286
27	99.5	6.2	298	2	JC7568
28	99	6.1	184	2	T03178
29	98	6.1	292	2	C88072

RESULT 1
148763
siab-1A protein - mouse
C;Species: Mus musculus (house mouse)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
C;Accession: I48763; S35753
R;Della, N.G.; Senior, P.V.; Bowtell, D.D.
Development 117, 1333-1343, 1993
A;Title: Isolation and characterisation of murine homologues of the Drosophila seven in ten protein
A;Reference number: I48763; MUID:94008536; PMID:8404535
A;Accession: I48763
A;Status: preliminary; translated from GE/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-282 <RES>
A;Cross-references: UNIPROT:P61092; EMBL:Z19579; NID:9297034; PIDN:CAA79630.1; PID:G297030;
C;Superfamily: Drosophila developmental protein sina; RING finger homology

Query Match 94.8%; Score 1528; DB 2; Length 282;
Best Local Similarity 99.6%; Pred. No. 2.9e-123;
Matches 281; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 17 MSRQTATATPTGTSKPPSORVPALGTATTASNDLASLFEPCVCFDYLPPILQCSGHL 76
Db 1 MSRQTATATPTGTSKPPSORVPALGTATTASNDLASLFEPCVCFDYLPPILQCSGHL 60
Qy 77 VCSNCRPKLTCCPTCRGLSIRNLAMEKVANSVLPCKYASSGCEITLPHTEKADHEEL 136
Db 61 VCSNCRPKLTCCPTCRGLSIRNLAMEKVANSVLPCKYASSGCEITLPHTEKADHEEL 120
Qy 137 CEFPRYSCPCPGASCKWQSLDAMPHLMHQHSITTLQGEDIVFLATDINLPGAVDWM 196
Db 121 CEFPRYSCPCPGASCKWQSLDAMPHLMHQHSITTLQGEDIVFLATDINLPGAVDWM 180
Qy 197 MQSCFGFHFMLVEKEKYDGHQOFFAIVQLIGTRKQAFNFAIRLEUNGHRRLTWTATP 256
Db 181 MQSCFGFHFMLVEKEKYDGHQOFFAIVQLIGTRKQAFNFAIRLEUNGHRRLTWTATP 240
Qy 257 RSTHEGIATAMNSDCLVFDTSIAQLFAENGNGINVTISMC 298
Db 241 RSIHEGIATAMNSDCLVFDTSIAQLFAENGNGINVTISMC 282

RESULT 2
335754
siab-1B protein - mouse
C;Species: Mus musculus (house mouse)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Jul-2004
C;Accession: I48764; S35754
R;Della, N.G.; Senior, P.V.; Bowtell, D.D.
Development 117, 1333-1343, 1993
A;Title: Isolation and characterisation of murine homologues of the Drosophila seven in ten protein
A;Reference number: I48763; MUID:94008536; PMID:8404535

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A;Accession: I48764
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-282 <RES>
A;Cross-references: UNIPROT:Q06985; EMBL:Z19580; NID:9297801; PIDN:CAA79631.1; PID:92978
C;Superfamily: Drosophila developmental protein sina; RING finger homology

Query Match 93.08; Score 1498; DB 2; Length 282;
Best Local Similarity 97.58; Pred. No. 1.1e-120; Indels 0; Gaps 0;
Matches 275; Conservative 4; Mismatches 3;

Qy 17 MSRTATALPTGTSKCPSPQSRVPAITTTASNNDLASLFECPVCFDYVLPPIILQCSGHL 76
Db 1 MSRQATALSTGTSKCPSPQSRVPAITTTASNNDLASLFECPVCFDYVLPPIILQCSGHL 60

Qy 77 VCSNCRPKLTCCPTCRPLGSIIRNLAMEKVANSVLPCKYASSGCEITLPHTEKADHEEL 136
Db 61 VCSNCRPKLTCCPTCRPLGSIIRNLAMEKVANSVLPCKYASSGCEITLPHTEKADHEEL 120

Qy 137 CERFPYSCPCGASCKWQSGISLDAVPHLMHOKHSITTLQGEDIVFLATDINLPGADVWM 196
Db 121 CERFPYSCPCGASCKWQSGISLDAVPHLMHOKHSITTLQGEDIVFLATDINLPGADVWM 180

Qy 197 MQSCFGFHFMVLVEKQEKYDGHQOFFAIVQLIGTRKQAEFAYRLELNGHRRRLTWEATP 256
Db 181 MQSCFGFHFMVLVEKQEKYDGHQOFFAIVQLIGTRKQAEFAYRLELNGHRRRLTWEATP 240

Qy 257 RSIHEGIATAMNSDCLVFTSTIAQLFAENGNGINVTISM 298
Db 241 RSIHEGIATAMNSDCLVFTSTIAQLFAENGNGINVTISM 282

RESULT 3
I48765
siah-2 protein - mouse
C;Species: Mus musculus (house mouse)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
C;Accession: I48765; S35755
R;Della, N.G.; Senior, P.V.; Bowtell, D.D.
Development 117, 1333-1343, 1993
A;Title: Isolation and characterisation of murine homologues of the Drosophila seven in
A;Reference number: I48763; MUID:94008536; PMID:8404535
A;Accession: I48765
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-325 <RES>
A;Cross-references: UNIPROT:Q06986; EMBL:Z19581; NID:9297036; PIDN:CAA79632.1; PID:92970
C;Superfamily: Drosophila developmental protein sina; RING finger homology

Query Match 73.9%; Score 1190; DB 2; Length 325;
Best Local Similarity 76.9%; Pred. No. 2.8e-94;
Matches 220; Conservative 27; Mismatches 31; Indels 8; Gaps 3;

Qy 21 TATALPTGTSKCPSPQSRV---PALTG----TTASNNDLASLFECPVCFDYVLPPIILQCS 73
Db 38 TISAAGPSSAVPAAAVISPGAGGADPVSPQHSLTSLFECPVCFDYVLPPIILQCS 97

Qy 74 GHLVCSNCRPKLTCCPTCRGPL-GSIRNLAMEKVANSVLPCKYASSGCEITLPHTEKAD 132
Db 98 GHLVCSNCRPKLTCCPTCRGALTFSIRNLAMEKVANSVLPCKYASSGCEITLPHTEKAD 157

Qy 133 HEELCEFRPYSCPCGASCKWQSGISLDAVPHLMHOKHSITTLQGEDIVFLATDINLPGAV 192
Db 158 HEDICEFRPYSCPCGASCKWQSGISLDAVPHLMHOKHSITTLQGEIVFLATDINLPGAV 217

Qy 193 DWVMQSCFGFHFMVLVEKQEKYDGHQOFFAIVQLIGTRKQAEFAYRLELNGHRRRLTW 252
Db 218 DWVMQSCFGFHFMVLVEKQEKYDGHQOFFAIVQLIGTRKQAEFAYRLELNGHRRRLTW 277

Qy 253 EATPRSIHEGIATAMNSDCLVFTSTIAQLFAENGNGINVTISM 298
Db 278 EATPRSIHDGVAALIMNSDCLVFTSTIAQLFAENGNGINVTISTC 323
```

```
RESULT 4
A36195
developmental protein sina - fruit fly (Drosophila melanogaster)
C;Species: Drosophila melanogaster
C;Date: 14-Dec-1990 #sequence_revision 13-Jan-1993 #text_change 09-Jul-2004
C;Accession: A36195
R;Carthew, R.W.; Rubin, G.M.
Cell 63, 561-577, 1990
A;Title: seven in absentia, a gene required for specification of R7 cell fate in the Dros
A;Reference number: A36195; MUID:91029488; PMID:2146028
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-314 <CAR>
A;Cross-references: UNIPROT:P21461; GB:M38384; NID:9158466; PID:9158467
C;Genetics:
A;Gene: FlyBase:sina
A;Cross-references: FlyBase:FBgn0003410
C;Superfamily: Drosophila developmental protein sina; RING finger homology
C;Keywords: DNA binding; nucleus; zinc finger

Query Match 71.6%; Score 1153.5; DB 2; Length 314;
Best Local Similarity 75.3%; Pred. No. 3.6e-91;
Matches 217; Conservative 18; Mismatches 42; Indels 11; Gaps 1;

Qy 21 TATALPTG-----TSKCPSPQSRVPAITTTASNNDLASLFECPVCFDYVLPPIIL 69
Db 26 TWTSTIGSSAGNTSSANTSSSSSSLSAGGAGMSADTSLFECPVCFDYVLPPIIL 85

Qy 70 QCQSGHLVCSNCRPKLTCCPTCRPLGSIIRNLAMEKVANSVLPCKYASSGCEITLPHTE 129
Db 86 QCQSGHLVCSNCRPKLTCCPTCRPLGSIIRNLAMEKVANSVLPCKYASSGCEITLPHTE 145

Qy 130 KADHEELCEFRPYSCPCGASCKWQSGISLDAVPHLMHOKHSITTLQGEDIVFLATDINLP 189
Db 146 KTEHEETCECRPYLCPGASCKWQSGISLDAVPHLMHOKHSITTLQGEDIVFLATDINLP 205

Qy 190 GAVDWMQSCFGFHFMVLVEKQEKYDGHQOFFAIVQLIGTRKQAEFAYRLELNGHRRR 249
Db 206 GAVDWMQSCFGFHFMVLVEKQEKYDGHQOFFAIVQLIGTRKQAEFAYRLELNGHRRR 265

Qy 250 LTWEATPRSIHEGIATAMNSDCLVFTSTIAQLFAENGNGINVTISM 297
Db 266 LTWEATPRSIHEGIATAMNSDCLVFTSTIAQLFAENGNGINVTISL 313

RESULT 5
A41544
developmental protein sina - fruit fly (Drosophila virilis)
C;Species: Drosophila virilis
C;Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 09-Jul-2004
C;Accession: A41544
R;Neufeld, T.P.; Carthew, R.W.; Rubin, G.M.
Proc. Natl. Acad. Sci. U.S.A. 88, 10203-10207, 1991
A;Title: Evolution of gene position: chromosomal arrangement and sequence comparison of t
A;Reference number: A41544; MUID:92052239; PMID:1946441
A;Accession: A41544
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-314 <NEU>
A;Cross-references: UNIPROT:P29304; GB:M77281
C;Genetics:
A;Gene: FlyBase:Dvir/sina
A;Cross-references: FlyBase:FBgn0013142
C;Superfamily: Drosophila developmental protein sina; RING finger homology
C;Keywords: zinc finger

Query Match 71.3%; Score 1149; DB 2; Length 314;
Best Local Similarity 75.3%; Pred. No. 8.7e-91;
Matches 216; Conservative 19; Mismatches 42; Indels 10; Gaps 1;

Qy 21 TATALPTG-----TSKCPSPQSRVPAITTTASNNDLASLFECPVCFDYVLPPIIL 70
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Db 194 VENATWMLTVFN-----CFGRQCL-----HFEAFQLGMAPVYMAFLRFMGD 235

Qy 231 RKOAEFAYLENGHRRRLTWATPRSIHEGATATMNSDCLVFTSIAQLPA--ENG 288

Db 236 ENEAKKFSYSLVGAHGRKLTQGIPIRSIRDSHRKVRDSQDGLIIPRNALALYFSGDROE 295

Qy 289 LGINVT 294

Db 296 LKLRVT 301

RESULT 9

hypothetical protein T27E11.120 - Arabidopsis thaliana

C:Species: Arabidopsis thaliana (mouse-ear cress)

C>Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 09-Jul-2004

C:Accession: T09027

R:Bevan, M.; Lennard, N.; Quail, M.; Harris, B.; Rajandream, M.A.; Barrell, B.G.; Bancroft submitted to the Protein Sequence Database, June 1999

A:Reference number: Z16533

A:Accession: T09027

A:Molecule type: DNA

A:Residues: 1-327 <BEV>

A:Cross-references: UNIPROT:Q9STN8; EMBL:AL078579; GSPDB:GN00062; ATSP:T27E11.120

A:Experimental source: cultivar Columbia; BAC clone T27E11

C:Genetics:

A:Gene: ATSP:T27E11.120

A:Map position: 4

A:Introns: 77/3; 206/3

C:Superfamily: Drosophila developmental protein sina; RING finger homology

Query Match 26.6%; Score 429; DB 2; Length 327;

Best Local Similarity 35.1%; Pred. No. 3.6e-29;

Matches 102; Conservative 45; Mismatches 126; Indels 18; Gaps 8;

Qy 11 YVFISEMSRQTATLPTGTSKCPSPORVPALTGTGTASNNDLASFECPCVDFYVLPILQ 70

Db 26 YQFSSTKTHGGAATAVTVNGTATAPA-----TSVYELLECPVCTYSMPPIHQ 77

Qy 71 QSGHLVCSNCRPKL--TCCTCRGPLGSIRNLAMEKVANSVLPFCYASSGCEITLPHTE 129

Db 78 CHNGHTLCTSKVRVHNRCPCTCRQELGDIRCLALEKVAESLELPCKFYNGCPEIFPYS 137

Qy 130 KADHEELCEFRPYSCPCGASCCKQGSGLDAMVPHLMHGHKSITTLQGEDIVFLATDINLP 189

Db 138 KKHESLGNFRPYSCPYAGSECGIVGDIPLVAHLRDDHK--VDMHAGSTENHRYVKN-P 195

Qy 190 GAVD---WVM-MQSCFGFHFMLVLEKQEKYDGHQOFFAIVOLIGTRKQAEFATRLLENG 245

Db 196 REVENATWMLTVFHCQGVYFCLHPEAFQLGGMG-PVYMAFLRFMGDEEDARSYSLEYVG 254

Qy 246 HRRRLTWATPRSIHEGATATMNSDCLVFTSIAQLPA--ENGMLGINVT 294

Db 255 SGKLTWEGTPRSIRDSHRKVRDSNDGLTIORNMALFFSGDGRKELKURVT 305

RESULT 10

probable RING zinc finger protein [imported] - Arabidopsis thaliana

C:Species: Arabidopsis thaliana (mouse-ear cress)

C>Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 09-Jul-2004

C:Accession: E84848

R:Liu, X.; Kaul, S.; Rounalev, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.; M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.; eus, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, Nature 402, 761-768, 1999

A:Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.

A:Reference number: A84420; MUID:20083487; PMID:10617197

A:Accession: E84848

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-305 <STO>

A:Cross-references: UNIPROT:P93748; GB:AE002093; NID:g1871185; PIDN:AAB63545.1; GSPDB:GN

C:Genetics:

A:Gene: At2g41980

A:Map position: 2

C:Superfamily: Drosophila developmental protein sina; RING finger homology

Query Match 26.2%; Score 422; DB 2; Length 305;

Best Local Similarity 31.2%; Pred. No. 1.3e-28;

Matches 94; Conservative 51; Mismatches 108; Indels 48; Gaps 7;

Qy 16 EMSRQTATLPTGTSKCPSPORVPALTGTGTASNNDLASFECPCVDFYVLPILQCSGH 75

Db 24 KMAKVEANSKPTKSGS-----GSIGKFSHNGYVELLECPVCTNLMPPIHQCPNGH 75

Qy 76 LVCSNCRPKL--TCCTCRGPLGSIRNLAMEKVANSVLPFCYASSGCEITLPHTEKADHE 134

Db 76 TLCSCKLVRQNTCTPRYELGNIRCLALEKVAESLEVPYQNLGCDIFFYYSKLKHE 135

Qy 135 ELCEFRPYSCPCGASCCKQGSGLDAMVPHLMHGHK-----SITTLQGEDIV 180

Db 136 QHCRFRFSYSCPYAGSECSVTGDIPTLVDLKDDHMDHGGCTFNHRYVKNPHEVENAT 195

Qy 181 ELATDINLPGAVDWVMQSCFGFHFMLVLEKQEKYDGHQ-----OFFAIVQLIGTRKQAE 235

Db 196 WMLTVFN-----CFGRQCL-----HFEAFQLGMAPVYMAFLRFMGDENEAK 237

Qy 236 NFAYRLLENGHRRRLTWATPRSIHEGATATMNSDCLVFTSIAQLP--AENGMLGINV 293

Db 238 KFSYSLEVGAKSKLTWQGIPIRSIRDSHRKVRDSQDGLIIPRNALALYFSGSKDELKRV 297

Qy 294 T 294

Db 298 T 298

RESULT 11

T47971

seven in absentia-like protein - Arabidopsis thaliana

N:Alternate names: protein F15G16.180

C:Species: Arabidopsis thaliana (mouse-ear cress)

C>Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 09-Jul-2004

C:Accession: T47971

R:De Haan, M.; Maarse, A.C.; Grivell, L.A.; Mewes, H.W.; Lemcke, K.; Mayer, K.F.X.; Quetf submitted to the Protein Sequence Database, January 2000

A:Reference number: Z24480

A:Accession: T47971

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-315 <DEH>

A:Cross-references: UNIPROT:Q84JL3; EMBL:AL132959

A:Experimental source: cultivar Columbia; BAC clone F15G16

C:Genetics:

A:Map position: 3

A:Introns: 65/3; 194/3

A:Note: F15G16.180

C:Superfamily: Drosophila developmental protein sina; RING finger homology

Query Match 26.0%; Score 419; DB 2; Length 315;

Best Local Similarity 34.0%; Pred. No. 2.5e-26;

Matches 91; Conservative 46; Mismatches 109; Indels 22; Gaps 7;

Qy 40 ALTGTASNNDLASFECPCVDFYVLPILQCSGHVLCNSCRPKL--TCCTCRGPLGSI 98

Db 35 AAGLLPTTTSVHLELCEPVCNTSMYPPIHQCHNGHTLCTCKARVHNRCPCTCRQELGDI 94

Qy 99 RNLAAMEKVANSVLPFCYASSGCEITLPHTEKADHELCERFPYSCPCGASCCKQGSGLD 158

Db 95 RCLALEKVAESLELPCKHMSLGCPEIFPYYSKLKHETVCNFRPYSCPYAGSECSVTGDI 154

Qy 159 AVMPHLMHGHK-----SITTLQGEDIVFLATDINLPGAVDWVM-MQSCFGFHFMLVLEKQE 213

Db 155 FLVAHLRDDHDKVDMHSGCTFNHRYVKNPHEVE---NATWMLTVFHCQGVYFCL----- 205

Qy 214 KYDGHQ-----OFFAIVQLIGTRKQAEFAYRLLENGHRRRLTWATPRSIHEGATATM 268

```
Db      206 HFEAFQMGAPVYMAFLRFMGDETEARNYNSLVGGYGRKLIWEGTPRSVRDHRKVRD 265
Qy      269 NSDCLVFTDTSIAQLFA--ENGNGLGNVT 294
Db      266 SHDGLIIRQNNALFFSGDRKELKLRVT 293

RESULT 12
T50561
SINA1 protein [imported] - Vitis vinifera
C:Species: Vitis vinifera
C:Date: 21-Jul-2000 #sequence_revision 21-Jul-2000 #text_change 09-Jul-2004
C:Accession: T50561
R;Brehm, I.; Korfei, M.; Preisig-Mueller, R.; Kindl, H.
submitted to the EMBL Data Library, November 1998
A:Description: A nuclear localized zinc finger protein found in a plant is homologous to
A:Reference number: 225132
A:Accession: T50561
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-315 <BRE>
A:Cross-references: UNIPROT:Q9XGC2; EMBL:Y18471; PIDN:CAB40577.1
C:Superfamily: Drosophila developmental protein sina; RING finger homology

Query Match      25.9%; Score 417; DB 2; Length 315;
Best Local Similarity 34.4%; Pred. No. 3.6e-28;
Matches 97; Conservative 43; Mismatches 102; Indels 40; Gaps 9;

Qy      29  TSKCPSPQRV--PALTGTASNNDLASLFCPCVCFDYLVPILQCSGHLVCSNCRPKL- 85
Db      28  SSSSKPSNVVSPAISPTS-----VHELLEPCVTNSMYPPIHQCHNGHTLCSTCKSRVH 83
Qy      86  TCPCPCRGLGSRNLAMEKANSVLPCKYASSGCEITLPHTEKADHEELCEFRPYSCP 145
Db      84  NRCPTCQELGDIKLALEKVAESLELPCKYCSLGCPEIPYYSKLKHEAQCNFRPYNCP 143
Qy      146  CPGASCKWQSLDAMVPHLMHQHSITTLQGEDIVFLATDINL-----PGAVD---W 194
Db      144  YAGSECAVVGDIPLVSLHRDDHK-----VDMHTGCTFNHRYVKNPREVENATW 193
Qy      195  VM-MQSCFGFHPMLVLEKQKYDGHQ-----OFFAIVQLIGTRKQAFNFAIRLELNGHRR 248
Db      194  MLTVNFCFGQYFCL-----HFEAFQMGAPVYMAFLRFMGDETEARNFYSLEVGANGR 247
Qy      249  RLWTWATPRSTHEGIATAIMNSDCLVFTDTSIAQLFAENGNLG 290
Db      248  KLIWEGTPRSIRDSHKVRDSDGLIIRQNNALFFLWVGQEG 289

RESULT 13
T50560
SINA1 protein [imported] - upland cotton
C:Species: Gossypium hirsutum (upland cotton)
C:Date: 21-Jul-2000 #sequence_revision 21-Jul-2000 #text_change 09-Jul-2004
C:Accession: T50560
R;Jaradat, T.T.
submitted to the EMBL Data Library, August 1999
A:Description: Studies of cotton cDNAs encoding a seven in absentia homolog, a potential
A:Reference number: 225131
A:Accession: T50560
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-336 <JAR>
A:Cross-references: UNIPROT:Q9SPH3; EMBL:AF175124; PIDN:RAD53877.1
C:Superfamily: Drosophila developmental protein sina; RING finger homology

Query Match      23.9%; Score 385.5; DB 2; Length 336;
Best Local Similarity 32.6%; Pred. No. 1.9e-25;
Matches 90; Conservative 46; Mismatches 101; Indels 39; Gaps 9;

Qy      39  PALTGTASNNDLASLFCPCVCFDYLVPILQCSGHLVCSNCRPKL-TCPCPCRGLG 97
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Db      62  PTAIAPAASVHE---LLECPVCTNSMYPPIHQCHNGHTLCSTCKIRVHDCRPTCQELGD 118
Qy      98  IRLNAMEKVANSVLPCKYASSGCEITLPHTEKADHEELCEFRPYSCPCPGASCKWQSL 157
Db      119  IRLALEKVAESLELPCKYKLGCPETFPYYSKLKHEGICIRPYNCPYAGSECSVVGDI 178
Qy      158  DAVMPHLMHQHSITTLQGEDIVFLATDINL-----PGAVD---WVM-MQSCFGFHP 205
Db      179  PFLVAHLRDDHK-----VDMHTGCTFNHRYVKNPREVENATWMLTVFHCQGYF 228
Qy      206  MLVLEKQEKYDGHQ-----OFFAIVQLIGTRKQAFNFAIRLELNGHRRRLTWATPRSIH 260
Db      229  CL-----HFEAFQMGAPVYMAFLRFMGDETEARNYNSLVFGANGKLRKSAPRSIR 282
Qy      261  EGIATAIMNSDCLVFTDTSIAQLFA--ENGNGLGNVT 294
Db      283  DSHRKVRDSDGLIIRQNNALFFSGDRKELKLRVT 318

RESULT 14
C96692
hypothetical protein T1217.8 [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
C:Accession: C96692
R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,
Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Creasy, T.H.; Dewar, K.;
ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.;
C.A.; Li, J.H.; Li, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziani,
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, I.
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A:Reference number: A86141; MUID:21016719; PMID:11130712
A:Accession: C96692
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-303 <STO>
A:Cross-references: UNIPROT:Q9C6H2; GB:AE005173; NID:gl1054584; PIDN:AAG27859.1; GSPDB:G
C:Geneid:8
A:Gene: T1217.8
A:Map position: 1

Query Match      14.4%; Score 232.5; DB 2; Length 303;
Best Local Similarity 32.5%; Pred. No. 2.1e-12;
Matches 49; Conservative 29; Mismatches 58; Indels 15; Gaps 5;

Qy      33  PPSQRPAL--TGTTASNNDLA-----SLFECPCVCFDYLVPILQCSGHLVCSNCR 82
Db      15  PKQRQPVSMENVGVTAGSEVSARSATLLELDLDCPICYHKLGAPIYQCDNGHIACSSCC 74
Qy      83  PKUTC-CPTCRGPLGSRNLAMEKVANSVLPCKYASSGCEITLPHTEKAD--HEELCEP 139
Db      75  KKVKYKCPYCSLRIGFRSRILEKIVEAVVVSFCNAKYGCTEKIPYDNESSESHERVCEP 134
Qy      140  RPYSCPCGASCKWQSLDAMVPHLMHQHS 170
Db      135  T-LCYCPEPECKYTVYTLRYHAEHKT 163

RESULT 15
B96692
hypothetical protein T1217.7 [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
C:Accession: B96692
R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,
Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Creasy, T.H.; Dewar, K.;
ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.
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C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A;Reference number: A86141; MUID:21016719; PMID:11130712
A;Accession: B96692
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-313 <STO>
A;Cross-references: UNIPROT:Q9C6H3; GB:AB005173; NID:G11054583; PIDN:AAG27858.1; GSPDB:G C;Genetics: T1217.7
A;Gene: T1217.7
A;Map position: 1

Query Match 13.4%; Score 215.5; DB 2; Length 313;
Best Local Similarity 30.6%; Pred.No. 6.3e-11;
Matches 44; Conservative 23; Mismatches 64; Indels 13; Gaps 3;
QY 36 QRVPALGTGTASNNDLA-----SLFECPCVCFDYVLPPILQCOGHLVGSNCRPKL 85
Db |||||:
13 QRVFSSVESVGGDDAVASGTLFELDLDCPICCHALTSPIFQCDNGHIACSSCCTKL 72
QY 86 -TCCPTCRGPIGSIRNLAMEKVANSVLFPCKYASSGCEITLPHTEKADHBEELCEFRPYSC 144
Db |||||:
73 RNKCPSCALPIGNFRSIRMERVVEAVVTCFNVKHGCTEKFSYKELIHEKDCRFA--LC 130
QY 145 PCPGASCKWOGSLDAVMPHLMQH 168
Db |||||:
131 YCPAPNCNYSGVYKDYSHFYVNH 154

Search completed: April 25, 2005, 06:39:13
Job time : 27 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 25, 2005, 03:59:42 ; Search time 82 Seconds
(without alignments)
1860.971 Million cell updates/sec

Title: US-10-679-246-2

Perfect score: 1611

Sequence: 1 MWIIIFLLPPYFISEMSRQ.....IAQLFAENGNGINVTISM 298

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt 03.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1532	95.1	282	1 SIH1 HUMAN	Q8iud4 homo sapien
2	1529	94.9	282	2 Q6GQJ5	Q6GQJ5 xenopus lae
3	1528	94.8	282	1 SIH1 MOUSE	P61092 mus musculus
4	1528	94.8	282	1 SIH1 RAT	Q920m9 rattus norv
5	1508	93.6	282	1 SIH1 BRARE	Q7zvg6 brachydanio
6	1494	92.7	282	1 SIH1 MOUSE	Q6985 mus musculus
7	1210	75.1	311	2 Q7Q520	Q7q520 anopheles g
8	1199	74.4	325	1 SIA2 MOUSE	Q06986 mus musculus
9	1199	74.4	325	1 SIA2 RAT	Q8r4t2 rattus norv
10	1198	74.4	324	1 SIA2 HUMAN	O43255 homo sapien
11	1192.5	74.0	331	1 SIA2 BRARE	Q7sy13 brachydanio
12	1177.5	73.1	313	1 SIA2 XENLA	Q8i8x5 xenopus lae
13	1156.5	71.8	331	1 SINA DROWI	Q8i147 drosophila
14	1153.5	71.6	314	1 SINA DROWI	P61093 drosophila
15	1153.5	71.6	314	1 SINA DROME	P21461 drosophila
16	1149	71.3	314	1 SINA DROWI	P29304 drosophila
17	1068	66.3	200	2 Q8JH27	Q8ihz7 gallus gall
18	1042.5	64.7	371	1 SINA SCHMA	Q86mw9 schistosoma
19	1037.5	64.4	339	1 SIAL CABEL	Q655x6 caenorhabdi
20	737	45.7	326	2 Q8I146	Q8i146 drosophila
21	729.5	45.3	354	2 Q8I1H9	Q8i1h9 drosophila
22	702.5	43.6	351	1 SINL DROME	Q8t3y0 drosophila
23	646.5	40.1	139	2 Q6X927	Q6x927 equus cabal
24	573	35.6	128	2 Q69DP6	Q69dp6 drosophila
25	571	35.4	128	2 Q69DM8	Q69dm8 drosophila
26	568	35.3	128	2 Q69DN2	Q69dn2 drosophila
27	568	35.3	128	2 Q69DN1	Q69dn1 drosophila
28	568	35.3	128	2 Q69DN2	Q69dn2 drosophila
29	568	35.3	128	2 Q69DN3	Q69dn3 drosophila
30	568	35.3	128	2 Q69DN7	Q69dn7 drosophila
31	568	35.3	128	2 Q69DP3	Q69dp3 drosophila

RESULT 1

SIH1_HUMAN	ID	SIH1_HUMAN	STANDARD;	PRT;	282 AA.
AC	Q8IU04	Q43269	Q92880;		
DT	05-JUL-2004	(Rel. 44, Created)			
DT	05-JUL-2004	(Rel. 44, Last sequence update)			
DT	25-OCT-2004	(Rel. 45, Last annotation update)			
DE	Ubiquitin ligase SIAH1 (EC 6.3.2.-) (Seven in absentia homolog 1)				
DE	(Siah-1) (Siah-1a).				
GN	Name=SIAH1; Synonyms=HUMSIAH;				
OS	Homo sapiens (Human)				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				
OX	NCBI_TaxID=9606;				
[1]					
RP	SEQUENCE FROM N.A. (ISOFORM 1).				
RC	TISSUE=Intestinal epithelium;				
RX	MEDLINE=96392362; PubMed=8799150; DOI=10.1073/pnas.93.17.9039;				
RA	Nemani M., Linares-Cruz G., Bruzoni-Giovanelli H., Roperch J.-P.,				
RA	Tuynder M., Bougueleret L., Cherif D., Medhioub M., Pasturaud P.,				
RA	Alvaro V., Der Sarkissian H., Cazes L., Le Paslier D., Le Gall I.,				
RA	Israeli D., Dausset J., Sigauf F., Chumakov I., Oren M., Calvo F.,				
RA	Amson R.B., Cohen D., Telerman A.;				
RT	"Activation of the human homologue of the Drosophila sina gene in				
RT	apoptosis and tumor suppression."				
RL	Proc. Natl. Acad. Sci. U.S.A. 93:9039-9042(1996).				
[2]					
RP	SEQUENCE FROM N.A. (ISOFORM 1), SUBCELLULAR LOCATION, AND TISSUE				
RC	SPECIFICITY.				
RC	TISSUE=Fetal brain;				
RX	MEDLINE=9806768; PubMed=9403064; DOI=10.1006/geno.1997.4997;				
RA	Hu G., Chung Y.-L., Glover T., Valentine V., Look A.T., Fearon E.R.;				
RT	"Characterization of human homologs of the Drosophila seven in				
RT	absentia (sina) gene."				
RL	Genomics 46:103-111(1997).				
[3]					
RP	SEQUENCE FROM N.A.				
RC	PubMed=10956387;				
RX	Medhioub M., Vaurty C., Hamelin R., Thomas G.;				
RA	"Lack of somatic mutation in the coding sequence of SIAH1 in tumors				
RT	hemixygous for this candidate tumor suppressor gene."				
RL	Int. J. Cancer 87:794-797(2000).				
[4]					
RP	SEQUENCE FROM N.A. (ISOFORM 2).				
RC	TISSUE=Retina;				
RA	Koehler K., Beyer A., Meves H.-W., Weil B., Amid C., Osanger A.,				
RA	Fobo G., Han M., Wiemann S.;				
RL	Submitted (AUG-2003) to the EMBL/GenBank/DBJ databases.				
[5]					
RP	SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).				
RC	TISSUE=Brain, and Pancreas;				
RX	MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;				
RA	Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,				
RA	Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,				

Q69dp4 drosophila
Q69dp5 drosophila
Q69dp7 drosophila
Q69dn6 drosophila
Q69dn9 drosophila
Q69dp2 drosophila
Q69dn4 drosophila
Q69dp1 drosophila
Q69dn5 drosophila
Q69dp0 drosophila
Q69dn0 drosophila
Q8iw03 homo sapien
Q8z6z3 oryza sativ
Q9xgc3 vitis vinif

- RA Altschul S.F., Zeeberg B., Buettow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Vallalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalusz D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
[6]
RN FUNCTION IN DEGRADATION OF DCC, SUBCELLULAR LOCATION, AND INTERACTION
RP WITH UBE21.
RX PubMed=9334332;
RA Hu G., Zhang S., Vidal M., Baer J.L., Xu T., Fearon E.R.;
RT "Mammalian homologs of seven in absentia regulate DCC via the
RT ubiquitin-proteasome pathway."
RL Genes Dev. 11:2701-2714(1997).
[7]
RN INTERACTION WITH BAG1, AND SUBCELLULAR LOCATION.
RP PubMed=958267; DOI=10.1093/emboj/17.10.2736;
RA Matsuzawa S., Takayama S., Froesch B.A., Zapata J.M., Reed J.C.;
RT "p53-inducible human homologue of Drosophila seven in absentia (Siah)
RT inhibits cell growth: suppression by BAG-1."
RL EMBO J. 17:2736-2747(1998).
[8]
RN FUNCTION, SUBCELLULAR LOCATION, AND MUTAGENESIS OF GLU-40; CYS-41;
RP CYS-44; CYS-55; HIS-59; ARG-66; LYS-68; ARG-76; HIS-152; HIS-202 AND
RP LEU-211.
RX PubMed=9858595;
RA Hu G., Fearon E.R.;
RT "Siah-1 N-terminal RING domain is required for proteolysis function,
RT and C-terminal sequences regulate oligomerization and binding to
RT target proteins."
RL Mol. Cell. Biol. 19:724-732(1999).
[9]
RN FUNCTION IN DEGRADATION OF KIF22, AND INTERACTION WITH ALPHA-TUBULIN.
RX PubMed=11146551; DOI=10.1038/sj.onc.1204002;
RA Germani A., Bruzzone-Giovanelli H., Fellous A., Gisselbrecht S.,
RA Varin-Blank N., Calvo F.;
RT "SIAH-1 interacts with alpha-tubulin and degrades the kinesin Kid by
RT the proteasome pathway during mitosis."
RL Oncogene 19:5997-6006(2000).
[10]
RN FUNCTION IN DEGRADATION OF MYB.
RX PubMed=10747903; DOI=10.1074/jbc.M000372200;
RA Tanikawa J., Ichikawa-Iwata E., Kanei-Ishii C., Nakai A.,
RA Matsuzawa S.-I., Reed J.C., Ishii S.;
RT "p53 suppresses the c-Myc-induced activation of heat shock
RT transcription factor 3."
RL J. Biol. Chem. 275:15578-15585(2000).
[11]
RN FUNCTION IN DEGRADATION OF CTNNB1, AND SUBUNIT OF A COMPLEX WITH
RP UBE2D1; CACYPB; SKP1A; APC AND TBL1X.
RX PubMed=11389839; DOI=10.1016/S1097-2765(01)00242-8;
RA Matsuzawa S.-I., Reed J.C.;
RT "Siah-1, SIP, and Ebi collaborate in a novel pathway for beta-catenin
RT degradation linked to p53 responses."
RL Mol. Cell. Biol. 21:915-926(2001).
[12]
RN FUNCTION IN DEGRADATION OF CTNNB1.
RX PubMed=11389840; DOI=10.1016/S1097-2765(01)00241-6;
RA Liu J., Stevens J., Rote C.A., Yost H.J., Hu Y., Neufeld K.L.,
RA White R.L., Matsunami N.;
RT "Siah-1 mediates a novel beta-catenin degradation pathway linking p53
RT to the adenomatous polyposis coli protein.";
RL Mol. Cell. Biol. 21:927-936(2001).
[13]
RN FUNCTION IN DEGRADATION OF POU2AF1, AND SUBCELLULAR LOCATION.
RX PubMed=11483517; DOI=10.1093/emboj/20.15.4143;
RA Tiedt R., Bartholdy B.A., Matthias G., Newell J.W., Matthias P.;
RT "The RING finger protein Siah-1 regulates the level of the
RT transcriptional coactivator OBF-1."
RL EMBO J. 20:4143-4152(2001).
[14]
RN FUNCTION IN DEGRADATION OF POU2AF1.
RX PubMed=11483518; DOI=10.1093/emboj/20.15.4153;
RA Boehm J., He Y., Greiner A., Staudt L., Wirth T.;
RT "Regulation of B0B.1/OBF.1 stability by SIAH."
RL EMBO J. 20:4153-4162(2001).
[15]
RN FUNCTION IN DEGRADATION OF NUBP.
RX PubMed=11752454; DOI=10.1073/pnas.261571998;
RA Susini L., Passer B.J., Amzallag-Elbaz N., Juven-Gershon T., Amson R.,
RA Prieur S., Privat N., Tuvynder M., Gendron M.-C., Israeeli A.,
RA Oren M., Telerman A.;
RT "Siah-1 binds and regulates the function of Numb."
RL Proc. Natl. Acad. Sci. U.S.A. 98:15067-15072(2001).
[16]
RN FUNCTION IN DEGRADATION OF TIEG1.
RX PubMed=12072443; DOI=10.1074/jbc.M204812200;
RA Johnsen S.A., Subramaniam M., Monroe D.G., Janknecht R.,
RA Spelsberg T.C.;
RT "Modulation of transforming growth factor beta (TGFbeta)/Smad
RT transcriptional responses through targeted degradation of TGFbeta-
RT inducible early gene-1 by human seven in absentia homologue."
RL J. Biol. Chem. 277:30754-30759(2002).
[17]
RN FUNCTION IN DEGRADATION OF SNCAIP, AND SUBCELLULAR LOCATION.
RX PubMed=14506261; DOI=10.1074/jbc.M306347200;
RA Negano Y., Yamashita H., Takahashi T., Kishida S., Nakamura T.,
RA Iseki E., Hattori N., Mizuno Y., Kikuchi A., Matsumoto M.;
RT "Siah-1 facilitates ubiquitination and degradation of synphilin-1."
RL J. Biol. Chem. 278:51504-51514(2003).
[18]
RN INTERACTION WITH PEG10.
RX PubMed=12810624;
RA Okabe H., Satoh S., Furukawa Y., Kato T., Hasegawa S., Nakajima Y.,
RA Yamaoka Y., Nakamura Y.;
RT "Involvement of PEG10 in human hepatocellular carcinogenesis through
RT interaction with SIAH1."
RL Cancer Res. 63:3043-3048(2003).
[19]
RN TISSUE SPECIFICITY.
RX PubMed=12557228; DOI=10.1002/gcc.10170;
RA Matsuo K., Satoh S., Okabe H., Nomura A., Maeda T., Yamaoka Y.,
RA Ikai I.;
RT "SIAH1 inactivation correlates with tumor progression in
RT hepatocellular carcinomas."
RL Genes Chromosomes Cancer 36:283-291(2003).
[20]
RN FUNCTION IN DEGRADATION OF RBBP8.
RX PubMed=14654780; DOI=10.1038/sj.onc.1206994;
RA Germani A., Prabel A., Mourah S., Podgorniak M.-P., Di Carlo A.,
RA Ehrlich R., Gisselbrecht S., Varin-Blank N., Calvo F.,
RA Bruzzone-Giovanelli H.;
RT "SIAH-1 interacts with CtIP and promotes its degradation by the
RT proteasome pathway."
RL Oncogene 22:8845-8851(2003).
[21]
RN INTERACTION WITH CACYPB, AND MUTANTS A; B; C; D AND E.
RX PubMed=12421809; DOI=10.1074/jbc.M210263200;
RA Matsuzawa S.-I., Li C., Ni C.-Z., Takayama S., Reed J.C., Ely K.R.;
RT "Structural analysis of Siah1 and its interactions with Siah-
RT interacting protein (SIP)."
RL J. Biol. Chem. 278:1837-1840(2003).
[22]
RN FUNCTION IN DEGRADATION OF PML, AND MUTANTS A AND D.
RP

RX PubMed=14645235; DOI=10.1074/jbc.M306407200;
RA Fanelli M., Fantozzi A., De Luca P., Caprodossi S., Matsuzawa S.-I.,
Query Match 95.1%; Score 1532; DB 1; Length 282;
Best Local Similarity 100.0%; Pred. No. 4.5e-127;
Matches 282; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 17 MSRTATATPTGTSKCPSPQSRVPALTTGTTASNNDLASLFECPCVDFVLPILQCSGHL 76
DB 1 MSRTATATPTGTSKCPSPQSRVPALTTGTTASNNDLASLFECPCVDFVLPILQCSGHL 60
QY 77 VCSNCRPKLTCCPTCRGPLGSIRNLAMEKANSVLPCKYASSCEITLPHTEKADHEEL 136
DB 61 VCSNCRPKLTCCPTCRGPLGSIRNLAMEKANSVLPCKYASSCEITLPHTEKADHEEL 120
QY 137 CEFRPYSCPCPGASCKWQSGSLDAMPHLMHQHSITTLQGEDIVFLATDINLPGAVDWM 196
DB 121 CEFRPYSCPCPGASCKWQSGSLDAMPHLMHQHSITTLQGEDIVFLATDINLPGAVDWM 180
QY 197 MQSCFGFHFMLVLEKQYDGHQOFFFAIVQLIGTRKQAFNFAVLELNGHRRRLTWEATP 256
DB 181 MQSCFGFHFMLVLEKQYDGHQOFFFAIVQLIGTRKQAFNFAVLELNGHRRRLTWEATP 240
QY 257 RSHIEGATAIMNSDCLVFTSIAQLFAENGNGINVTISM 298
DB 241 RSHIEGATAIMNSDCLVFTSIAQLFAENGNGINVTISM 282
RESULT 2
Q6GQJ5 PRELIMINARY; PRT; 282 AA.
ID Q6GQJ5
AC Q6GQJ5
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE MSC79105 protein.
GN Name=MGC79105;
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidea; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Ovary;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Atschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Vallalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
Krzyszinski M.I., Skalska U., Smallos D.E., Schnerch A., Schein J.E.,
Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences".
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Ovary;
RA Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
Richardson P.;
RT "Genetic and genomic tools for Xenopus research: The NIH Xenopus

initiative".
RL Dev. Dyn. 225:384-391 (2002).
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Ovary;
RA Klein S., Gerhard D.S.;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC072747; AAH72747.1; .
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0000151; C:ubiquitin-protein ligase complex; IEA.
DR GO; GO:0004842; F:ubiquitin-protein ligase activity; IEA.
DR GO; GO:0008270; F:zinc ion binding; IEA.
DR GO; GO:0007275; P:development; IEA.
DR GO; GO:0016567; P:protein ubiquitination; IEA.
DR GO; GO:0006511; P:ubiquitin-dependent protein catabolism; IEA.
DR InterPro; IPR004162; Sina.
DR InterPro; IPR008974; Traf like.
DR InterPro; IPR001841; Znf_Ring.
DR Pfam; PF03145; Sina; 1.
DR PROSITE; PS00089; ZF_RING_2; 1.
SQ SEQUENCE 282 AA; 31109 MW; 21629CB20DDFE793 CRC64;
Query Match 94.9%; Score 1529; DB 2; Length 282;
Best Local Similarity 99.3%; Pred. No. 8.3e-127;
Matches 280; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
QY 17 MSRTATATPTGTSKCPSPQSRVPALTTGTTASNNDLASLFECPCVDFVLPILQCSGHL 76
DB 1 MSRTATATPTGTSKCPSPQSRVPALTTGTTASNNDLASLFECPCVDFVLPILQCSGHL 60
QY 77 VCSNCRPKLTCCPTCRGPLGSIRNLAMEKANSVLPCKYASSCEITLPHTEKADHEEL 136
DB 61 VCSNCRPKLTCCPTCRGPLGSIRNLAMEKANSVLPCKYASSCEITLPHTEKADHEEL 120
QY 137 CEFRPYSCPCPGASCKWQSGSLDAMPHLMHQHSITTLQGEDIVFLATDINLPGAVDWM 196
DB 121 CEFRPYSCPCPGASCKWQSGSLDAMPHLMHQHSITTLQGEDIVFLATDINLPGAVDWM 180
QY 197 MQSCFGFHFMLVLEKQYDGHQOFFFAIVQLIGTRKQAFNFAVLELNGHRRRLTWEATP 256
DB 181 MQSCFGFHFMLVLEKQYDGHQOFFFAIVQLIGTRKQAFNFAVLELNGHRRRLTWEATP 240
QY 257 RSHIEGATAIMNSDCLVFTSIAQLFAENGNGINVTISM 298
DB 241 RSHIEGATAIMNSDCLVFTSIAQLFAENGNGINVTISM 282
RESULT 3
SIIA MOUSE
ID SIIA MOUSE STANDARD; PRT; 282 AA.
AC P61092; Q06984;
DT 05-JUL-2004 (Rel. 44, Created)
DT 05-JUL-2004 (Rel. 44, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Ubiquitin ligase SIIA1A (EC 6.3.2.-) (Seven in absentia homolog 1a)
DE (SIIA1a) (SIIA-1a) (mSIIA-1a).
GN Name=SIIA1a;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A. AND TISSUE SPECIFICITY.
RC STRAIN=Swiss; TISSUE=Eye;
RX MEDLINE=94008536; PubMed=8404535;
RA Della N.G., Senior P.V., Bowtell D.D.L.;
RT "Isolation and characterisation of murine homologues of the Drosophila
seven in absentia gene (sina)".
RL Development 117:1333-1343 (1993).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6; TISSUE=olfactory epithelium;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

complex composed of UBE2D1, SIAH1, CACYBP/SIP, SKP1A, APC and
TbLx. Interacts with UBE2L. Interacts with alpha-tubulin.
Interacts with PEG10, which may inhibit its activity (By
similarity). Interacts with DAB1, which may inhibit its activity.
SUBCELLULAR LOCATION: Cytoplasmic; predominantly. Nuclear;
partially.
TISSUE SPECIFICITY: Widely expressed at low level in embryos and
adults. Expressed at higher level in testis. Due to the high
similarity between SIAH1 and SIAH2, it is difficult to
distinguish its own tissue specificity, suggesting that it may be
required to modulate TP53 response. The relevance of such activity
in vivo is however unclear and may not exist.
DOMAIN: The RING-type zinc finger domain is essential for
ubiquitin ligase activity.
DOMAIN: The SBD domain (substrate-binding domain) mediates the
homodimerization and the interaction with substrate proteins. It
is related to the TRAF family.
SIMILARITY: Belongs to the SINA (seven in absentia) family.
SIMILARITY: Contains 1 C2HC-type zinc finger.
SIMILARITY: Contains 1 RING-type zinc finger.
SIMILARITY: Contains 1 SIAH-type zinc finger.
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EMBL; Z19579; CAA79630.1; -
EMBL; BC046317; AAH46317.1; -
PIR; I48763; I48763
PDB; 1K2F; X-ray; A/B--
MGI; MGI:108064; Siah1a.
InterPro; IPR004162; Sina.
InterPro; IPR008974; Traf dom.
InterPro; IPR001841; Znf ring.
PROSITE; PS00518; ZF_RING_1; FALSE_NEG.
PROSITE; PS00089; ZF_RING_2; 1.
3D-structure; Apoptosis; Cell cycle; Ligase; Metal-binding;
Nuclear protein; Spermatogenesis; Ub conjugation pathway; Zinc;
Zinc-finger.
Zn FING 41 76 RING-type.
ZN FING 96 121 C2HC-type.
ZN FING 126 152 SIAH-type.
DOMAIN 90 282 SBD.
METAL 98 98 Zinc 1.
METAL 105 105 Zinc 1.
METAL 117 117 Zinc 1.
METAL 121 121 Zinc 1.
METAL 128 128 Zinc 2.
METAL 135 135 Zinc 2.
METAL 147 147 Zinc 2.
METAL 152 152 Zinc 2.
SEQUENCE 282 AA; 852ADCD5DD4A4FFA CRC64;
Query Match 94.8%; Score 1528; DB 1; Length 282;
Best Local Similarity 99.6%; Pred. No. 1e-126;
Matches 281; Conservative 1; Mismatches 0; Gaps 0;
QY 17 MSROTATLPTGTSKCPQSRVPAITCTTASNDLASLFEPCVCFDVLPPILQCSGHL 76
DB 1 MSROTATLPTGTSKCPQSRVPAITCTTASNDLASLFEPCVCFDVLPPILQCSGHL 60
QY 77 VCSNCRPKLTCCPTCRGPLGSIRNLAMEKVANSVLPFCYVASSGCEITLPHTEKADHEEL 136
DB 61 VCSNCRPKLTCCPTCRGPLGSIRNLAMEKVANSVLPFCYVASSGCEITLPHTEKADHEEL 120
QY 137 CEFRPSCPCPGASCKWQGSGLDVAVPHLMHQHKSITTLQGHEDIVFLATDINLPGAVDWM 196
DB 121 CEFRPSCPCPGASCKWQGSGLDVAVPHLMHQHKSITTLQGHEDIVFLATDINLPGAVDWM 180

RT "Isolation of 10 differentially expressed cDNAs in p53-induced
RT apoptosis: activation of the vertebrate homologue of the Drosophila
RT seven in absentia gene.";
RN Proc. Natl. Acad. Sci. U.S.A. 93:3953-3957(1996).
RN [4]
RN TISSUE SPECIFICITY.
RP PubMed=12842817; DOI=10.1152/ajpheart.00983.2002;
RP Pavre C.J., Mancuso M., Maas K., McLean J.W., Baluk P., McDonald D.M.;
RA "Expression of genes involved in vascular development and angiogenesis
RT in endothelial cells of adult lung.";
RT Am. J. Physiol. 285:H1917-H1938(2003).
RN [5]
RN INDUCTION
RP PubMed=14985507; DOI=10.1073/pnas.0400177101;
RP Flucci G., Beaucourt S., Dufaut D., Lespagnol A.,
RA Stumpner-Cuvellette P., Gaent A., Buchwalter G., Teyndler M.,
RA Susini L., Lassel J.-M., Wasylyk C., Wasylyk B., Oren M., Amson R.,
RA Telerman A.;
RT "Siah-1b is a direct transcriptional target of p53: Identification of
RT the functional p53 responsive element in the siah-1b promoter.";
RN Proc. Natl. Acad. Sci. U.S.A. 101:3510-3515(2004).
CC -!- FUNCTION: E3 Ubiquitin ligase protein that mediates ubiquitination
CC and subsequent proteasomal degradation of target proteins. E3
CC ubiquitin ligases accept ubiquitin from an E2 ubiquitin-
CC conjugating enzyme in the form of a thioester and then directly
CC transfers the ubiquitin to targeted substrates. Mediates E3
CC ubiquitin ligase activity either through direct binding to
CC substrates or by functioning as the essential RING domain subunit
CC of larger E3 complexes. Probably triggers the ubiquitin-mediated
CC degradation of many substrates (By similarity).
CC -!- PATHWAY: Ubiquitin conjugation; third step.
CC -!- SUBCELLULAR LOCATION: Cytoplasmic; predominantly. Nuclear;
CC partially (By similarity).
CC -!- TISSUE SPECIFICITY: Widely expressed at low level in embryos and
CC adults. Due to the high similarity between SIAH1A and SIAH1B, it
CC is difficult to distinguish its own tissue specificity.
CC Overexpressed in endothelial cells of adult lung.
CC -!- INDUCTION: Induced by TP53/p53, suggesting that it may be required
CC to modulate TP53 response.
CC -!- DOMAIN: The RING-type zinc finger domain is essential for
CC ubiquitin ligase activity.
CC -!- DOMAIN: The SBD domain (substrate-binding domain) mediates the
CC homodimerization and the interaction with substrate proteins. It
CC is related to the TRAF family (By similarity).
CC -!- SIMILARITY: Belongs to the SINA (Seven in absentia) family.
CC -!- SIMILARITY: Contains 1 C2HC-type zinc finger.
CC -!- SIMILARITY: Contains 1 RING-type zinc finger.
CC -!- SIMILARITY: Contains 1 SIAH-type zinc finger.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
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CC or send an email to license@sib-sib.ch).
CC -----
DR EMBL; Z19580; CAA79631.1; -.
DR EMBL; BC052887; AAH52887.1; -.
DR PIR; I48764; S35754.
DR HSP; Q06984; I42F.
DR MGD; MG1:108063; Siah1b.
DR InterPro; IPR004162; Sina.
DR InterPro; IPR008974; Traf.dom.
DR InterPro; IPR001841; Znf_ring.
DR Pfam; PF03145; Sina; 1.
DR SMART; SM00184; RING; 1.
DR PROSITE; PS00518; ZF_RING_1; FALSE_NEG.
DR PROSITE; PS50089; ZF_RING_2; 1.
KW Ligase; Metal-binding; Nuclear protein; Ubl conjugation pathway; Zinc;
KW Zinc-finger. 41 76 RING-type.
FT ZN_FING 96 C2HC-type.

FT	ZN_FING	126	152	SIAH-type.
FT	DOMAIN	90	282	SBD.
FT	METAL	98		Zinc 1 (By similarity).
FT	METAL	105		Zinc 1 (By similarity).
FT	METAL	117		Zinc 1 (By similarity).
FT	METAL	121		Zinc 1 (By similarity).
FT	METAL	128		Zinc 2 (By similarity).
FT	METAL	135		Zinc 2 (By similarity).
FT	METAL	147		Zinc 2 (By similarity).
FT	METAL	152		Zinc 2 (By similarity).
FT	CONFLICT	87		V -> M (in Ref. 1).
SQ	SEQUENCE	282 AA;	31122 MW;	A09F5D3DEEB39AC2 CRC64;

Query Match 92.7%; Score 1494; DB 1; Length 282;
Best Local Similarity 97.2%; Pred. No. 1e-123;
Matches 274; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

QY	17	MSRQTATATPTGTSKCPSPORVPALCTGTATSNNDLASLFECPCVDFVLPILQCSGHL	76
DB	1	MSRQAATATLTGTSKCPSPORVPALCTGTATSNNDLASLFECPCVDFVLPILQCSGHL	60
QY	77	VCNCRPKLTCCPTCRGLGSIIRNLAMEKVANSVLPFCVYASSCEITLPHTEKADHEEL	136
DB	61	VCNCRPKLTCCPTCRGLGSIIRNLAMEKVANSVLPFCVYASSCEITLPHTEKADHEEL	120
QY	137	CEFRPVSCTPCGASCKWQSLDAMPVHLMHQHSITTTLOGEDIVFLATDINLPGAVDWM	196
DB	121	CEFRPVSCTPCGASCKWQSLDAMPVHLMHQHSITTTLOGEDIVFLATDINLPGAVDWM	180
QY	197	MQSCFGFHFMLVLEKQEKYDGHQOFFAIVQLIGTRKQAEFAVRLNGLNHRRLTWEATP	256
DB	181	MQSCFGFHFMLVLEKQEKYDGHQOFFAIVQLIGTRKQAEFAVRLNGLNHRRLTWEATP	240
QY	257	RSIHGIATAIMNSDCLVFTSTIAQLFAENGNGINVTISMC	298
DB	241	RSIHGIATAIMNSDCLVFTSTIAQLFAENGNGINVTISMC	282

RESULT 7
ID Q7Q5Z0 PRELIMINARY; PRT; 311 AA.
AC Q7Q5Z0;
DT 01-MAR-2004 (TrEMBLrel. 26, Created)
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE EbiP5924 (Fragment).
GN Name=ebic5924; ORFNames=ENSANGG0000004508;
OS Anopheles gambiae str. PEST.
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Anopheles.
OX NCBI_TaxID=180454;
[1]
RP SEQUENCE FROM N.A.
RC STRAIN=PEST;
RA Anopheles Genome Sequencing Consortium;
RL Submitted (Mar-2002) to the EMBL/GenBank/DBJ databases.
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
CC EMBL; AAAB01008960; EAA11451.1; -.
DR HSP; P61092; I42F.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:000151; C:ubiquitin ligase complex; IEA.
DR GO; GO:0004842; F:ubiquitin-protein ligase activity; IEA.
DR GO; GO:0008270; F:zinc ion binding; IEA.
DR GO; GO:0007275; P:development; IEA.
DR GO; GO:0016567; P:protein ubiquitination; IEA.
DR GO; GO:0006511; P:ubiquitin-dependent protein catabolism; IEA.
DR InterPro; IPR004162; Sina.
DR InterPro; IPR008974; Traf.like.
DR InterPro; IPR001841; Znf_Ring.
DR Pfam; PF03145; Sina; 1.
DR PROSITE; PS50089; ZF_RING_2; 1.

FT NON_TER 1 1
FT NON_TER 311 311
SQ SEQUENCE 311 AA; 34029 MW; 6F79749EF318FC86 CRC64;
Query Match 75.1%; Score 1210; DB 2; Length 311;
Best Local Similarity 72.7%; Pred. No. 1.4e-98;
Matches 226; Conservative 32; Mismatches 29; Indels 24; Gaps 3;
QY 9 PPVVFISEMSRQTATLPTGTSKCP-----PSORVPALTGTTASNN-----49
Db 2 PSHTETAQTAETTAATTTTTTTTTTTMSNKLNNPKER--EVTGSSSSNSSISSVAGDGS 59
QY 50 ---DLASLFCPCVDFVLPPILOCSGHLVCSNCRPKLTCCPTCRGPLGSIIRNLAMEKV 106
Db 60 ISADLASLFCPCVDFVLPPILOCSGHLVCSNCRPKLTCCPTCRGPLGSIIRNLAMEKV 119
QY 107 ANSVLPFPCKVASSGCEITLPHTEKADHEELCEFRPSCPCPGASCCKWQGSGLDVMPLMH 166
Db 120 ASNVKFPCKSHNGCTVSLVYTEKAHEEACEFRPYLPCPCPGASCCKWQGSGLDVMPLMH 179
QY 167 QHSITTLQGEDIVFLATDINLPGADVMMQSCFGHFMVLVEKQKDYDGHQOQFAIVQ 226
Db 180 SHKSITTLQGEDIVFLATDINLPGADVMMQSCFGHFMVLVEKQKDYDGHQOQFAIVQ 239
QY 227 LIGTRKQAEFAYLELNGHRRRLTWEATPRSIHEGIATAIMNSDCLVFTDSIAQLFAEN 286
Db 240 LIGSRKQAEFAYLELNGHRRRLTWEATPRSIHEGVASAILNSDCLVFTDSIAQLFADN 299
QY 287 GNLGINTVISM 297
Db 300 GNLGINTVISV 310
RESULT 8
SIA2 MOUSE STANDARD; PRT; 325 AA.
AC Q06986;
DT 05-JUL-2004 (Rel. 44, Created)
DT 05-JUL-2004 (Rel. 44, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Ubiquitin ligase SIAH2 (EC 6.3.2.-) (Seven in absentia homolog 2) (Siah2) (msiah2).
GN Name=Siah2;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OC NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A., AND TISSUE SPECIFICITY.
RC STRAIN=Swiss;
RX MEDLINE=94008536; PubMed=8404535;
RA Della N.G., Senior P.V., Bowtell D.D.L.;
RT "Isolation and characterisation of murine homologues of the Drosophila seven in absentia gene (sina).";
RL Development 117:1333-1343(1993).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6; TISSUE=Brain;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Schuler G.D., Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D., Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J., Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickinson M.C.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.N., Krzywinski M.I., Skalski U., Smailus D.E., Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [3]
RP FUNCTION IN DEGRADATION OF BAG1.
RX PubMed=11257006;
RA Sourisseau T., Desbois C., Debure L., Bowtell D.D.L., Cato A.C.B., Schneikert J., Moysse E., Michel D.;
RT "Alteration of the stability of Bag-1 protein in the control of olfactory neuronal apoptosis.";
RL J. Cell Sci. 114:1409-1416(2001).
RN [4]
RP TISSUE SPECIFICITY.
RX PubMed=7895278;
RA Della N.G., Bowtell D.D.L., Beck F.;
RT "Expression of Siah-2, a vertebrate homologue of Drosophila sina, in germ cells of the mouse ovary and testis.";
RL Cell Tissue Res. 279:411-419(1995).
RN [5]
RP FUNCTION IN DEGRADATION OF NCOR1.
RX PubMed=9637679;
RA Zhang J., Guenther M.G., Carthew R.W., Lazar M.A.;
RT "Proteasomal regulation of nuclear receptor corepressor-mediated repression.";
RL Genes Dev. 12:1775-1780(1998).
RN [6]
RP INDUCTION.
RX PubMed=12417719; DOI=10.1128/MCB.22.23.8155-8164.2002;
RA Frew I.J., Dickens R.A., Cuddihy A.R., Del Rosario M., Reinhard C., O'Connell M.J., Bowtell D.D.L.;
RT "Normal p53 function in primary cells deficient for Siah genes.";
RL Mol. Cell. Biol. 22:8155-8164(2002).
RN [7]
RP FUNCTION.
RX PubMed=14645526; DOI=10.1128/MCB.23.24.9150-9161.2003;
RA Frew I.J., Hammond V.E., Dickens R.A., Quinn J.M.W., Walkley C.R., Sims N.A., Schnall R., Della N.G., Holloway A.J., Digby M.R., James P.W., Tarlington D.M., Purton L.E., Gillespie M.T., Bowtell D.D.L.;
RT "The coiled-coil domain is the structural determinant for mammalian homologues of Drosophila Sina-mediated degradation of promyelocytic leukemia protein and other tripartite motif proteins by the proteasome.";
RL J. Biol. Chem. 279:5374-5379(2004).
RN [8]
RP FUNCTION IN DEGRADATION OF PML.
RX PubMed=14645235; DOI=10.1074/jbc.M306407200;
RA Fanelli M., Fantozzi A., De Luca P., Caprodossi S., Matsuzawa S.-I., Lazar M.A., Pelicci P.G., Minucci S.;
RT "The coiled-coil domain is the structural determinant for mammalian homologues of Drosophila Sina-mediated degradation of promyelocytic leukemia protein and other tripartite motif proteins by the proteasome.";
RL J. Biol. Chem. 279:5374-5379(2004).
RN [9]
RP FUNCTION: E3 Ubiquitin ligase protein that mediates ubiquitination and subsequent proteasomal degradation of target proteins. E3 ubiquitin ligases accept ubiquitin from an E2 ubiquitin-conjugating enzyme in the form of a thioester and then directly transfers the ubiquitin to targeted substrates. Mediates E3 ubiquitin ligase activity either through direct binding to substrates or by functioning as the essential RING domain subunit of larger E3 complexes. Triggers the ubiquitin-mediated degradation of many substrates, including proteins involved in transcription regulation (POU2AF1, PML, NCOR1), a cell surface receptor (DCC), an antiapoptotic protein (BAG1), and a protein involved in synaptic vesicle function in neurons (SYN). It is thereby involved in apoptosis, tumor suppression, cell cycle, transcription and signaling processes. Has some overlapping function with SIAH1. Triggers the ubiquitin-mediated degradation of TRAF2, whereas SIAH1 can not.
RN [10]
RP PATHWAY: Ubiquitin conjugation; third step.
RN [11]
RP SUBUNIT: Homodimer. Interacts with UBE2E2. Interacts with VAV1, without mediating its ubiquitin-mediated degradation. Interacts

CC with CACVBP/SIP. Probable component of some large E3 complex
 CC possibly composed of UBE2D1, SIAH2, CACVBP/SIP, SKP1A, APC and
 CC TBLIX. Interacts with UBE2D1. Interacts with PEG10, which may
 CC inhibit its activity (By similarity).
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic; predominantly Nuclear;
 CC partially (By similarity).
 CC -1- TISSUE SPECIFICITY: Widely expressed at low level in embryos and
 CC adults. Expressed in a specific population of germ cells within
 CC both the mouse ovary and testis. Absent in primordial oocytes but
 CC expressed in all growing oocytes, coincident with their
 CC recruitment from the pool of quiescent cells. Its level of
 CC expression increases as the oocytes mature. Expressed in Graafian
 CC follicles and in fertilized zygotes up until the two cell stage, a
 CC time of extensive maternal transcript degradation and zygotic gene
 CC activation. Expressed in the testis from postmeiotic spermatids.
 CC -1- INDUCTION: May be induced by TP53/p53, suggesting that it may be
 CC required to modulate TP53 response. The relevance of such activity
 CC in vivo is however unclear and may not exist.
 CC -1- DOMAIN: The RING-type zinc finger domain is essential for
 CC ubiquitin ligase activity.
 CC -1- DOMAIN: The SBD domain (substrate-binding domain) mediates the
 CC homodimerization and the interaction with substrate proteins. It
 CC is related to the TRAF family (By similarity).
 CC -1- SIMILARITY: Belongs to the SINA (Seven in Absentia) family.
 CC -1- SIMILARITY: Contains 1 C2HC-type zinc finger.
 CC -1- SIMILARITY: Contains 1 RING-type zinc finger.
 CC -1- SIMILARITY: Contains 1 SIAH-type zinc finger.
 CC -----
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 CC -----
 DR EMBL; Z19581; CAA79632.1; --
 DR EMBL; BC058400; AAH58400.1; --
 DR PIR; I48765; I48765.
 DR HSSP; Q06984; IK2F.
 DR MGD; MGI:108062; Siah2.
 DR InterPro; IPR004162; Sina.
 DR InterPro; IPR008974; Traf_dom.
 DR InterPro; IPR001841; Znf_ring.
 DR Pfam; PF03145; Sina; 1.
 DR SMART; SM00184; RING; 1.
 DR PROSITE; PS00518; ZF_RING_1; FALSE_NEG.
 DR PROSITE; PS00089; ZF_RING_2; 1.
 DR Apoptosis; Cell cycle; Ligase; Metal-binding; Nuclear protein;
 KW Ub1 conjugation pathway; Zinc; Zinc-finger.
 FT ZN FING 81 116 RING-type.
 FT ZN FING 137 162 C2HC-type.
 FT ZN FING 167 193 SIAH-type.
 FT DOMAIN 131 323 SBD.
 FT METAL 139 139 Zinc 1 (By similarity).
 FT METAL 146 146 Zinc 1 (By similarity).
 FT METAL 158 158 Zinc 1 (By similarity).
 FT METAL 162 162 Zinc 1 (By similarity).
 FT METAL 169 169 Zinc 2 (By similarity).
 FT METAL 176 176 Zinc 2 (By similarity).
 FT METAL 188 188 Zinc 2 (By similarity).
 FT METAL 193 193 Zinc 2 (By similarity).
 FT CONFLICT 203 204 DI -> ET (in Ref. 1).
 SQ SEQUENCE 325 AA; 34757 MW; 1CB73AD3B4C9982F CRC64;
 Query Match 74.4%; Score 1199; DB 1; Length 325;
 Best Local Similarity 77.6%; Pred. No. 1.4e-97;
 Matches 222; Conservative 26; Mismatches 8; Gaps 3;
 QY 21 TATPAGTGTSCPPSQRV---PALTG---TTASNDLASLFCPCVCFVLPPILOQCS 73
 DB TTSAGFGSSAVAAAVISGPGAGGADVPSPQHELTSFPCPCVCFVLPPILOQCA 97

QY 74 GHLYVCSNCRPKLTCCPTCRGPL-GSIRNLAMEKVANSVLPCKYASSGCCBITLPHTEKAD 132
 DB GHLYVCSNCRPKLTCCPTCRGPL-GSIRNLAMEKVANSVLPCKYASSGCCBITLPHTEKPE 157
 QY 133 HEELCEFRPVPSCPCPGASCKWQSLDAMPHLMHOKHSITTLQGEDIVFLATDINLPGAV 192
 DB HEELCEFRPVPSCPCPGASCKWQSLDAMPHLMHOKHSITTLQGEDIVFLATDINLPGAV 217
 QY 193 DWYMMQSCFGFHMVLVLEKOEKDYDGHQOFPFAIVOLIGTRKQAFYRLELNGHRRRLTW 252
 DB DWYMMQSCFGFHMVLVLEKOEKDYDGHQOFPFAIVOLIGTRKQAFYRLELNGHRRRLTW 277
 QY 253 EATPSRIHGGIATAMNSDCLVDTSTIAQLFAENGNGINVTISMC 298
 DB EATPSRIHGGIATAMNSDCLVDTSTIAQLFAENGNGINVTISMC 323
 RESULT 9
 SIA2_RAT STANDARD; PRT; 325 AA.
 AC Q8R4T2; Q920M8;
 DT 05-JUL-2004 (Rel. 44, Created)
 DT 05-JUL-2004 (Rel. 44, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Ubiquitin ligase SIAH2 (EC 6.3.2.-) (Seven in Absentia homolog 2)
 DE (Siah-2).
 DE Names=Siah2;
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OC NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Yamaguchi A., Hori O., Tohyama M.;
 RT "Rat Siah1a";
 RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP INTERACTION OF 71-325 FROM N.A., FUNCTION IN SYP DEGRADATION, AND
 RP INTERACTION WITH UBE2E2.
 RC STRAIN=Sprague-Dawley;
 RX MEDLINE=21895831; PubMed=11786535; DOI=10.1074/jbc.M107857200;
 RA Wheeler T.C., Chin L.-S., Li Y., Roudabush F.L., Li L.;
 RT "Regulation of synaptophysin degradation by mammalian homologues of
 RT Seven in Absentia";
 RL J. Biol. Chem. 277:10273-10282(2002).
 CC -1- FUNCTION: E3 Ubiquitin ligase protein that mediates ubiquitination
 CC and subsequent proteasomal degradation of target proteins. E3
 CC ubiquitin ligases accept ubiquitin from an E2 ubiquitin-
 CC conjugating enzyme in the form of a thioester and then directly
 CC transfers the ubiquitin to targeted substrates. Mediates E3
 CC ubiquitin ligase activity either through direct binding to
 CC substrates or by functioning as the essential RING domain subunit
 CC of larger E3 complexes. Triggers the ubiquitin-mediated
 CC degradation of many substrates, including proteins involved in
 CC transcription regulation (POU2AF1, PML, NCOR1), a cell surface
 CC receptor (DCC), an antiapoptotic protein (BAG1), and a protein
 CC involved in synaptic vesicle function in neurons (SYP). It is
 CC thereby involved in apoptosis, tumor suppression, cell cycle,
 CC transcription and signaling processes. Has some overlapping
 CC function with SIAH1. Triggers the ubiquitin-mediated degradation
 CC of TRAF2, whereas SIAH1 can not.
 CC -1- PATHWAY: Ubiquitin conjugation; third step.
 CC -1- SUBUNIT: Homodimer. Interacts with VAV1, without mediating its
 CC ubiquitin-mediated degradation. Probable component of some large
 CC E3 complex possibly composed of UBE2D1, SIAH2, CACVBP/SIP, SKP1A,
 CC APC and TBLIX. Interacts with UBE2E2. Interacts with UBE2E1.
 CC Interacts with PEG10, which may inhibit its activity (By
 CC similarity). Interacts with UBE2E2.
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic; predominantly Nuclear;
 CC partially (Probable).
 CC -1- DOMAIN: The RING-type zinc finger domain is essential for
 CC ubiquitin ligase activity.
 CC -1- DOMAIN: The SBD domain (substrate-binding domain) mediates the

CC CC homodimerization and the interaction with substrate proteins. It
 CC is related to the TRAF family (By similarity).
 CC DE -1- SIMILARITY: Belongs to the SIAH (seven in absentia) family.
 CC CC -1- SIMILARITY: Contains 1 C2HC-type zinc finger.
 CC CC -1- SIMILARITY: Contains 1 RING-type zinc finger.
 CC CC -1- SIMILARITY: Contains 1 SIAH-type zinc finger.
 CC -----
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 CC -----
 CC EMBL; AB067815; BAB70754.1; -;
 CC EMBL; AF389477; AAL91363.1; -;
 CC HSP; O06984; IK2F.
 CC RGD; 620778; Siah2.
 CC InterPro; IPR004162; Sina
 CC InterPro; IPR008974; Traf dom.
 CC InterPro; IPR001841; Znf_Fing.
 CC Pfam; PF03145; Sina; 1.
 CC SMART; SM00184; RING; 1.
 CC PROSITE; PS00518; ZF_RING_1; FALSE_NEG.
 CC PROSITE; PS00083; ZF_RING_2; 1.
 CC Apoptosis; Cell cycle; Ligase; Metal-binding; Nuclear protein;
 CC Ub1 conjugation pathway; Zinc; Zinc-finger.
 CC FT ZN_FING 81 116 RING-type.
 CC FT ZN_FING 137 162 C2HC-type.
 CC FT ZN_FING 167 193 SIAH-type.
 CC FT DOMAIN 131 323 SBD.
 CC FT METAL 139 139 Zinc 1 (By similarity).
 CC FT METAL 146 146 Zinc 1 (By similarity).
 CC FT METAL 158 158 Zinc 1 (By similarity).
 CC FT METAL 162 162 Zinc 1 (By similarity).
 CC FT METAL 169 169 Zinc 2 (By similarity).
 CC FT METAL 176 176 Zinc 2 (By similarity).
 CC FT METAL 188 188 Zinc 2 (By similarity).
 CC FT METAL 193 193 Zinc 2 (By similarity).
 CC SQ SEQUENCE 325 AA; 34699 MW; 0E273AD30959982E CRC64;
 CC
 CC Query Match 74.4%; Score 1199; DB 1; Length 325;
 CC Best Local Similarity 77.6%; Pred. No. 1.4e-97;
 CC Matches 222; Conservative 26; Mismatches 30; Indels 8; Gaps 3;
 CC
 CC QY 21 TATALTPTGTSKCPSPQSV---PALTG---TASNDIASLFECPVCFDYVLPILQCS 73
 CC DB 38 TISAAGFGSSAVPAAAVISGFGAGGAGPVSPQHSLTSLFECPCFDYVLPILQCSA 97
 CC
 CC QY 74 GHLVCSNCRPKLTCCPTCRGPL-GSIRNLAMEKVANSVLPCKYASSGCEITLPHTEKAD 132
 CC DB 98 GHLVCNCRKQLSCCPTCRGALTSPSIRNLAMEKVASVLPCKYATGCSLTHTTEKPE 157
 CC
 CC QY 133 HEELCEFPYSPCPGASCKQWGLDAVPHLMHOKHSITTLQGEDIVFLATDINLPGAV 192
 CC DB 158 HEDICEYRYPSPCPGASCKQWGLSLEAVSHLMHAHSITTLQGEDIVFLATDINLPGAV 217
 CC
 CC QY 193 DWVMQSCFGHFHMLVLEKQEKYDGHQOFAIVQLIGTRKQAEAFAYELELNGHRRRLTW 252
 CC DB 218 DWVMQSCFGHFHMLVLEKQEKYDGHQOFAIVQLIGTRKQAEAFAYELELNGHRRRLTW 277
 CC
 CC QY 253 EATPRSIHEGATATMNSDCLVFTDSIAQLFAENGLNGLNVTISMC 298
 CC DB 278 EATPRSIHGDVAAIMNSDCLVFTDAIAHLFADNGLNGLNVTISMC 323
 CC
 CC RESULT 10
 CC SIA2 HUMAN
 CC ID SIA2 HUMAN STANDARD; PRT; 324 AA.
 CC AC Q43255; O43270;
 CC DT 05-JUL-2004 (Rel. 44, Created)
 CC PT 05-JUL-2004 (Rel. 44, Last sequence update)

DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Ubiquitin ligase SIAH2 (EC 6.3.2.-) (seven in absentia homolog 2)
 GN (Siah-2) (hsiah2).
 GN Name-SIAH2;
 OS Homo sapiens (Human)
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OC NCBI_TaxID=9606;
 RN [1] SEQUENCE FROM N.A., AND TISSUE SPECIFICITY.
 RP MEDLINE=98066768; PubMed=9403064; DOI=10.1006/geno.1997.4997;
 RX Hu G., Chung T.-L., Glover T., Valentine V., Look A.T., Fearon E.R.;
 RA "Characterization of human homologs of the Drosophila seven in
 RT absentia (sina) gene.";
 RL Genomics 46:103-111(1997).
 RN [2] SEQUENCE FROM N.A., AND INTERACTION WITH VAV1.
 RP PubMed=10207103;
 RX Germani A., Romero F., Houlard M., Canonis J., Gisselbrecht S.,
 RA Fischer S., Varin-Blank N.;
 RT "hsiah2 is a new Vav binding protein which inhibits Vav-mediated
 RT signaling pathways.";
 RL Mol. Cell. Biol. 19:3798-3807(1999).
 RN [3] SEQUENCE FROM N.A.
 RP TISSUE=Brain;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahy J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RA "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [4] FUNCTION IN DEGRADATION OF DCC, AND INTERACTION WITH UBE2I.
 RP PubMed=9334332;
 RX Hu G., Zhang S., Vidal M., Baer J.L., Xu T., Fearon E.R.;
 RT "Mammalian homologs of seven in absentia regulate DCC via the
 RT ubiquitin-proteasome pathway.";
 RL Genes Dev. 11:2701-2714(1997).
 RN [5] FUNCTION IN DEGRADATION OF POU2AF1.
 RP PubMed=11483518; DOI=10.1093/emboj/20.15.4153;
 RX Boehm J., He Y., Greiner A., Staudt L., Wirth T.;
 RT "Regulation of BOB.1/OBF.1 stability by SIAH.";
 RL EMBO J. 20:4153-4162(2001).
 RN [6] INTERACTION WITH CACYBP.
 RP PubMed=11389839; DOI=10.1016/S1097-2765(01)00242-8;
 RX Matsuzawa S.-I., Reed J.C.;
 RT "Siah-1, SIP, and Ebi collaborate in a novel pathway for beta-catenin
 RT degradation linked to p53 responses.";
 RL Mol. Cell 7:915-926(2001).
 RN [7] FUNCTION IN DEGRADATION OF TRAF2.
 RP PubMed=12411493; DOI=10.1093/emboj/cdf576;
 RX Habelhah H., Frew I.J., Laine A., Janes P.W., Relaix F., Sassoon D.,
 RA Bowtell D.D.L., Ronai Z.;
 RT "Stress-induced decrease in TRAF2 stability is mediated by Siah2.";
 RL Mol. Cell 7:915-926(2001).
 RN

EMBO J. 21:5756-5765(2002).
 [8]
 RL INTERACTION WITH PEG10.
 RP PubMed:12810624;
 RX Okabe H., Satoh S., Furukawa Y., Kato T., Hasegawa S., Nakajima Y.,
 RA Yamaoka Y., Nakamura Y.;
 RT "Involvement of PEG10 in human hepatocellular carcinogenesis through
 interaction with SIAH1.";
 RL Cancer Res. 63:3043-3048(2003).
 CC -!- FUNCTION: E3 Ubiquitin ligase protein that mediates ubiquitination
 and subsequent proteasomal degradation of target proteins. E3
 ubiquitin ligases accept ubiquitin from an E2 ubiquitin-
 conjugating enzyme in the form of a thioester and then directly
 transfers the ubiquitin to targeted substrates. Mediates E3
 ubiquitin ligase activity either through direct binding to
 substrates or by functioning as the essential RING domain subunit
 of larger E3 complexes. Triggers the ubiquitin-mediated
 degradation of many substrates, including proteins involved in
 transcription regulation (POU2AF1, PML, NCOR1), a cell surface
 receptor (DCC), an antiapoptotic protein (BAG1), and a protein
 involved in synaptic vesicle function in neurons (SYP). It is
 thereby involved in apoptosis, tumor suppression, cell cycle,
 transcription and signaling processes. Has some overlapping
 function with SIAH1. Triggers the ubiquitin-mediated degradation
 of TRAF2, whereas SIAH1 can not.
 CC -!- PATHWAY: Ubiquitin conjugation; third step.
 CC -!- SUBUNIT: Homodimer. Interacts with UBE2E2 (By similarity).
 CC Interacts with VAV1, without mediating its ubiquitin-mediated
 degradation. Interacts with CACYPB/SIP. Probable component of some
 large E3 complex possibly composed of UBE2D1, SIAH2, CACYBP/SIP,
 SKP1A, APC and TBL1X. Interacts with PEG10, which may inhibit its
 activity.
 CC -!- SUBCELLULAR LOCATION: Cytoplasmic; predominantly. Nuclear;
 partially (Probable).
 CC -!- TISSUE SPECIFICITY: Widely expressed at low level.
 CC -!- DOMAIN: The RING-type zinc finger domain is essential for
 ubiquitin ligase activity.
 CC -!- DOMAIN: The SBD domain (substrate-binding domain) mediates the
 homodimerization and the interaction with substrate proteins. It
 is related to the TRAF family (By similarity).
 CC -!- SIMILARITY: Belongs to the SINA (Seven in Absentia) family.
 CC -!- SIMILARITY: Contains 1 C2HC-type zinc finger.
 CC -!- SIMILARITY: Contains 1 RING-type zinc finger.
 CC -!- SIMILARITY: Contains 1 SIAH-type zinc finger.
 CC -----
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 or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL; Y6248; AAC51908.1; -;
 DR EMBL; Y1268; AAH5557.1; -;
 DR EMBL; BC013082; AAH13082.1; -;
 DR HSSP; Q06984; 1K2F.
 DR Genep; HGNC:10858; SIAH2.
 DR MIM; 602213; -;
 DR GO; GO:0005737; Cytoplasm; TAS.
 DR GO; GO:0003714; F:transcription corepressor activity; TAS.
 DR GO; GO:0007264; F:small GTPase mediated signal transduction; TAS.
 DR GO; GO:0006511; P:ubiquitin-dependent protein catabolism; TAS.
 DR InterPro; IPR004162; Sina.
 DR InterPro; IPR008974; Traf like.
 DR InterPro; IPR001841; Znf_fing.
 DR Pfam; PF03145; Sina; 1.
 DR SMART; SM00184; RING; 1.
 DR PROSITE; PS00518; ZF_RING_1; FALSE_NEG.
 DR PROSITE; PS00089; ZF_RING_2; 1.
 KW Apoptosis; Cell cycle; Ligase; Metal-binding; Nuclear protein;
 KW Ub1 conjugation pathway; Zinc; Zinc-finger.
 FT ZN_FING 80 115 RING-type.

FT	ZN_FING	136	161	C2HC-type.
FT	ZN_FING	166	192	SIAH-type.
FT	DOMAIN	130	322	SBD.
FT	METAL	138	138	Zinc 1 (By similarity).
FT	METAL	145	145	Zinc 1 (By similarity).
FT	METAL	157	157	Zinc 1 (By similarity).
FT	METAL	161	161	Zinc 1 (By similarity).
FT	METAL	168	168	Zinc 2 (By similarity).
FT	METAL	175	175	Zinc 2 (By similarity).
FT	METAL	187	187	Zinc 2 (By similarity).
FT	METAL	192	192	Zinc 2 (By similarity).
FT	CONFLICT	200	200	G -> E (in Ref. 1).
SO	SEQUENCE	324 AA;	34614 MW;	2D5DD845666EC924 CRC64;

Query Match 74.4%; Score 1198; DB 1; Length 324;
 Best Local Similarity 77.3%; Pred. No. 1.7e-97;
 Matches 221; Conservative 27; Mismatches 30; Indels 8; Gaps 2;

Qy	21	TATALPTGTSKPPSQRPVLTG-----TTASNNDLALSFECPCFVYVLPPILOQCS	73
Db	37	TISAAGFSSAVPAAAVISGPGGGGAGVPSPQHBLTSLFECPCFVYVLPPILOQCA	96
Qy	74	GHVCSNCRPKLTCCPTCRGPL-GSIENLAMEKVANSVLPCKYASSGCEITLPHTEKAD	132
Db	97	GHVCSNCRPKLTCCPTCRGPL-GSIENLAMEKVANSVLPCKYASSGCEITLPHTEKPE	156
Qy	133	HEELCEPRYPSCPCGASCKQSGSLDAVPHLMHQHKSITTLQGEDIVFLATDINLPQAV	192
Db	157	HEDICEVYPSCPCGASCKQSGSLDAVPHLMHQHKSITTLQGEDIVFLATDINLPQAV	216
Qy	193	DWVMQSCFGFHFMLEKQEKYDGHQFPFAIVOLITRKOAEAFYRLELNGHRRRLTW	252
Db	217	DWVMQSCFGFHFMLEKQEKYDGHQFPFAIVOLITRKOAEAFYRLELNGHRRRLTW	276
Qy	253	EATPRSIHEGTAIWNISDCLVETSTAOIQAENGNGINVTISMIC	298
Db	277	EATPRSIHGVAAIWNISDCLVETSTAOIQAENGNGINVTISTC	322

RESULT 11
 SIA2 BRARE STANDARD; PRT; 331 AA.
 AC Q/SYL3; Q8JH29;
 DT 05-JUL-2004 (Rel. 44, Created)
 DT 05-JUL-2004 (Rel. 44, Last sequence update)
 DT 25-OCT-2004 (Rel. 45, Last annotation update)
 DE Ubiquitin ligase SIAH2 (EC 6.3.2.-) (Seven in Absentia homolog 2)
 DE (Siah-2).
 GN Name=siah2; Synonyms=siaz;
 OS Brachydanio rerio (Zebrafish) (Danio rerio).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
 OC Cyprinidae; Danio.
 OC NCBI_TaxID=7955;
 OX [1]
 RP SEQUENCE FROM N.A. (ISOFORM 1), TISSUE SPECIFICITY, AND DEVELOPMENTAL
 STAGE.
 RC TISSUE=Embryo;
 RC PubMed=12915316; DOI=10.1016/S1567-133X(03)00061-9;
 RA Ro H., Kim K.E., Huh T.L., Lee S.-K., Rhee M.;
 RT "Expression pattern of Siaz gene during the zebrafish embryonic
 development.";
 .RL Gene Expr. Patterns 3:483-488(2003).
 RN [2]
 RP SEQUENCE FROM N.A. (ISOFORM 2).
 RG NIH - Zebrafish Gene Collection (ZGC) project;
 RL Submitted (JUL-2003) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RN FUNCTION, AND DOMAIN.
 RP PubMed=15055544;
 RA Ro H., Jang Y., Rhee M.;
 RT "The RING domain of Siaz, the zebrafish homologue of Drosophila seven
 in Absentia, is essential for cellular growth arrest.";
 RT

RL Mol. Cells 17:160-165(2004).

CC -|- FUNCTION: E3 Ubiquitin ligase protein that mediates ubiquitination

CC and subsequent proteasomal degradation of target proteins. E3

CC ubiquitin ligases accept ubiquitin from an E2 ubiquitin-

CC conjugating enzyme in the form of a thioester and then directly

CC transfers the ubiquitin to targeted substrates. It probably

CC triggers the ubiquitin-mediated degradation of different

CC substrates. Induces cellular growth arrest by inhibiting the G2/M

CC transition.

CC -|- PATHWAY: Ubiquitin conjugation; third step.

CC -|- SUBUNIT: Homodimer (By similarity).

CC -|- ALTERNATIVE PRODUCTS:

CC Event=Alternative splicing; Named isoforms=2;

CC Name=1;

CC IsoId=Q7SYL3-1; Sequence=Displayed;

CC Name=2;

CC IsoId=Q7SYL3-2; Sequence=VSP_010167, VSP_010168;

CC Note=No experimental conformation available;

CC -|- TISSUE SPECIFICITY: In embryos it is expressed in all blastomers

CC starting at the mid-blastula. After 20 somite stage, it is

CC expressed mainly in the posterior part. Expressed in brain,

CC including the eye, the cranial cavity, otic vesicle, optic chiasm

CC and in the gut.

CC -|- DEVELOPMENTAL STAGE: Expressed both maternally and zygotically.

CC -|- DOMAIN: The RING-type zinc finger domain is essential for

CC ubiquitin ligase activity (By similarity).

CC -|- DOMAIN: The SBD domain (substrate-binding domain) mediates the

CC homodimerization and the interaction with substrate proteins. It

CC is related to the TRAF family.

CC -|- SIMILARITY: Belongs to the SINA (Seven in absentia) family.

CC -|- SIMILARITY: Contains 1 C2HC-type zinc finger.

CC -|- SIMILARITY: Contains 1 RING-type zinc finger.

CC -|- SIMILARITY: Contains 1 SIAH-type zinc finger.

CC -----

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CC or send an email to license@sib-sib.ch).

CC -----

CC EMBL; AF411696; AAN03677.1; --

CC EMBL; BC054674; AAN54674.1; --

CC HSPF; Q06984.1; K2F.

CC InterPro; IPR004162; Sina.

CC InterPro; IPR008974; Traf_dom.

CC InterPro; IPR001841; Znf_Fing.

CC Pfam; PF03145; Sina; 1.

CC SMART; SM00184; RING; 1.

CC PROSITE; PS00518; 2F_RING_1; FALSE_NEG.

CC PROSITE; PS00518; 2F_RING_2; 1.

CC Alternative splicing; Cell cycle; Ligase; Metal-binding;

CC Ub conjugation pathway; Zinc; Zinc-finger.

CC FT ZN_FING 89 124

CC FT ZN_FING 145 170

CC FT ZN_FING 175 201

CC FT ZN_FING 139 331

CC FT DOMAIN 147 147

CC FT METAL 154 154

CC FT METAL 166 166

CC FT METAL 170 170

CC FT METAL 177 177

CC FT METAL 184 184

CC FT METAL 196 196

CC FT METAL 201 201

CC FT VARSPLFC 197 208

CC /FTId=VSP_010167.

CC FT VARSPLFC 209 331

CC /FTId=VSP_010168.

CC FT CONFLICT 34 34

CC FT SEQUENCE 331 AA; 3493 MW; 1059490BF60F4B2 CRC64;

Query Match 74.0%; Score 1192.5; DB 1; Length 331;

Best Local Similarity 79.5%; Pred. No. 5.3e-97;

Matches 221; Conservative 23; Mismatches 19; Indels 15; Gaps 3;

QY 22 AFALPTGTGSKCPPSRVPAITGTTASNNDLASLFECPVCFDVLPPILQCSGHVCSNC 81

DB 68 AVALP-----VAALPG--QSPETALFECPVCFDVLPPILQCSGHVCSNC 113

QY 82 RPLTCCCTCRGPL--GSTRNLAMEKVANSVLPCKYASSGCEITLPHTEKADHEELCEFR 140

DB 114 ROKLSCTCCPTCRGPLTPSRNLAMEKVASTLPPCKYSSAGCLLSLHSEKPEHEVCEFR 173

QY 141 PYSCPCPGASCKWQSGSLDAVMPHLMHQHSITTLQGEDIVFLATDINLPAGVDWMQSC 200

DB 174 PYTCPCPGASCKWQSGSLDAVMPHLMHQHSITTLQGEDIVFLATDINLPAGVDWMQSC 233

QY 201 FGFHMLVLEKQEKYDGHQOFPFAIVOLIGTRKQAFNFAIRLENGHRRRLTWEATPRSH 260

DB 234 FGFHMLVLEKQEKYDGHQOFPFAIVOLIGTRKQAFNFAIRLENGHRRRLTWEATPRSH 293

QY 261 EGIATAMNSDCLVFDTSIAQLFAENGNGINVTISM 298

DB 294 DGVAAAIMNSDCLVFDTSIAHLFADNGNGINVTISM 331

RESULT 12

SIA2_XENLA STANDARD; PRT; 313 AA.

ID SIA2_XENLA

AC Q918X5; 2004 (Rel. 44, Created)

DT 05-JUL-2004 (Rel. 44, Last sequence update)

DE 05-JUL-2004 (Rel. 44, Last annotation update)

DE Ubiquitin ligase SIAH2 (BC 6.3.2.-) (Seven in absentia homolog 2)

DE (Xsiah-2).

GN Name=XIAH2; Synonyms=STAH2;

OS Xenopus laevis (African clawed frog).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;

OC Xenopodinae; Xenopus.

OX NCBI_TaxID=8355;

RN [1]

RP SEQUENCE FROM N.A., FUNCTION, SUBCELLULAR LOCATION, TISSUE

RP SPECIFICITY, AND DEVELOPMENTAL STAGE.

RX MEDLINE=21233021; PubMed=11335112; DOI=10.1016/S0925-4773(01)00332-X;

RA Bogdan S., Senkel S., Esser F., Ryffel G.U., Pogge von Strandmann E.;

RT "Misexpression of Xsiah-2 induces a small eye phenotype in Xenopus.";

RL Mech. Dev. 103:61-69(2001).

CC -|- FUNCTION: E3 Ubiquitin ligase protein that mediates ubiquitination

CC and subsequent proteasomal degradation of target proteins. E3

CC ubiquitin ligases accept ubiquitin from an E2 ubiquitin-

CC conjugating enzyme in the form of a thioester and then directly

CC transfers the ubiquitin to targeted substrates. Involved in eye

CC morphogenesis, probably triggers the ubiquitin-mediated

CC degradation of different substrates.

CC -|- PATHWAY: Ubiquitin conjugation; third step.

CC -|- SUBUNIT: Homodimer (By similarity).

CC -|- SUBCELLULAR LOCATION: Cytoplasmic.

CC -|- TISSUE SPECIFICITY: Widely expressed in early embryos until stage

CC 40. It is then expressed in brain, spinal cord and in the

CC developing and mature eye.

CC -|- DEVELOPMENTAL STAGE: Expressed both maternally and zygotically.

CC -|- DOMAIN: The RING-type zinc finger domain is essential for

CC ubiquitin ligase activity (By similarity).

CC -|- DOMAIN: The SBD domain (substrate-binding domain) mediates the

CC homodimerization and the interaction with substrate proteins. It

CC is related to the TRAF family (By similarity).

CC -|- SIMILARITY: Belongs to the SINA (Seven in absentia) family.

CC -|- SIMILARITY: Contains 1 C2HC-type zinc finger.

CC -|- SIMILARITY: Contains 1 RING-type zinc finger.

CC -|- SIMILARITY: Contains 1 SIAH-type zinc finger.

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CC -----
DR EMBL; AF155509; AAF080255.1; -;
DR HSSP; Q06984; IK2F.
DR InterPro; IPR004162; Sina.
DR InterPro; IPR008974; Traf_lik.
DR InterPro; IPR001841; Znf_Fing.
DR Pfam; PF03145; Sina; 1.
DR SMART; SM00184; RING; 1.
DR PROSITE; PS00518; ZF_RING_1; FALSE_NEG.
DR PROSITE; PS00089; ZF_RING_2; 1.
DR Ligase; Metal-binding; Ubl conjugation pathway; Zinc; Zinc-finger.
KW ZN_FING 69 104 RING-type.
FT ZN_FING 125 150 C2HC-type.
FT ZN_FING 155 181 SIAH-type.
FT DOMAIN 119 311 SBD.
FT METAL 127 127 Zinc 1 (By similarity).
FT METAL 134 134 Zinc 1 (By similarity).
FT METAL 146 146 Zinc 1 (By similarity).
FT METAL 150 150 Zinc 1 (By similarity).
FT METAL 157 157 Zinc 2 (By similarity).
FT METAL 164 164 Zinc 2 (By similarity).
FT METAL 176 176 Zinc 2 (By similarity).
FT METAL 181 181 Zinc 2 (By similarity).
SQ SEQUENCE 313 AA; 34099 MW; 9CF9C291C49B19EB CRC64;

Query Match 73.1%; Score 1177.5; DB 1; Length 313;
Best Local Similarity 73.7%; Pred. No. 1.1e-95;
Matches 219; Conservative 27; Mismatches 34; Indels 17; Gaps 4;

QY 9 PPVVFISEMSRQTATLPTGTS-----KCPSPQSRVPLTG-TTASNDLASLFCPCVCFD 62
DB 25 PPH-----APSLPATISGPGASAPPAPTAATGSLPSOOHQLSLFCPCVCFD 74
QY 63 YVLPPIQLQCOSHLVCSNCRPKLCCPTCRGPL-GSRINLAMEKVANSVLPCKYASSGC 121
DB 75 YVLPPIQLCQAGHLVCSNCRPKLCCPTCRGPL-GSRINLAMEKVANSVLPCKYASTGC 134
QY 122 EITLPHTKADHELCBFRPVSFCPCGASCKWQSGSLDAMPHLMHOKHSITTLQGEDIVF 181
DB 135 SLSLHTEKPEHEDICEYRPSYSCPCGASCKWQSGSLDAMPHLMHOKHSITTLQGEDIVF 194
QY 182 LATDINLPGAVDWMQSCFGFHMVLEKQEKYDGHQOPFAIVQLIGTRKQAEYAYRL 241
DB 195 LATDINLPGAVDWMQSCFGFHMVLEKQEKYDGHQOPFAIVQLIGTRKQAEYAYRL 254
QY 242 ELNGRRRLTWEATPRSHIEGIATAMNSDCLVDTSTIAOLFARNGLGNVTISM 298
DB 255 ELNGRRRLTWEATPRSHIEGIATAMNSDCLVDTSTIAOLFARNGLGNVTISM 311

RESULT 13
SINA DROWI STANDARD; PRT; 331 AA.
AC Q81147;
DT 05-JUL-2004 (Rel. 44, Created)
DT 05-JUL-2004 (Rel. 44, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Ubiquitin ligase sina (EC 6.3.2.-) (Seven in absentia protein).
GN Name=sina;
OS Drosophila willistoni (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7260;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Tucson 14030-0814.10;

RX MEDLINE=22426072; PubMed=12537575;
RA Bergman C.M., Pfeiffer B.D., Rincon-Limas D.E., Hoskins R.A.,
RA Gnirke A., Mungall C.J., Wang A.M., Krommiller B., Pacleb J., Park S.,
RA Stapleton M., Wan K., George R.A., de Jong P.J., Botas J., Rubin G.M.,
RA Celniker S.E.;
RT Assessing the impact of comparative genomic sequence data on the
functional annotation of the Drosophila genome.;
RL Genome Biol. 3:RESEARCH0086.1-RESEARCH0086.20(2002).
CC -!- FUNCTION: E3 Ubiquitin ligase protein that is required for
specification of R7 photoreceptor cell fate in the eye by
mediating the ubiquitination and subsequent proteasomal
degradation of Tramtrack (ttk). E3 Ubiquitin ligases accept
ubiquitin from an E2 ubiquitin-conjugating enzyme in the form of a
thioester and then directly transfers the ubiquitin to targeted
substrates. Acts via the formation of a complex with ebi and phyl
that ubiquitinates the transcription repressor ttk, a general
inhibitor of photoreceptor differentiation, in a subset of
photoreceptor cells in the eye, leading to the differentiation of
cells into neurons. Also involved in external sensory organ
development (By similarity).
CC -!- PATHWAY: Ubiquitin conjugation; third step.
CC -!- SUBUNIT: Component of some E3 complex at least composed of sina,
ebi and phyl. Interacts with ebf (By similarity).
CC -!- SUBCELLULAR LOCATION: Nuclear and cytoplasmic (By similarity).
CC -!- DOMAIN: The RING-type zinc finger domain is essential for
ubiquitin ligase activity (By similarity).
CC -!- DOMAIN: The SBD domain (substrate-binding domain) mediates the
interaction with substrate proteins. It is related to the TRAF
family (By similarity).
CC -!- SIMILARITY: Belongs to the SINA (Seven in absentia) family.
CC -!- SIMILARITY: Contains 1 C2HC-type zinc finger.
CC -!- SIMILARITY: Contains 1 RING-type zinc finger.
CC -!- SIMILARITY: Contains 1 SIAH-type zinc finger.
CC -----
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or send an email to license@isb-sib.ch.
CC -----
DR EMBL; AY190961; AA001124.1; -;
DR HSSP; Q06984; IK2F.
DR FlyBase; FBgn0064264; Dwa1\ sina.
DR InterPro; IPR004162; Sina.
DR InterPro; IPR008974; Traf_lik.
DR InterPro; IPR001841; Znf_Fing.
DR Pfam; PF03145; Sina; 1.
DR SMART; SM00184; RING; 1.
DR PROSITE; PS00518; ZF_RING_1; FALSE_NEG.
DR PROSITE; PS00089; ZF_RING_2; 1.
KW Developmental protein; Ligase; Metal-binding; Nuclear protein;
KW Ubl conjugation pathway; Vision; Zinc; Zinc-finger.
FT ZN_FING 90 125 RING-type.
FT ZN_FING 145 170 C2HC-type.
FT ZN_FING 175 201 SIAH-type.
FT DOMAIN 139 331 SBD.
FT METAL 147 147 Zinc 1 (By similarity).
FT METAL 154 154 Zinc 1 (By similarity).
FT METAL 166 166 Zinc 1 (By similarity).
FT METAL 170 170 Zinc 1 (By similarity).
FT METAL 177 177 Zinc 2 (By similarity).
FT METAL 184 184 Zinc 2 (By similarity).
FT METAL 196 196 Zinc 2 (By similarity).
FT METAL 201 201 Zinc 2 (By similarity).
SQ SEQUENCE 331 AA; 34963 MW; 64893444AB70BC5 CRC64;

Query Match 71.8%; Score 1156.5; DB 1; Length 331;
Best Local Similarity 73.5%; Pred. No. 8.1e-94;
Matches 219; Conservative 19; Mismatches 35; Indels 25; Gaps 2;

QY 21 TATALTGTGSKPPSQSRVPLTGTASNN-----DLASLFCPCV 59

Cell 63:561-577(1990).

[2] SEQUENCE FROM N.A.

RC STRAIN=Berkeley;

RA MEDLINE=20196006; PubMed=10731132; DOI=10.1126/science.287.5461.2185;

RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,

RA Anantides P.G., Scherz S.E., Li P.W., Hoskins R.A., Galie R.F.,

RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,

RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,

RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,

RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,

RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,

RA Ballwe R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,

RA Beeson D.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,

RA Borkova D., Botchan M.R., Bouck J., Brockstein P., Brottier P.,

RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,

RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,

RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,

RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,

RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,

RA Glöck A., Gong F., Gorrell J.H., Gu Z., Guan P., Harries M.,

RA Harris N.L., Harvey D.A., Heiman T.J., Hernandez J.R., Houck J.,

RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,

RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,

RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,

RA Lasko P., Lei Y., Levitsky A.A., Li J.H., Li Z., Liang Y., Lin X.,

RA Liu X., Mattei G., McIntosh T.C., McLeod M.P., McPherson D.,

RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,

RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,

RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,

RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,

RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Smith H.,

RA Shue B.C., Siden-Kiamos I., Simpson M.C., Skupski M.P., Smith T.,

RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,

RA Svirskas R., Tector R., Turner R., Venter E., Wang A.H., Wang X.,

RA Wang Z.-Y., Wasserman D.A., Weinstein G.M., Weissenbach J.,

RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,

RA Ye J., Yeh R.-P., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,

RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu H.O.,

RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.

RT "The genome sequence of *Drosophila melanogaster*."

RL Science 287:2185-2195(2000).

[3] GENOME REANNOTATION.

RP MEDLINE=22426069; PubMed=12537572;

RA Mitra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,

RA Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochnik S.E.,

RA Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Herman B.P.,

RA Bettencourt B.R., Celniker S.E., de Grey A.D.N.J., Drysdale R.A.,

RA Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,

RA Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,

RA Lewis S.E.

RT "Annotation of the *Drosophila melanogaster* euchromatic genome: a

RT systematic review."

RL Genome Biol. 3:RESEARCH0083.1-RESEARCH0083.22(2002).

[4] SEQUENCE FROM N.A.

RC STRAIN=Berkeley; TISSUE=Head;

RX MEDLINE=22426066; PubMed=12537569;

RA Stapleton M., Carlson J.W., Brockstein P., Yu C., Champe M.,

RA George R.A., Guarin H., Kronmiller B., Pacleb J.M., Park S., Wan K.H.,

RA Rubin G.M., Celniker S.E.

RT "A *Drosophila* full-length cDNA resource."

RL Genome Biol. 3:RESEARCH0080.1-RESEARCH0080.8(2002).

[5] FUNCTION IN TTK DEGRADATION, AND INTERACTIONS WITH PHYL AND EFF.

RP PubMed=9267026; DOI=10.1016/S0092-8674(00)80506-1;

RA Tang A.H., Neufeld T.P., Kwan E., Rubin G.M.

RT "PHYL acts to down-regulate TTK88, a transcriptional repressor of

RT neuronal cell fates, by a SINA-dependent mechanism."

RL Cell 90:459-467(1997).

[6] FUNCTION IN TTK DEGRADATION, AND INTERACTION WITH PHYL.

RP PubMed=9267027; DOI=10.1016/S0092-8674(00)80507-3;

RA Li S., Li Y., Carthew R.W., Lai Z.-C.

RT "Photoreceptor cell differentiation requires regulated proteolysis of

RT the transcriptional repressor Tramtrack."

RL Cell 90:469-478(1997).

[7] COMPONENT OF A COMPLEX WITH EBI AND PHYL.

RP PubMed=11032805; DOI=10.1093/emboj/19.20.5376;

RA Boulton S.J., Brook A., Staehling-Hampton K., Heitzler P., Dyson N.

RT "A role for Ebi in neuronal cell cycle control."

RL EMBO J. 19:5376-5386(2000).

[8] FUNCTION.

RP PubMed=11526076;

RA Pi H., Wu H.-J., Chien C.-T.

RT "A dual function of phyllopo in *Drosophila* external sensory organ

RT development: cell fate specification of sensory organ precursor and

RT its progeny."

RL Development 128:2699-2710(2001).

[9] FUNCTION OF THE COMPLEX.

RP PubMed=12215542; DOI=10.1128/MCB.22.19.6854-6865.2002;

RA Li S., Xu C., Carthew R.W.

RT "Phyllopo acts as an adaptor protein to link the *sina* ubiquitin

RT ligase to the substrate protein tramtrack."

RL Mol. Cell. Biol. 22:6854-6865(2002).

CC "FUNCTION: E3 Ubiquitin ligase protein that is required for

CC specification of R7 photoreceptor cell fate in the eye by

CC mediating the ubiquitination and subsequent proteasomal

CC degradation of tramtrack (ttk). E3 Ubiquitin ligases accept

CC ubiquitin from an E2 ubiquitin-conjugating enzyme in the form of a

CC thioester and then directly transfers the ubiquitin to targeted

CC substrates. Acts via the formation of a complex with ebi and phyl

CC that ubiquitinates the transcription repressor ttk, a general

CC inhibitor of photoreceptor differentiation, in a subset of

CC photoreceptor cells in the eye, leading to the differentiation of

CC cells into neurons. Also involved in external sensory organ

CC development.

CC "PATHWAY: Ubiquitin conjugation; third step.

CC "SUBUNIT: Component of some E3 complex at least composed of *sina*,

CC ebi and phyl. Interacts with eff.

CC "SUBCELLULAR LOCATION: Nuclear and cytoplasmic.

CC "TISSUE SPECIFICITY: In many ommatidial precursor cells.

CC "DOMAIN: The RING-type zinc finger domain is essential for

CC ubiquitin ligase activity (By similarity).

CC "DOMAIN: The SBD domain (substrate-binding domain) mediates the

CC interaction with substrate proteins. It is related to the TRAF

CC family (By similarity).

CC "SIMILARITY: Belongs to the SINA (seven in absentia) family.

CC "SIMILARITY: Contains 1 C2HC-type zinc finger.

CC "SIMILARITY: Contains 1 RING-type zinc finger.

CC "SIMILARITY: Contains 1 SIAH-type zinc finger.

CC "SIMILARITY: Contains 1 SIAH-type zinc finger.

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CC -----

DR EMBL; M38384; AAA28901.1; -.

DR EMBL; AE003526; AAF49403.1; -.

DR EMBL; AY060358; AAL25397.1; -.

DR FIR; A36195; A36195.

DR HSSP; Q06984; 1K2F.

DR IntAct; P21461; -.

DR FlyBase; FBgn003410; *sina*.

DR GO; GO:0007423; P:sensory organ development; IMP.

DR InterPro; IPR004162; Sina.

DR InterPro; IPR008974; Traf_like.

DR InterPro; IPR001841; Znf_ring.

Search completed: April 25, 2005, 06:38:42
Job time : 85 secs

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OM protein - protein search, using sw model

Run on: April 25, 2005, 05:57:40 ; Search time 25 Seconds
(without alignments)
889.817 Million cell updates/sec

Title: US-10-679-246-2
Perfect score: 1611
Sequence: 1 MWIIIFLLPPYVFISEMSRQ.....IAQLFAENGNGINVTISMC 298

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:*
1: /cgn2_6/prodata/1/iaa/5A_COMB.pep.*
2: /cgn2_6/prodata/1/iaa/5B_COMB.pep.*
3: /cgn2_6/prodata/1/iaa/6A_COMB.pep.*
4: /cgn2_6/prodata/1/iaa/6B_COMB.pep.*
5: /cgn2_6/prodata/1/iaa/POCUS_COMB.pep.*
6: /cgn2_6/prodata/1/iaa/backfile1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1611	100.0	298	US-09-591-694-2	Sequence 2, Appli
2	1516	94.1	282	US-09-544-618-17	Sequence 17, Appl
3	1512	93.9	282	US-09-544-618-18	Sequence 18, Appl
4	1489	92.4	282	US-09-544-618-12	Sequence 12, Appl
5	1482	92.0	282	US-09-544-618-19	Sequence 19, Appl
6	1122.5	69.7	314	US-09-544-618-20	Sequence 20, Appl
7	447	27.7	313	US-09-362-506-2	Sequence 2, Appli
8	326	20.2	325	US-09-325-932A-83	Sequence 83, Appl
9	325	20.2	325	US-09-325-932A-201	Sequence 201, App
10	123.5	7.7	299	US-09-270-767-45308	Sequence 45308, A
11	121.5	7.5	172	US-09-270-767-60801	Sequence 60801, A
12	107.5	6.7	120	US-09-325-932A-84	Sequence 84, Appl
13	107	6.6	485	US-08-724-194A-8	Sequence 8, Appli
14	106	6.6	522	US-08-639-237-2	Sequence 2, Appli
15	106	6.6	522	US-08-375-405-2	Sequence 2, Appli
16	105.5	6.5	22	US-08-012-269A-4	Sequence 4, Appli
17	102.5	6.4	474	US-09-949-016-7120	Sequence 7120, Ap
18	99.5	6.2	298	US-09-127-928-2	Sequence 2, Appli
19	99.5	6.2	299	US-09-949-016-7820	Sequence 7820, Ap
20	97.5	6.1	50	US-09-270-767-34977	Sequence 34977, A
21	97.5	6.1	50	US-09-270-767-50194	Sequence 50194, A
22	96.5	6.0	326	US-09-538-092-1019	Sequence 1019, Ap
23	96.5	6.0	343	US-09-949-016-11007	Sequence 11007, A
24	96	6.0	913	US-09-248-796A-15734	Sequence 15734, A
25	93.5	5.8	366	US-09-908-988B-2	Sequence 2, Appli
26	93.5	5.8	487	US-09-949-016-11205	Sequence 11205, A
27	93.5	5.8	600	US-09-327-984A-6	Sequence 6, Appli

ALIGNMENTS

RESULT 1

US-09-591-694-2
; Sequence 2, Application US/09591694
; Patent No. 6638734
; GENERAL INFORMATION:
; APPLICANT: John C. Reed
; APPLICANT: Shu-ichi Matsumura
; TITLE OF INVENTION: Nucleic Acid Encoding Proteins Involved
; TITLE OF INVENTION: in Protein Degradation, Products and Methods Related Thereto
; FILE REFERENCE: P-LJ 4220
; CURRENT APPLICATION NUMBER: US/09/591,694
; CURRENT FILING DATE: 2000-06-09
; EARLIER APPLICATION NUMBER: US 09/330,517
; EARLIER FILING DATE: 1999-06-11
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 298
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-591-694-2

Query Match	100.0%;	Score 1611;	DB 4;	Length 298;
Best Local Similarity	100.0%;	Pred. No. 3.2e-159;		
Matches	298;	Conservative	0;	Mismatches 0; Indels 0; Gaps 0;
QY	1	MWIIIFLLPPYVFISEMSRQTATLPTGTSKCPSPQRPVLPALTGTTASNNNDLASLFCPCVC	60	
DB	1	MWIIIFLLPPYVFISEMSRQTATLPTGTSKCPSPQRPVLPALTGTTASNNNDLASLFCPCVC	60	
QY	61	FQYVLPPILOCGSHLVCSNCPKLTCCPTCGPLGSIIRNLAMEKVANSVLPCKYASSG	120	
DB	61	FQYVLPPILOCGSHLVCSNCPKLTCCPTCGPLGSIIRNLAMEKVANSVLPCKYASSG	120	
QY	121	CSITLPHTEKADHEELCEFRPSCPCGASCKWQGSGLDAMPHLMHOKHSITTLQGEDIV	180	
DB	121	CSITLPHTEKADHEELCEFRPSCPCGASCKWQGSGLDAMPHLMHOKHSITTLQGEDIV	180	
QY	181	FLATDINLPAGVDVMMWQSCFGFHEMLVLEKEKYDGHQFFAIVQLIGTRKQAFAYR	240	
DB	181	FLATDINLPAGVDVMMWQSCFGFHEMLVLEKEKYDGHQFFAIVQLIGTRKQAFAYR	240	
QY	241	LELNGHRRRLTWEATPRSIHEGIAIATMNSDCLVFDTSIAQLFAENGNGINVTISMC	298	
DB	241	LELNGHRRRLTWEATPRSIHEGIAIATMNSDCLVFDTSIAQLFAENGNGINVTISMC	298	

RESULT 2

US-09-544-618-17
; Sequence 17, Application US/09544618

```

; Patent No. 6503502
; GENERAL INFORMATION:
; APPLICANT: Telerman, Adam
; APPLICANT: Amson, Robert
; APPLICANT: Cohen, Daniel
; TITLE OF INVENTION: NUCLEOTIDE SEQUENCES, PROTEINS, DRUGS AND DIAGNOSTIC
; TITLE OF INVENTION: AGENTS OF USE IN TREATING CANCER
; FILE REFERENCE: 065691-0139
; CURRENT APPLICATION NUMBER: US/09/544,618
; CURRENT FILING DATE: 2000-03-06
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 17
; LENGTH: 282
; TYPE: PRT
; ORGANISM: HUMAN
US-09-544-618-17

Query Match          94.1%; Score 1516; DB 4: Length 282;
Best Local Similarity 99.3%; Pred. No. 2.2e-149;
Matches 280; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 17 MSRQTATALPTGTSKCPSPQRVPALTGTTASNNDLASLFFPCVCFDVLPPILQCQSGHL 76
Db 1 MSRQTATALPTGTSKCPSPQRVPALTGTTASNNDLASLFFPCVCFDVLPPILQCQSGHL 60

Qy 77 VCSNCRPLKLTCCPTCRGPLGSIRNLAMEKVANSVLPCKYASSGCEITLPHTEKADHEEL 136
Db 61 VCSMCRPLKLTCCPTCRGPLGSIRNLAMEKVANSVLPCKYASSGCEITLPHTEKADHEEL 120

Qy 137 CEFPPYSCPCGASCKWQGSILDAWPHLMHOKHSITTLQGEDIVFLATDINLPGADVWM 196
Db 121 CEFPPYSCPCGASCKWQGSILDAWPHLMHOKHSITTLQGEDIVFLATDINLPGADVWM 180

Qy 197 MQSCFGFHFMVLVEKQKYDGHQOFFFAIVQLIGTRKQAFENPAYLELNGHRRRLTWEATP 256
Db 181 MQSCFGFHFMVLVEKQKYDGHQOFFFAIVQLIGTRKQAFENPAYLELNGHRRRLTWEATP 240

Qy 257 RSTHEGIATAIMNSDCLVFDFTSIAQLFAENGNLGINVTISM 298
Db 241 RSTHEGIATAIMNSDCLVFDFTSIAQLFAENGNLGINVTISM 282

```

RESULT 3
US-09-544-618-18
; Sequence 18, Application US/09544618
; Patent No. 6503502
; GENERAL INFORMATION:
; APPLICANT: Telerman, Adam
; APPLICANT: Amson, Robert
; APPLICANT: Cohen, Daniel
; TITLE OF INVENTION: NUCLEOTIDE SEQUENCES, PROTEINS, DRUGS AND DIAGNOSTIC
; FILE OF INVENTION: AGENTS OF USE IN TREATING CANCER
; FILE REFERENCE: 065691-0139
; CURRENT APPLICATION NUMBER: US/09/544, 618
; CURRENT FILING DATE: 2000-03-06
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn ver. 2.0
; SEQ ID NO 18
; LENGTH: 282
; TYPE: PRT
; ORGANISM: MOUSE
US-09-544-618-18

	Query Match	93.9%;	Score 1512;	DB 4;	Length 282;	
	Best Local Similarity	98.9%;	Pred. No. 5.8e-149;			
	Matches 279; Conservative	2;	Mismatches 2;	Indels	0;	Gaps 0
Qy	17 MSROTATALPTGTSCKPPSQRPVALTGTTASNNDLASLFECPVCDFYVLPPILQCQSGLH	76				
Dd	1 MSROTATALPTGTSCKPPSQRPVALTGTTASNNDLASLFECPVCDFYVLPPILQCQSGLH	60				
Ov	77 VCSNCRPKITCCPTCGRDPIGSTRNIAAMEKANSVLPCKYASSGCETIPLPHEKADHBEEL	136				

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Db      61  VCSWCRPKLTCCPTCRGPLGSIRNLAMEKVANSVLPFCKYASSCEITLPHTEKAEHEEL 120
Qy      137 CERFPYSCPCPGASCKWQSGLDVMPHLMHOKHSITTLQGEDIVFLATDINLPGAVDWM 196
Db      121 CERFPYSCPCPGASCKWQSGLDVMPHLMHOKHSITTLQGEDIVFLATDINLPGAVDWM 180
Qy      197 MQSCFGFHFMVLVEKQKYGHQGFPAIVOLIIGTRKQAEFAFYKLELNGHRRRLTWEATP 256
Db      181 MQSCFGFHFMVLVEKQKYGHQGFPAIVOLIIGTRKQAEFAFYKLELNGHRRRLTWEATP 240
Qy      257 RSTHEGATAIMNSDCILVFDTSTIAQLFAENGNGLINVTTSMC 298
Db      241 RSTHEGATAIMNSDCILVFDTSTIAQLFAENGNGLIMVTSMC 282

RESULT 4
US-09-544-618-12
; Sequence 12, Application US/09544618
; Patent No. 6503502
; GENERAL INFORMATION:
; APPLICANT: Telerman, Adam
; APPLICANT: Amson, Robert
; APPLICANT: Cohen, Daniel
; TITLE OF INVENTION: NUCLEOTIDE SEQUENCES, PROTEINS, DRUGS AND DIAGNOSTIC
; TITLE OF INVENTION: AGENTS OF USE IN TREATING CANCER
; FILE REFERENCE: 065691-0139
; CURRENT APPLICATION NUMBER: US/09/544,618
; CURRENT FILING DATE: 2000-03-06
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 12
; LENGTH: 282
; TYPE: PRT
; ORGANISM: TSAP 3
US-09-544-618-12

```

Query Match	92.4%	Score 1489	DB 4	Length 282
Best Local Similarity	96.8%	Prod. No. 1.4e-146		
Matches 273	Conservative	2	Mismatches 7	Indels 0
Matches 273	Conservative	2	Mismatches 7	Indels 0
QY	17	MSRQTATALPTGTGSKCPSQVRPALTGTTASNNDIASLFECPVFDYVLPPILOQSGHL	76	
DB	1	MSRQTATALPTGTGSKCPSQVRPALTGTTASNNDIASLFECPVFDYVLPPILOQSGHL	60	
QY	77	VCSNCRPKLTCCTPCRGLSGIRNLAMEKVANSVLPCKYASSGCEITLPHTEKADHEEL	136	
DB	61	VCSNCRPKLTCCTPCRGLSGIRNLAMEKVANSVLPCKYASSGCEITLPHTEKADHEEL	120	
QY	137	CEFRPYSCPCGASCCKWGSLDVAVMPHLMHQHSITTLQGEDIVFLATDINILPGAVDWM	196	
DB	121	CEFRPYSCPCGASCCKWGSLDVAVMPHLMHQHSITTLQGEDIVFLATDINILPGAVDWM	180	
QY	197	MOSCFGHFMLVLEKQEKYDGHQQFAIVOLLGTRKQAFNFAIRLELNGHRRRLTWEATP	256	
DB	181	MOSCFGHFMLVLEKQEKYDGHQQFAIVOLLGTRKQAFNFAIRLELNGHRRRLTWEATP	240	
QY	257	RSIIHEGIATAMNSCLVFDTSIAQLFAENGNLGINVTISM	238	
DB	241	RSIIHEGIATAMNSCLVFDTSIAQLFAENGNLGINVTISM	282	

RESULT 5
US-09-544-618-19
; Sequence 19, Application US/09544618
; Patent No. 6503502
; GENERAL INFORMATION:
; APPLICANT: Telerman, Adam
; APPLICANT: Amson, Robert
; APPLICANT: Cohen, Daniel
; TITLE OF INVENTION: NUCLEOTIDE SEQUENCES, PROTEINS, DRUGS AND DIAGNOSTIC
; TITLE OF INVENTION: AGENTS OF USE IN TREATING CANCER
; FILE REFERENCE: 065691-0139

; CURRENT APPLICATION NUMBER: US/09/544,618
; CURRENT FILING DATE: 2000-03-06
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 19
; LENGTH: 282
; TYPE: PRT
; ORGANISM: MOUSE
US-09-544-618-19

Query Match 92.0%; Score 1482; DB 4; Length 282;
Best Local Similarity 96.8%; Pred. No. 7.7e-146;
Matches 273; Conservative 4; Mismatches 5; Indels 0; Gaps 0;
QY 17 MSRTATLPTGTSKPPSRVPALTGTTASNNDLASLFECPVCFDYVLPPIQCSGHL 76
Db 1 MSRQAATLSTGTSKPPSRVPALDTTASNNDLASLFECPVCFDYVLPPIQCSGHL 60
QY 77 VCSNCRPKLTCCPTCRGPIGSRINLAMEKVANSVLPCKYASSGCCITLPHTEKADHEEL 136
Db 61 VCSNCRPKLTCCPTCRGPIGSRINLAMEKVANSVLPCKYASSGCCITLPHTEKADHEEL 120
QY 137 CEFRPYSCPCGASCKWQSLDAMPHLMHOKSIITLQGEDIVFLATDINLPGVDWVM 196
Db 121 CEFRPYSCPCGASCKWQSLDAMPHLMHOKSIITLQGEDIVFLATDINLPGVDWVM 180
QY 197 MOSCFGFHMLVLEKQEKYDGHQOFFAIVQLIGTRKQAFNFAIRLELNGHRRRLTWEATP 256
Db 181 MOSCFGFHMLVLEKQEKYDGHQOFFAIVQLIGTRKQAFNFAIRLELNGHRRRLTWEATP 240
QY 257 RSIHEGIATAMNSDCLVFDTSIAQLPAENGNGINVTISM 298
Db 241 RSIHEGIATAMNSDCLVFDTSIAQLPAENGNGINVTISM 282

RESULT 6

US-09-544-618-20
; Sequence 20, Application US/09544618
; Patent No. 6503502
; GENERAL INFORMATION:
; APPLICANT: Telerman, Adam
; APPLICANT: Anson, Robert
; APPLICANT: Cohen, Daniel
; TITLE OF INVENTION: NUCLEOTIDE SEQUENCES, PROTEINS, DRUGS AND DIAGNOSTIC
; FILE REFERENCE: AGENTS OF USE IN TREATING CANCER
; FILE REFERENCE: 065691-0139
; CURRENT APPLICATION NUMBER: US/09/544,618
; CURRENT FILING DATE: 2000-03-06
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 20
; LENGTH: 314
; TYPE: PRT
; ORGANISM: DROSINA
US-09-544-618-20

Query Match 69.7%; Score 1122.5; DB 4; Length 314;
Best Local Similarity 73.0%; Pred. No. 2.3e-108;
Matches 211; Conservative 21; Mismatches 44; Indels 13; Gaps 1;
QY 22 ATALPTGTSKPPSRVPALTGTTASNN-----DLASLFECPVCFDYVLPPI 68
Db 25 ATNTSTGSSAGNTSSAMTSSSSSSLSAGGGGAGMSADLTSLFECPVCFDYVLPPI 84
QY 69 LQCSGHLVCSNCRPKLTCCPTCRGPIGSRINLAMEKVANSVLPCKYASSGCCITLPHTE 128
Db 85 LQCSSGHLVCSNCRPKLTCCPTCRGPIGSRINLAMEKVANSVLPCKYASSGCCITLPHTE 144
QY 129 EKADHEELCEFRPYSCPCGASCKWQSLDAMPHLMHOKSIITLQGEDIVFLATDINL 188
Db 145 EKTEHEETCEFRPYSCPCGASCKWQSLDAMPHLMHOKSIITLQGEDIVFLATDINL 204
QY 189 PGAVDWMVMQSCFGFHMVLVLEKQEKYDGHQOFFAIVQLIGTRKQAFNFAIRLELNGHRR 248

Db 205 PGAVDWMVMQSCFGFHMVLVLEKQEKYDGHQOFFAIVQLIGTRKQAFNFAIRLELNGHRR 264
QY 249 RLTTWEATPRSIHEGIATAMNSDCLVFDTSIAQLFAENGNGINVTISM 297
Db 265 RLTTWEATPRSIHEGIATAMNSDCLVFDTSIAQLFADMGMLGIMVTISL 313
RESULT 7
US-09-362-506-2
; Sequence 2, Application US/09362506
; Patent No. 6111167
; GENERAL INFORMATION:
; APPLICANT: Mahajan, Pramod B.
; TITLE OF INVENTION: Maize SINA Orthologue-1 and Uses Thereof
; FILE REFERENCE: 0936
; CURRENT APPLICATION NUMBER: US/09/362,506
; CURRENT FILING DATE: 1999-07-27
; EARLIER APPLICATION NUMBER: 60/100,258
; EARLIER FILING DATE: 1998-09-14
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 313
; TYPE: PRT
; ORGANISM: Zea mays
US-09-362-506-2

Query Match 27.7%; Score 447; DB 3; Length 313;
Best Local Similarity 37.6%; Pred. No. 4.3e-38;
Matches 103; Conservative 44; Mismatches 101; Indels 26; Gaps 9;
QY 39 PALTGTTASNNDLAS-----LFECPVCFDYVLPPIQCSGHLVCSNCRPKL-TCCPTC 91
Db 39 PASTSASLANVALSSLCGLNDLLECPVCTNSMRPPILOCPNGHTICSSCKHRVNHCPCTC 98
QY 92 RGPLGSIRNLAMEKVANSVLPCKYASSGCCITLPHTEKADHEELCEFRPYSCPCGASC 151
Db 99 ROELGNIRCLAEKVAEQQLFECKYQSTGCTEIHPIYKSLKHEELCRFRPYSCPYAGSEC 158
QY 152 KWQGSILDAMPHLMHOKSIITLQGEDIVFLATDINLPGAVD---WVM-MQSCFGFPHML 207
Db 159 LIAGDVPPVLSHLNDHK-VDLHEGCTFNHRVTKPN-PYEVENATWMLTVFKCFGHFL 216
QY 208 -----VLEKQEKYDGHQOFFAIVQLIGTRKQAFNFAIRLELNGHRRRLTWEATPRSIHEG 262
Db 217 HFEAFVLGWAPVY-----MAFLRFMGESSEAQFGYSLGVGGGGRKLTWQGTFRSVD 270
QY 263 IATAMNSDCLVFDTSIAQLPAENG--NLGINVT 294
Db 271 HRKVRDSFDGLIHRNMALFFSGGGRQELKLRVT 304

RESULT 8

US-09-325-932A-83
; Sequence 83, Application US/09325932A
; Patent No. 6451604
; GENERAL INFORMATION:
; APPLICANT: Flinn, Barry
; APPLICANT: Lasham, Annette
; TITLE OF INVENTION: Compositions affecting programmed cell
; FILE REFERENCE: 1022
; CURRENT APPLICATION NUMBER: US/09/325,932A
; CURRENT FILING DATE: 1999-06-04
; NUMBER OF SEQ ID NOS: 206
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 83
; LENGTH: 325
; TYPE: PRT
; ORGANISM: Pinus radiata
US-09-325-932A-83

for forestry plant develop

[illegible]

Query Match	20.2%	Score 325;	DB 4;	Length 325;
Best Local Similarity	31.7%	Pred. No. 2.2e-25;		
Matches	90;	Conservative 42;	Mismatches 114;	Indels 38; Gaps 9;
Qy	36	QRVPALTG-----TTASNNDL--ASLPKPCPVCFDVLPPILQCQSGHLVCSNCRPKLT-C	87	
Db	50	RRFAVRDKTEQVATRSFGDLLGASLIETP-GRETQLQIVITECPNTRTVCSGCKSRLSNW	108	
Qy	88	CPTCRGPGLGSIRNLAMEKAVNSVLPPCKYASSGCEITLPHTEKADHEELCEFRYSCPCP	147	
Db	109	CPSRCNLGNFRCLAPETETSSQELTCMYQSYGCEDMYPYYSSELURHEAHCNFRYPNCPYA	168	
Qy	148	GASCKWQSGSLVAVPHLMHOKH-----SITTLQGGEDIVFLATDINLPGAVD	193	
Db	169	GSECKLVGDIFFLVVAHLRDDHKVYMHNSCTFDHRYVKSNPLEVENAIWMPTVIN-----	222	
Qy	194	WMMQSCRGFFHMLVLEKQEKVDGHOQFAIVOLIGTRKOENFAYRLKELNGHRRRLTWE	253	
Db	223	-----CFGQFCFLHFE-AFLIDMAPVVIAFILFMGDDNEAKNFSYCLETGNGKRLIWH	275	
Qy	254	ATPASIHEGIATAINNSDCLVFTDTSIAOLFKAENGLG-INVTIS	296	
Db	276	GVPSIRPCHRKVHDSSDGLIIORDVA-LFFSGGDIINELNRLT	318	

RESULT 10
US-09-270-767-45308
: Sequence 45308. Application US/09270767

```

; Patent No. 6703491
;
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 45308
; LENGTH: 299
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
; FEATURE:
; OTHER INFORMATION: Xaa means any amino acid
US-09-270-767-45308

Query Match          7.7%; Score 123.5; DB 4; Length 299;
Best Local Similarity 19.6%; Pred. No. 0.00018;
Matches 50; Conservative 32; Mismatches 64; Indels 109; Gaps 13;

Qy 63 YVLPPILOQSGHLVCSNCPKLTCCPTCRGPLG---SIRNLAMEKIVANSVLPCKVASS 119
Db 16 YSLPSL-----RDQATCNCRVSEIKSKTSRNLAVLVEKAASELDPSCQF--- 59

Qy 120 GCEITLPHTEKADHEE-LCSFRPYSCPCPGASCKWQGSLDVAMPH---LMHQHKSITTLQ 175
Db 60 -CNKEFPYKSLRHEHQECQERPTKCKYHRIGCQWRGPYHETNEHNRNCLHPQKS----- 113

Qy 176 GEDIVFLATDINLPQAVDWMQSCGFHFHMLVLE-----KQKYDGHQOQFAIVQLIG 229
Db 114 -----GYEVMAALEAHDDRIKEEK-----KMFNTLIDLLS 143

Qy 230 TRK-----QAEINFAYRL-----ELN-----GHRRLITW 252
Db 144 YEKLIIFNDLQMKPRTDEYVHKLFEYETARFSAFNQWVVKARINNSQRDPHQSNERITY 203

Qy 253 E-----ATPRSTH 260
Db 204 HLLIKTKTSTPMSIH 218

```

RESULT 11
US-09-270-767-60801
; Sequence 60801, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of *Drosophila melanogaster*
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 60801
; LENGTH: 172
; TYPE: PRT
; ORGANISM: *Drosophila melanogaster*
US-09-270-767-60801

	Query Match	7.5%; Score 121.5; DB 4; Length 172;
	Best Local Similarity	22.4%; Pred. No. 0.00013;
	Matches	41; Conservative 22; Mismatches 55; Indels 65; Gaps 8;
QY	63 YLPILOQSGHLVCSNCRKFLTCCCTCGPLG---	SIRNLAMEKVANSVLFPCKVASS 119
	:	: : : : :
	:	: : : : :
Db	16 YSLPSL-----	RDOIATPCNCRVIEISKASRNLAWEKAASELPSCQP--- 59
	:	: : : : :
	:	: : : : :
QY	120 GCETTLPTHEKADHEE-LCEFRPYSCP CGASCWKQSGLDAVMPH---	LMEHQHSITTLQ 175
	:	: : : : :
	:	: : : : :
Db	60 -CNKEFFPKSLERHQEHCEQRPYTKVKHRCQWRGPYHETNEHERNLHPQKS-----	113
	:	: : : : :
	:	: : : : :
QY	176 GEDIVFLATDINLPGADVMMWQSGFGFHFMLVLE-----	KQSYGDGHQOFAIVQLIG 229
	:	: : : : :
	:	: : : : :

NAME: Brezner, David J
REGISTRATION NUMBER: 24,7747
REFERENCE/DOCKET NUMBER: T96-004/A63312
TELEPHONE: (415) 781-1989
TELEFAX: (415) 781-1989
TELEPHONE: (415) 781-1989
TELEFAX: (415) 398-3249
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 522 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-975-405-2

Query Match 6.6%; Score 106; DB 1; Length 522;
Best Local Similarity 19.3%; Pred. No. 0.027;
Matches 72; Conservative 43; Mismatches 115; Indels 144; Gaps 17;

QY 30 SKCPPSQRPVATGTASNN-----DLASFECPCVCFDYVLPPILOQ 71
DB 25 SSCSAVTKDDSVGGTASTGNLSSSFMBEIQGYDVDFPPLSKYECPICL-MALREAVQT 83
QY 72 QSHLVCSNCRPKLTCCPTCRGPLGSIRN-----LAMEKVANSVLPCKYA----- 117
DB 84 PCGRFCKACIIK-----SIRDAHGKCPVDNEILLENLQFPDNFAKREILSLM 131
QY 118 ----SSGC--EITLPHTEKADHEELCEFRPYSCP-----CPGASCKW 153
DB 132 VKCPNEGCLHMKWELHLE--DQAHCEPALMDCPQCQRPFOKFHINIHLKDCP---RR 185
QY 154 QGSLDAMPHLMHQHSITITLOGEDIVFLATDINLPGA-----VDWVMQ----- 198
DB 186 QVSCDNCAASMAFEDKEI-----HDQNCPLANVCEYCNLTILIREQMPNHYDL 233
QY 199 -----SCFGFHEM-----LVLEKQEKYDGHQOQFFA-----IVOLIGTRKQAE 235
DB 234 DCPTAPICTFTFCGCKEKQNRHLARHLQENTQSHRMMLAQAVHLSVIPDSGYISEVR 293
QY 236 NFAY-----RLELNGHRRRLTWEATPSIHEGATATMNSDCLVFTDTSIAQLFAEN-- 286
DB 294 NFQETIHQLEGLRVRQDQHIR---ELTAKMETQSMYVSELKRTITRTLEDKVAIEAQOQN 350
QY 287 -----GNLGINV 293
DB 351 GIYIWKIGNFGMHL 364

Search completed: April 25, 2005, 06:39:44
Job time : 28 secs

TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 781-1989
TELEFAX: (415) 398-3249
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 522 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-639-237-2

Query Match 6.6%; Score 106; DB 1; Length 522;
Best Local Similarity 19.3%; Pred. No. 0.027;
Matches 72; Conservative 43; Mismatches 115; Indels 144; Gaps 17;

QY 30 SKCPPSQRPVATGTASNN-----DLASFECPCVCFDYVLPPILOQ 71
DB 25 SSCSAVTKDDSVGGTASTGNLSSSFMBEIQGYDVDFPPLSKYECPICL-MALREAVQT 83
QY 72 QSHLVCSNCRPKLTCCPTCRGPLGSIRN-----LAMEKVANSVLPCKYA----- 117
DB 84 PCGRFCKACIIK-----SIRDAHGKCPVDNEILLENLQFPDNFAKREILSLM 131
QY 118 ----SSGC--EITLPHTEKADHEELCEFRPYSCP-----CPGASCKW 153
DB 132 VKCPNEGCLHMKWELHLE--DQAHCEPALMDCPQCQRPFOKFHINIHLKDCP---RR 185
QY 154 QGSLDAMPHLMHQHSITITLOGEDIVFLATDINLPGA-----VDWVMQ----- 198
DB 186 QVSCDNCAASMAFEDKEI-----HDQNCPLANVCEYCNLTILIREQMPNHYDL 233
QY 199 -----SCFGFHEM-----LVLEKQEKYDGHQOQFFA-----IVOLIGTRKQAE 235
DB 234 DCPTAPICTFTFCGCKEKQNRHLARHLQENTQSHRMMLAQAVHLSVIPDSGYISEVR 293
QY 236 NFAY-----RLELNGHRRRLTWEATPSIHEGATATMNSDCLVFTDTSIAQLFAEN-- 286
DB 294 NFQETIHQLEGLRVRQDQHIR---ELTAKMETQSMYVSELKRTITRTLEDKVAIEAQOQN 350
QY 287 -----GNLGINV 293
DB 351 GIYIWKIGNFGMHL 364

RESULT 15
US-08-975-405-2
Sequence 2, Application US/08975405
Patent No. 5767244
GENERAL INFORMATION:
APPLICANT: Goeddel, David V.
APPLICANT: Xiong, Jessie
TITLE OF INVENTION: No. 5767244el Protein - TRAF6
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: Flehr, Hobbach, Test, Albritton & Herbert
STREET: 4 Embarcadero Center, Suite 3400
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/975,405
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/639,237
FILING DATE:
ATTORNEY/AGENT INFORMATION:

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OM protein - protein search, using sw model

Run on: April 25, 2005, 06:38:49 ; Search time 403 Seconds
(without alignments)
246.084 Million cell updates/sec

Title: US-10-679-246-2

Perfect score: 1611

Sequence: 1 MWIIIFLLPPYVFIEMSRQ.....IAQLFAENGLNINTWISMC 298

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1424015 seqs, 332791073 residues

Total number of hits satisfying chosen parameters: 1424015

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

- Database : Published Applications_AA.*
- 1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep.*
 - 2: /cgn2_6/ptodata/2/pubpaa/PT_NEW_PUB.pep.*
 - 3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep.*
 - 4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep.*
 - 5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep.*
 - 6: /cgn2_6/ptodata/2/pubpaa/PTUS_PUBCOMB.pep.*
 - 7: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep.*
 - 8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep.*
 - 9: /cgn2_6/ptodata/2/pubpaa/US09A_PUBCOMB.pep.*
 - 10: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep.*
 - 11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep.*
 - 12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep.*
 - 13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep.*
 - 14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep.*
 - 15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep.*
 - 16: /cgn2_6/ptodata/2/pubpaa/US10D_PUBCOMB.pep.*
 - 17: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep.*
 - 18: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep.*
 - 19: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*
 - 20: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1611	100.0	298	16 US-10-679-246-2	Sequence 2, Appli
2	1603	99.5	298	15 US-10-108-260A-2712	Sequence 2712, Ap
3	1198	74.4	324	14 US-10-177-293-425	Sequence 425, App
4	1190	73.9	324	16 US-10-755-889-124	Sequence 124, App
5	462.5	28.7	308	16 US-10-437-963-185899	Sequence 185899,
6	432	26.8	89	9 US-09-925-297-543	Sequence 543, App
7	422	26.2	302	15 US-10-437-963-187446	Sequence 187446,
8	419	26.0	422	16 US-10-424-599-241141	Sequence 241141,
9	417	25.9	305	15 US-10-425-114-43471	Sequence 43471, A
10	416	25.8	324	15 US-10-424-599-164340	Sequence 164340,
11	415	25.8	693	16 US-10-437-963-111838	Sequence 111838,
12	413.5	25.7	311	15 US-10-424-599-161695	Sequence 161695,
13	411	25.5	309	16 US-10-324-120-1	Sequence 1, Appli

14	407.5	25.3	498	16 US-10-437-963-158317	Sequence 158317,
15	405	25.1	309	16 US-10-324-120-3	Sequence 3, Appli
16	404	25.1	309	15 US-10-424-599-158683	Sequence 158683,
17	401	24.9	309	16 US-10-324-120-2	Sequence 2, Appli
18	398.5	24.7	375	16 US-10-437-963-132004	Sequence 132004,
19	397	24.6	310	15 US-10-424-599-161694	Sequence 161694,
20	392	24.3	327	15 US-10-424-599-164338	Sequence 164338,
21	332	20.6	192	16 US-10-767-701-34707	Sequence 34707, A
22	326	20.2	325	14 US-10-219-220-83	Sequence 83, Appl
23	326	20.2	325	14 US-10-219-220-83	Sequence 201, App
24	325	20.2	325	14 US-10-219-220-83	Sequence 270, App
25	325	20.2	325	14 US-10-219-220-83	Sequence 3779, Ap
26	276.5	17.2	187	16 US-10-767-701-50920	Sequence 50920, A
27	260.5	16.2	223	16 US-10-437-963-127636	Sequence 127636,
28	237.5	14.7	358	15 US-10-424-599-271409	Sequence 271409,
29	236.5	14.7	214	16 US-10-767-701-41512	Sequence 41512, A
30	235.5	14.6	341	15 US-10-425-114-67688	Sequence 67688, A
31	235.5	14.6	417	16 US-10-437-963-169168	Sequence 169168,
32	227	14.1	304	16 US-10-437-963-180489	Sequence 180489,
33	225	14.0	292	16 US-10-437-963-172205	Sequence 172205,
34	211.5	13.1	151	16 US-10-767-701-53418	Sequence 53418, A
35	203.5	12.6	307	16 US-10-437-963-173045	Sequence 173045,
36	178	11.0	159	16 US-10-767-701-38997	Sequence 38997, A
37	174.5	10.8	128	16 US-10-437-963-181637	Sequence 181637,
38	173.5	10.8	285	15 US-10-425-114-65663	Sequence 65663, A
39	170.5	10.6	203	16 US-10-437-963-113170	Sequence 113170,
40	169.5	10.5	90	15 US-10-424-599-273575	Sequence 273575,
41	169.5	10.5	332	16 US-10-437-963-131170	Sequence 131170,
42	168	10.4	261	16 US-10-437-963-159080	Sequence 159080,
43	165.5	10.3	386	16 US-10-437-963-194113	Sequence 194113,
44	159	9.9	289	16 US-10-437-963-179909	Sequence 179909,
45	154.5	9.6	105	16 US-10-767-701-60980	Sequence 60980, A

ALIGNMENTS

RESULT 1

US-10-679-246-2
; Sequence 2, Application US/10679246
; Publication No. US20040163138A1
; GENERAL INFORMATION:
; APPLICANT: Reed, John C.
; TITLE OF INVENTION: Nucleic Acid Encoding Proteins Involved
; TITLE OF INVENTION: in Protein Degradation, Products and Methods Related Thereto
; FILE REFERENCE: 66821-235
; CURRENT APPLICATION NUMBER: US/10/679,246
; PRIOR FILING DATE: 2003-10-02
; PRIOR APPLICATION NUMBER: US 09/591,694
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 298
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-679-246-2

Query Match	100.0%	Score 1611;	DB 16;	Length 298;
Best Local Similarity	100.0%	Pred. No. 2.3e-148;		
Matches 298;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	1	MVIIIFLLPPYVFIEMSRQTATLPTGTSKCPSPORVPALGTGTASNNDLASLRECPVC	60	
Db	1	MVIIIFLLPPYVFIEMSRQTATLPTGTSKCPSPORVPALGTGTASNNDLASLRECPVC	60	
QY	61	FDYVLPPIIQCSGHLVCSNCRPKLTCCPTCRGLGSRINLAMEKVANSVLPFCYASSG	120	
Db	61	FDYVLPPIIQCSGHLVCSNCRPKLTCCPTCRGLGSRINLAMEKVANSVLPFCYASSG	120	
QY	121	CSBITPHTEKADHELCFRPVSFCPCGASCKWQCSLDAVPHLMHQHSITTLQGEDIV	180	

Db 121 CEITLPHTEKADHEELCEFRPYSFCPCGASCKWQSLDAMVPHLMHQHKSITTLQGEDIV 180
Qy 181 FLATDINLPAGVDWVMQSCFGFHFMLVLEKQEKYDGHQOQFAIVOLIGTRKQAEAFYR 240
Db 181 FLATDINLPAGVDWVMQSCFGFHFMLVLEKQEKYDGHQOQFAIVOLIGTRKQAEAFYR 240
Qy 241 LEINLGHRRRLTWEATPRSIHEGIATAIMNSDCLVFDTSIAQLFAENGNGINVTISMC 298
Db 241 LEINLGHRRRLTWEATPRSIHEGIATAIMNSDCLVFDTSIAQLFAENGNGINVTISMC 298

RESULT 2

US-10-108-260A-2712
; Sequence 2712, Application US/10108260A
; Publication No. US20040005560A1
; GENERAL INFORMATION:
; APPLICANT: HELIX RESEARCH INSTITUTE
; TITLE OF INVENTION: NO. US20040005560A1 full length cDNA
; FILE REFERENCE: H1-A0106
; CURRENT APPLICATION NUMBER: US/10/108,260A
; CURRENT FILING DATE: 2002-03-27
; NUMBER OF SEQ ID NOS: 5458
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 2712
; LENGTH: 298
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-108-260A-2712

Query Match 99.5%; Score 1603; DB 15; Length 298;
Best Local Similarity 99.7%; Pred. No. 1.4e-147;
Matches 297; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MWIIIFLLPPYVFISEMSQTATLPTGTSKPPSORVPALTGTASNNDLASLSECPVC 60
Db 1 MWIIIFLLPPYVFISEMSQTATLPTGTSKPPSORVPALTGTASNNDLASLSECPVC 60
Qy 61 FDVLPPILOQSGHLVCSNCRPKLTCCPTCRGLGSIIRNLAMEKVANSVLPFCYASSG 120
Db 61 FDVLPPILOQSGHLVCSNCRPKLTCCPTCRGLGSIIRNLAMEKVANSVLPFCYASSG 120
Qy 121 CEITLPHTEKADHEELCEFRPYSFCPCGASCKWQSLDAMVPHLMHQHKSITTLQGEDIV 180
Db 121 CEITLPHTEKADHEELCEFRPYSFCPCGASCKWQSLDAMVPHLMHQHKSITTLQGEDIV 180
Qy 181 FLATDINLPAGVDWVMQSCFGFHFMLVLEKQEKYDGHQOQFAIVOLIGTRKQAEAFYR 240
Db 181 FLATDINLPAGVDWVMQSCFGFHFMLVLEKQEKYDGHQOQFAIVOLIGTRKQAEAFYR 240
Qy 241 LEINLGHRRRLTWEATPRSIHEGIATAIMNSDCLVFDTSIAQLFAENGNGINVTISMC 298
Db 241 LEINLGHRRRLTWEATPRSIHEGIATAIMNSDCLVFDTSIAQLFAENGNGINVTISMC 298

RESULT 3

US-10-177-293-425
; Sequence 425, Application US/10177293
; Publication No. US20030124128A1
; GENERAL INFORMATION:
; APPLICANT: Lillie, James
; APPLICANT: Glatt, Karen
; APPLICANT: Zhao, Xumei
; APPLICANT: Gannavarpu, Manjula
; APPLICANT: Kamatkar, Shubhangi
; APPLICANT: Mertens, Maureen
; APPLICANT: Myer, Vic
; APPLICANT: Wang, Youzhen
; APPLICANT: Xu, Yongyao
; APPLICANT: Hoersch, Sebastian
; APPLICANT: Monahan, John
; APPLICANT: Meyers, Rachel E.
; APPLICANT: Bast Jr., Robert C.
; APPLICANT: Hortobagyi, Gabriel N.

; APPLICANT: Pusztai, Lajos
; APPLICANT: Mexic, Funda
; APPLICANT: Sahin, Aysegul
; APPLICANT: Mills, Gordon B.
; TITLE OF INVENTION: COMPOSITIONS, KITS, AND METHODS FOR IDENTIFICATION, ASSESSMENT,
; FILE REFERENCE: PREVENTION, AND THERAPY OF BREAST CANCER
; TITLE OF INVENTION: MRI-038
; CURRENT APPLICATION NUMBER: US/10/177,293
; CURRENT FILING DATE: 2002-06-21
; PRIOR APPLICATION NUMBER: US 60/299,887
; PRIOR FILING DATE: 2001-06-21
; PRIOR APPLICATION NUMBER: US 60/301,572
; PRIOR FILING DATE: 2001-06-27
; PRIOR APPLICATION NUMBER: US 60/306,501
; PRIOR FILING DATE: 2001-07-18
; PRIOR APPLICATION NUMBER: US 60/325,002
; PRIOR FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: US 60/362,585
; PRIOR FILING DATE: 2002-03-05
; PRIOR APPLICATION NUMBER: US 60/xxx,xxx
; PRIOR FILING DATE: 2002-05-14
; NUMBER OF SEQ ID NOS: 506
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 425
; LENGTH: 324
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-177-293-425

Query Match 74.4%; Score 1198; DB 14; Length 324;
Best Local Similarity 77.3%; Pred. No. 4.4e-108;
Matches 221; Conservative 27; Mismatches 30; Indels 8; Gaps 2;
Qy 21 TATLPTGTSKPPSORVPALTGTASNNDLASLSECPVCDFYVLPPILOQCS 73
Db 37 TISAAGPSSAVPAAAVISGPGGGAGPVSPOHHELTSLFECPVCDFYVLPPILOQCS 96
Qy 74 GHLVCSNCRPKLTCCPTCRGPI-GSIRNLAMEKVANSVLPFCYASSGCEITLPHTEKAD 132
Db 97 GHLVCSNCRPKLTCCPTCRGPI-GSIRNLAMEKVANSVLPFCYASSGCEITLPHTEKAD 156
Qy 133 HEELCEFRPYSFCPCGASCKWQSLDAMVPHLMHQHKSITTLQGEDIVFLATDINLPAGV 192
Db 157 HEDICEYRPYSFCPCGASCKWQSLDAMVPHLMHQHKSITTLQGEDIVFLATDINLPAGV 216
Qy 193 DWVMQSCFGFHFMLVLEKQEKYDGHQOQFAIVOLIGTRKQAEAFYRLNNGHRRRLTW 252
Db 217 DWVMQSCFGFHFMLVLEKQEKYDGHQOQFAIVOLIGTRKQAEAFYRLNNGHRRRLTW 276
Qy 253 EATPRSIHEGIATAIMNSDCLVFDTSIAQLFAENGNGINVTISMC 298
Db 277 EATPRSIHEGIATAIMNSDCLVFDTSIAQLFAENGNGINVTISMC 322

RESULT 4

US-10-755-889-124
; Sequence 124, Application US/10755889
; Publication No. US20040171823A1
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES ASSOCIATED WITH THE NF-KB
; FILE REFERENCE: D0284 NP
; CURRENT APPLICATION NUMBER: US/10/755,889
; CURRENT FILING DATE: 2004-01-13
; PRIOR APPLICATION NUMBER: U.S. 60/440,068
; PRIOR FILING DATE: 2003-01-14
; PRIOR APPLICATION NUMBER: U.S. 60/469,757
; PRIOR FILING DATE: 2003-05-12
; NUMBER OF SEQ ID NOS: 823
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 124
; LENGTH: 324

QY 8 LPYVYFISEMSRQTATATPTGTS-----KCPBSQRV-----PALGTGTASN- 48
DB |||:
78 LPPH-----LPGAVGVGPGRAFPKANVAGVGGGGAAGAPAGGAVAGG 124
QY 49 -----NDLASLFPCCPVCFDVLPPILQCSGHLVCSNCRPKL--TCCTCRGPLGSIR 99
DB |||:
125 GFGGPPATSVHELLECPVCTMSMPPHQCQNGHTLCTCKARVHNRCTCRQELGDIR 184
QY 100 NLAMEKVANSVLFPCKYASSGCEITLPHTEKADHEELCEFRPYSCPCPGASCKWOGSIDA 159
DB |||:
185 CLALEKVAESLELPCCKYSLGCPPIPPYYSKIKHEAQCSTRPNCYPYAGSECAVAGDIPF 244
QY 160 VNPMLMHQK---SITTLQGEDIVFLATDINLPGAVDWM--MQSCFGFHEMLVLEKQEK 214
DB |||:
245 LVAHLRDDHDKVDMHSCTFNHRYVKSNPREE---NATWMLTVFHCFGQYFCL-----H 295
QY 215 YDGHQ-----QFFAIVQLIGTRKQAFNAYRLELNGHRRRLTWEATPRSIHEGIATAMN 269
DB |||:
296 FEAFLGMAPVYMAFLRFMGDENEARNYYSLEVGNGRKMVWEGTTPRSIRDSHRKVRDS 355
QY 270 SDCLVFDTSLAQLFA--ENGNLGINVT 294
DB |||:
356 HDGLIIQRNMLFFSGGDRKELKLRVT 382

RESULT 8
US-10-424-599-241141
; Sequence 241141, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 241141
; LENGTH: 322
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_5979C.1.pap
US-10-424-599-241141

Query Match 26.0%; Score 419; DB 15; Length 322;
Best Local Similarity 34.4%; Pred. No. 3.5e-32;
Matches 94; Conservative 49; Mismatches 108; Indels 22; Gaps 9;
QY 34 PSQRPALTGTATASNDLASLFPCCPVCFDVLPPILQCSGHLVCSNCRPKL--TCCTPCR 92
DB |||:
53 PAOTALKPGTVSSS--VRELLECPVCLNAMYPIHQCNSNGHTLCSGCKPRVHNRCTCR 110
QY 93 GPLGSIRNLAMEKVANSVLFPCKYASSGCEITLPHTEKADHEELCEFRPYSCPCPGASCK 152
DB |||:
111 HELGNIRCLALEKVAESLELPCCKYQCGGCGIGIYYSKLEHESQCAHRPNCYPYAGSECS 170
QY 153 WQSLDAMPHLMHQHSITTLQGEDIVFLATDINLPGAVD---WM--MQSCFGFHEMLV 208
DB |||:
171 IMGDIPLYVAHLKDDHK--VDMHNGSTFNHRYVKS--PQEVENATWMLTVFSCFGQYFCL- 227
QY 209 LEKQEKVDGHQ-----OFFAIVQLIGTRKQAFNAYRLELNGHRRRLTWEATPRSIHEGI 263
DB |||:
228 -----HFEAFQLGMAPVYIAFLRFMGDDDAKNYSYSLVGGNGRKMVWOGVPRSDSH 282
QY 264 ATAIMNSDCLVFTDSIAQLFA--ENGNLGINVT 294
DB |||:
283 RKVRDSFDGLIIQRNMLFFSGGDRKELKLRVT 315

RESULT 9
US-10-425-114-43471
; Sequence 43471, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 43471
; LENGTH: 305
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: 700349579_FLI.pap
US-10-425-114-43471

Query Match 25.9%; Score 417; DB 15; Length 305;
Best Local Similarity 35.2%; Pred. No. 5e-32;
Matches 92; Conservative 48; Mismatches 101; Indels 20; Gaps 8;
QY 46 ASNDLASLFPCCPVCFDVLPPILQCSGHLVCSNCRPKL--TCCTPCRGLGSIRNLAME 104
DB |||:
46 ASYGNVRELLECPVCLNAMYPIHQCNSNGHTLCSGCKPRVHNRCTCRHELGNIRCLALE 105
QY 105 KVANSVLFPCKYASSGCEITLPHTEKADHEELCEFRPYSCPCPGASCKWQSLDAMPHL 164
DB |||:
106 KVAASLELPCCKYQNGCGGIGIYYSKLEHESQCAHRPNCYPYAGSECTVAGDIPYLVNHL 165
QY 165 MHQHSITTLQGEDIVFLATDINLPGAVD---WM--MQSCFGFHEMLVLEKQEKVDGHQ- 219
DB |||:
166 KDDHK--VDMHNGSTFNHRYVKS--PHEVENATWMLTVFSCFGQYFCL-----HFEAFQL 217
QY 220 -----OFFAIVQLIGTRKQAFNAYRLELNGHRRRLTWEATPRSIHEGIATAMNSDCLVF 275
DB |||:
218 GMAPVYIAFLRFMGDDDAKNYSYSLVGGNGRKMVWOGVPRSDSHRKVRDSYDGLII 277
QY 276 DTSIAQLFA--ENGNLGINVT 294
DB |||:
278 QRNMLFFSGGDRKELKLRVT 298

RESULT 10
US-10-424-599-164340
; Sequence 164340, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 164340
; LENGTH: 324
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_119417C.1.pap
US-10-424-599-164340

Query Match 25.8%; Score 416; DB 15; Length 324;
Best Local Similarity 33.8%; Pred. No. 6.8e-32;
Matches 98; Conservative 44; Mismatches 102; Indels 46; Gaps 10;

QY 35 SQRVPALTGTASN-----NDLA-----SLFECPCVDFYVLPPILOQSGHLVCSNCRPK 84
DB 31 SSKPRNGTSTNSVCPNGIAPATSVHELLECPVCTNSMYPPIHQCHNGHTLCTCKTR 90
QY 85 L-TCCPTCRGPLGSIRNLAMEKANSVLFPCKYASSGCEITLPHTEKADHEELCEPRYS 143
DB 91 VHNRCPTCRQELGDIRCALEKVAESLELPCKYSLGCPPEIFPYYSKLKHEITVCNFRYS 150
QY 144 CPCGASCKQGSLDVAMPHLMHQKSIITLQGEDIVFLATDNL-----PGAVD-- 193
DB 151 CPVAGSECVVGDIPFLVAHLRDDHK-----VDMETGCTFNHRYKSNPREVENA 200
QY 194 -WVM-MQSCFGFHMVLEKQKVDGHQ-----OFFAIVOLIGTRKOAENFAYRLLENGH 246
DB 201 TWMLTVFHCFGQYFCL-----HFEAFQLGMAPVYMAFLRPMGDENEARNSYSLEVGAN 254
QY 247 RRLTWEATPRSIHEGIATATMNSDCLVFDTSIAQLFA--ENGNLGINVT 294
DB 255 GRKLIWGTFRSVDRSHRKVRDSDHGLIIQRNMALFFSGGDRKELKLRVT 304

RESULT 11
US-10-437-963-111838
; Sequence 111838, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 111838
; LENGTH: 693
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_1577C.1.pep
US-10-437-963-111838

Query Match 25.8%; Score 415; DB 16; Length 693;
Best Local Similarity 34.7%; Pred. No. 2.3e-31;
Matches 90; Conservative 50; Mismatches 99; Indels 20; Gaps 8;

QY 48 NNDLASLFEPCVDFYVLPPILOQSGHLVCSNCRPKL-TCCPTCRGPLGSIRNLAMEKV 106
DB 436 SGNVRELLECPVCLNAMYPIHQCSNGHTLCSGCKPRVHNRCTCRHELGNIRCLAEKV 495
QY 107 ANSVLPFCYASSGCEITLPHTEKADHEELCEPRYS CPCPGASCKWQGS LDVAMPHLMH 166
DB 496 AASLELPCKYQNGFGLIYPPYCKLKHESQCYRPTCTPVAGSECTVAGDIQYLVSHLKD 555
QY 167 QHKSITTLQGEDIVFLATDNLPGAVD---WVM-MQSCFGFHMVLEKQKVDGHQ--- 219
DB 556 DHK-VDMHNGSTFNHRYVKS-N-PHEVENATWMLTVFSCFGYFCL-----HFEAFQLGM 607
QY 220 --OFFAIVOLIGTRKOAENFAYRLLENGHRRRLTWEATPRSIHEGIATATMNSDCLVFD 277
DB 608 APVTIAFLRPMGDAAENKNSYSLEVGSGGRKMTQGVPRSIKSHRKRVDSDYDGLIIQR 667

QY 278 SIAQLFA--ENGNLGINVT 294
DB 668 NMALFFSGGDKKELKLRVT 686

RESULT 12
US-10-424-599-161695
; Sequence 161695, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 161695
; LENGTH: 311
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_117028C.1.pep
US-10-424-599-161695

Query Match 25.7%; Score 413.5; DB 15; Length 311;
Best Local Similarity 32.6%; Pred. No. 1.1e-31;
Matches 89; Conservative 51; Mismatches 90; Indels 43; Gaps 7;

QY 44 TTASNDLASLFEPCVDFYVLPPILOQSGHLVCSNCRPKL-TCCPTCRGPLGSIRNLA 102
DB 39 TTTSVHD---LLEPCVCTNSMYPPIHQCHNGHTLCTCKTRVHNRCTCRQELGDIRCLA 95
QY 103 MEKANSVLFPCKYASSGCEITLPHTEKADHEELCEPRYS CPCPGASCKWQGS LDVAMP 162
DB 96 LEKIAESLELPCKYISLGCPEIFPYYSKLKHEAICNFRPYNCYPYAGSDCVVGDIPCLVA 155
QY 163 HLM-----HOHKSITTLQGEDIVFLATDNLPGAVDWMVMQSCFGFHEMLV 208
DB 156 HLRRDHRVDMHSGCTFNHRYVKS-NPMEVENATWMLTVFH-----CFGQYFCL- 202
QY 209 LEKQEKYDGHQ-----OFFAIVOLIGTRKOAENFAYRLLENGHRRRLTWEATPRSIHEGI 263
DB 203 -----HFEAFQLGMAPVYMAFLRPMGDENEARNSYSLEVGNGRKLTFPGSPRSDSH 257
QY 264 ATAIMNSDCLVFDTSIAQLFA--ENGNLGINVT 294
DB 258 KKVDRSDHGLIIYRNMALFFSGGDRKELKLRVT 290

RESULT 13
US-10-324-120-1
; Sequence 1, Application US/10324120
; Publication No. US20040123349A1
; GENERAL INFORMATION:
; APPLICANT: TENASEK LIFE SCIENCES LABORATORY
; TITLE OF INVENTION: SINAT5, an Arabidopsis thaliana gene involved in lateral root dev
; FILE REFERENCE: 2577-157
; CURRENT APPLICATION NUMBER: US/10/324,120
; CURRENT FILING DATE: 2002-12-20
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 309
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-10-324-120-1

Query Match 25.5%; Score 411; DB 16; Length 309;
Best Local Similarity 33.3%; Pred. No. 2e-31;

Search completed: April 25, 2005, 06:51:41
Job time : 404 secs

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: April 25, 2005, 06:39:49 ; Search time 4911 Seconds
(without alignments)
2940.268 Million cell updates/sec

Title: US-10-679-246-2

Perfect score: 1611

Sequence: 1 MWIIIFLPPYVFIEMSRQ.....IAQLFAENGLNINVTISM 298

Scoring table:

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Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

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-O=/cgn2.1/USPTO.spool/US10679246/runat.22042005.185510.7685/app_query.fasta.1.455
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-UNITS=bits -START=1 -END=-1 -MATRIX=blomsu62 -TRANS=human40.cdi -LIST=45
-DOALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
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-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

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- 2: gb.htg.*
- 3: gb.in.*
- 4: gb.om.*
- 5: gb.ov.*
- 6: gb.pat.*
- 7: gb.ph.*
- 8: gb.pl.*
- 9: gb.pr.*
- 10: gb.ro.*
- 11: gb.sts.*
- 12: gb.sv.*
- 13: gb.un.*
- 14: gb.vi.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1611	100.0	1274	6	AR411820 Sequence
2	1611	100.0	1274	6	AX058082 Sequence
3	1611	100.0	2128	9	AK056051 Homo sapi
4	1611	100.0	2440	6	AR380043 Sequence

5	1611	100.0	2924	6	CQ491092	CQ491092 Sequence	
6	1611	100.0	2924	6	CQ493590	CQ493590 Sequence	
7	1611	100.0	2924	6	CQ496955	CQ496955 Sequence	
8	1611	100.0	31705	9	HSAA00626	AJ400626 Homo sapi	
9	1611	100.0	173304	9	AC023818	AC023818 Homo sapi	
10	1603	99.5	2829	6	AX833145	AX833145 Sequence	
11	1603	99.5	2829	9	AK094663	AK094663 Homo sapi	
12	1596	99.1	2972	9	HSMB07215	BX647064 Homo sapi	
C	13	1565	97.1	4090	6	AX780380	AX780380 Sequence
14	1553.5	96.4	220157	2	AC105462	AC105462 Rattus no	
15	1542	95.7	175636	10	AC142211	AC142211 Mus muscu	
C	16	1541.5	95.7	232382	2	AC098991	AC098991 Rattus no
17	1540	95.6	1540	9	BC035562	BC035562 Homo sapi	
18	1540	95.6	2048	9	HSU76247	U76247 Human HSI	
19	1537	95.4	1874	6	CQ719559	CQ719559 Sequence	
20	1537	95.4	2454	9	BC042550	BC042550 Homo sapi	
21	1536	95.3	1645	10	BC046317	BC046317 Mus muscu	
22	1536	95.3	1968	6	AX305603	AX305603 Sequence	
23	1536	95.3	1968	10	MMSIAH1A	Z19579 M.musculus	
24	1534	95.2	1246	5	BC072747	BC072747 Xenopus l	
25	1532	95.1	1886	9	HSU63295	U63295 Homo sapien	
26	1528	94.8	1465	10	AF389476	AF389476 Rattus no	
27	1527	94.8	2034	9	BC018193	BC018193 Homo sapi	
C	28	1514.5	94.0	120810	5	BX649644	BX649644 Zebrafish
29	1514.5	94.0	241301	5	BX470163	BX470163 Zebrafish	
30	1513	93.9	2419	5	BC045870	BC045870 Danio rer	
31	1504	93.4	1713	10	MMSIAH1B	Z19580 M.musculus	
C	32	1504	93.4	112893	10	AL732294	AL732294 Mouse DNA
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34	1500	93.1	1720	10	BC052887	BC052887 Mus muscu	
35	1489	92.4	1884	6	A63558	A63558 Sequence 11	
36	1489	92.4	1884	6	AR271267	AR271267 Sequence 11	
37	1486	92.2	1457	10	AB067814	AB067814 Rattus no	
38	1405	87.2	194622	10	AC133654	AC133654 Mus muscu	
39	1270	78.8	711	5	CR386772	CR386772 Gallus ga	
C	40	1262	78.3	168091	10	AC139553	AC139553 Mus muscu
41	1262	78.3	182733	10	AC123941	AC123941 Mus muscu	
42	1214	75.4	1441	3	AK112696	AK112696 Ciona inc	
43	1208.5	75.0	2511	10	BC058400	BC058400 Mus muscu	
44	1206	74.9	2347	9	BC013082	BC013082 Homo sapi	
45	1205.5	74.8	2048	10	AB067815	AB067815 Rattus no	

ALIGNMENTS

RESULT 1	AR411820	Sequence 1 from patent US 6638734.	1274 bp	DNA	linear	PAT 18-DB-2003
LOCUS	AR411820	Sequence 1 from patent US 6638734.	1274 bp	DNA	linear	PAT 18-DB-2003
DEFINITION	AR411820	Sequence 1 from patent US 6638734.	1274 bp	DNA	linear	PAT 18-DB-2003
ACCESSION	AR411820	Sequence 1 from patent US 6638734.	1274 bp	DNA	linear	PAT 18-DB-2003
VERSION	AR411820.1	GI:40164258				
KEYWORDS	Unknown.					
SOURCE	Unknown.					
ORGANISM	Unclassified.					
REFERENCE	1 (bases 1 to 1274)					
AUTHORS	Reed, J.C. and Matsuzawa, S.-i.					
TITLE	Nucleic acid encoding proteins involved in protein degradation, products and methods related thereto					
JOURNAL	Patent: US 6638734-A 1 28-OCT-2003;					
FEATURES	Location/Qualifiers					
source	1..1274					
	/organism="unknown"					
	/mol_type="genomic DNA"					

ORIGIN

Alignment Scores:						
Pred. No.:	2.79e-121	Length:	1274			
Score:	1611.00	Matches:	298			
Percent Similarity:	100.00%	Conservative:	0			
Best Local Similarity:	100.00%	Mismatches:	0			
Query Match:	100.00%	Indels:	0			
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QY 201 PheGlyPheHisPheMetLeuValLeuGluLeuGlnGlyLysTrpAspGlyHisGlnGln 220
Db 874 TTTCGGCTTTTCACTTTCATGTTAGTCTTAGAGAACAGGAAAAATACGATGTCACCAAGCAG 933
QY 221 PhePheAlaValGlnLeuIleGlyThrArgLysGlnAlaGluAsnPheAlaTrpArg 240
Db 934 TTCTTCGCAATCGTACAGCTGATAGAACACGCAAGCAGCTGAAAAATTTGCTTACCGA 993
QY 241 LeuGluLeuAsnGlyHisArgArgLysLeuThrTrpGluAlaThrProArgSerIleHis 260
Db 994 CTTGACTAAATGGTCATAGGCGACCAATTGACTTGGAGAGCACTCTCGACTATTCAT 1053
QY 261 GluGlyLeuAlaThrAlaIleMetAsnSerAspCysLeuValPheAspThrSerIleAla 280
Db 1054 GAAGGAATTCGAACGCCATTATGAATAGCAGCTGCTAGTCTTTGACACCAAGCATTGCA 1113
QY 281 GlnLeuPheAlaGluAsnGlyLeuGlyIleAsnValThrIleSerMetCys 298
Db 1114 CAGCTTTTTCGAGAAATGCAATTTAGGCATCAATGTAACTATTTCATGTGT 1167

RESULT 3
AK056051/c
LOCUS Homo sapiens cDNA FLJ31489 fis, clone NT2NE2003308. PRI 30-JAN-2004
DEFINITION AK056051
VERSION AK056051.1 GI:16551141
KEYWORDS oligo capping; fis (full insert sequence).
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE
1
Ota, T., Suzuki, Y., Nishikawa, T., Otsuki, T., Sugiyama, T., Irie, R., Wakamatsu, A., Hayashi, K., Sato, H., Negai, K., Kimura, K., Makita, H., Sekine, M., Ohyashi, M., Nishi, T., Shibahara, T., Tanaka, T., Ishii, S., Yamamoto, J., Saito, K., Kawai, Y., Isono, Y., Nakamura, Y., Nagahari, K., Murakami, K., Yasuda, T., Iwayanagi, T., Wagatsuma, M., Shizatori, A., Sudo, H., Hosolri, T., Kaku, Y., Kodaira, H., Kondo, H., Sugawara, M., Takahashi, M., Kanda, K., Yokoi, T., Furuya, T., Kikkawa, E., Omura, Y., Abe, K., Kamihara, K., Katsuta, N., Sato, K., Tanikawa, M., Yamazaki, M., Ninomiya, K., Ishibashi, T., Yamashita, H., Murakawa, K., Fujimori, K., Tanai, H., Kimata, M., Watanabe, M., Hirakawa, S., Chiba, Y., Ishida, S., Ono, Y., Takiguchi, S., Watanabe, S., Yosida, M., Hotuta, T., Kusano, J., Kanehori, K., Takahashi-Fujii, A., Hara, H., Tanase, T., Nomura, Y., Togiya, S., Komai, F., Hara, R., Takeuchi, K., Arita, M., Imose, N., Musashino, K., Yuuki, H., Oshima, A., Sasaki, N., Aotsuka, S., Yoshikawa, Y., Matsunawa, H., Ichihara, T., Shiohata, N., Sano, S., Moriya, S., Momiyama, H., Satoh, N., Takami, S., Terashima, Y., Suzuki, O., Nakagawa, S., Senoh, A., Mizoguchi, H., Goto, Y., Shimizu, F., Wakebe, H., Hishigaki, H., Watanabe, T., Sugiyama, A., Takemoto, M., Kawakami, B., Yamazaki, M., Watanabe, K., Kumagai, A., Itakura, S., Fukuzumi, Y., Fujimori, Y., Komiyama, M., Tashiro, K., Tanigami, A., Fujiwara, T., Ono, T., Yamada, K., Fujii, Y., Ozaki, K., Hiro, M., Ohmori, Y., Kawabata, A., Hiki, J., Kobatake, N., Inagaki, H., Ikem, Y., Okamoto, S., Okitani, R., Kawakami, T., Noguchi, S., Itoh, T., Shigetani, K., Senba, T., Matsumura, K., Nakajima, Y., Mizuno, T., Morinaga, M., Sasaki, M., Togashi, T., Oyama, M., Hata, H., Watanabe, M., Komatsu, T., Mizushima-Sugano, J., Satoh, T., Shirai, Y., Takahashi, Y., Nakagawa, K., Okumura, K., Nagase, T., Nomura, N., Kikuchi, H., Masuho, Y., Yamashita, R., Nakai, K., Yada, T., Nakamura, Y., Ohara, O., Isogai, T. and Sugano, S. Complete sequencing and characterization of 21,243 full-length human cDNAs Nat. Genet. 36 (1), 40-45 (2004).

REFERENCE
2
Ninomiya, K., Wagatsuma, M., Kanda, K., Kondo, H., Yokoi, T., Kodaira, H., Furuya, T., Takahashi, M., Kikkawa, E., Omura, Y., Abe, K., Kamihara, K., Katsuta, N., Sato, K., Tanikawa, M., Yamazaki, M., Sugiyama, T., Irie, R., Otsuki, T., Sato, H., Wakamatsu, A., Ishii, S., Yamamoto, J., Isono, Y., Kawai-Hio, Y., Saito, K., Nishikawa, T.,

Kimura, K., Yamashita, H., Matsuo, K., Nakamura, Y., Sekine, M., Kikuchi, H., Murakawa, K., Kanehori, K., Takahashi-Fujii, A., Oshima, A., Sugiyama, A., Kawakami, B., Suzuki, Y., Sugano, S., Nagahari, K., Masuho, Y., Nagai, K. and Isogai, T. NEDO human cDNA sequencing project Unpublished JOURNAL 3 (bases 1 to 2128) Isogai, T., Otsuki, T. and Sugiyama, T. Direct Submission JOURNAL 3 (bases 1 to 2128) Submitted (24-OCT-2001) Takao Isogai, Helix Research Institute, Genomics Laboratory; 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan (E-mail: genomics@hri.co.jp, Tel: 81-438-52-3975, Fax: 81-438-52-3986) NEDO human cDNA sequencing project supported by Ministry of Economy, Trade and Industry of Japan; cDNA full insert sequencing: Research Association for Biotechnology (RAB); cDNA library construction: Helix Research Institute (HRI) (supported by Japan Key Technology Center etc.); 5'- & 3'-end one pass sequencing: RAB, HRI, and Biotechnology Center, National Institute of Technology and Evaluation; clone selection for full insert sequencing: RAB and HRI.

Location/Qualifiers
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/clone="NT2NE2003308"
/cell_line="NT2"
/cell_type="teratocarcinoma"
/clone_lib="NT2NE2"
/note="cloning vector: pME18SFL3-mRNA from NT2 neuron after the differentiation of NT2 neuronal precursor cells."

ALIGNMENT SCORES
Pred. No.: 5,17e-121 Length: 2128
Score: 1611.00 Matches: 298
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 9 Gaps: 0

US-10-679-246-2 (1-298) x AK056051 (1-2128)

QY 1 MetValIleIlePheLeuLeuProProTyrValPheIleSerGluMetSerArgGln 20
Db 2025 ATGGTTATATATTTTCTCTCTGCTCTCTATGATATTATTTCAGAAATGAGCCCTCAG 1966

QY 21 ThrAlaThrAlaLeuProThrGlyThrSerLysCysProProSerGlnArgValProAla 40
Db 1965 ACTGCTACAGCATTACCTACCGGTACCTCGAAGTGTCCACCATCCAGAGGGTGCCTGCC 1906

QY 41 LeuThrGlyThrThrAlaSerAsnAspLeuAlaSerLeuPheGluCysProValCys 60
Db 1905 CTGACTGGCACAACATGATCCAAACAAATGACTTGGCGAGTCTTTTGGAGTGCAGTCTGC 1846

QY 61 PheAspTyrValLeuProProIleLeuGlnCysGlnSerGlyHisLeuValCysSerAsn 80
Db 1845 TTTCGATATGTTTACCGCCCATCTTCAATGTCAGATGGCCATCTTGTGTAGCAAC 1786

QY 81 CysArgProLysLeuThrCysCysProThrCysArgGlyProLeuGlySerIleArgAsn 100
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QY 101 LeuAlaMetGluLysValAlaAsnSerValLeuPheProCysLysTyrAlaSerSerGly 120
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QY 121 CysGluIleThrLeuProHisThrGluLysAlaAspHisGluGluLeuCysGluPheArg 140
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QY 141 ProTyrSerCysProCysProGlyAlaSerCysLysTrpGlnGlySerLeuAspAlaVal 160

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	Ddb	1113	TGTGAATAACTCTGCACACACAGAAAAGCAGACCATTGAAGAGCTCTGTGAGTTAGG	1172		
	Oy	141	ProTyrSerCysProCysProGlyAlaSerCysIysTrpGlnGlySerLeuAspAlaVal	160		
	Ddb	1173	CCTTATTCTCTCGTGCCCTGGTCTCTCTGTGTAATGGCAAGCTCTCTGGATGCTGTGA	1232		
	Oy	161	MetProHisLeuMetHisGlnHisIysSerIleThrThrLeuGlnGlyGluAspIleVal	180		
	Ddb	1233	ATGCCCATCTGATGCATCACATAAGTCCATTACACCTTACAGGGNAGAGATATAGTT	1292		
	Oy	181	PheLeuAlaThrAspIleAsnLeuProGlyAlaValAspTrpValMetMetGlnSerCys	200		
	Ddb	1293	TTTTCTGCTACAGACATTAATCTTCTGGTCTGTTCAGTCGGTGATGATCGAGTCTCTGT	1352		
	Oy	201	PheGlyPheHisPheMetLeuValLeuGluLysGlnGluLysTrpAspGlyHisGlnGln	220		
	Ddb	1353	TTTGCTTTTCACTTCATGTTTGTCTTAGAGAAACAGGAAAAATACGATGTCACAGCAG	1412		
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	Ddb	1413	TTCTTCGCAATCGTACAGCTGATAGAACACGCAAGCAAGCTGAAAAATTTTGTCTTACGGA	1472		
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	Ddb	1473	CTTGAGCTAAATGGTCAVAGCGCAGATTGACTTGGGAAGCGGACTCTCTCGATCTATTTCAT	1532		
	Oy	261	GluGlyIleAlaThrAlaIleMetAsnSerAspCysLeuValPheAspThrSerIleAla	280		
	Ddb	1533	GAAGGAATTGCACAGCCATTATGATAGGACTCTCTAGICTTTTGACACAGCAGATTGCA	1592		
	Oy	281	GlnLeuPheAlaGluAAsnGlyAsnLeuGlyIleAsnValThrIleSerMetCys	298		
	Ddb	1593	CAGCTTTTTCGAGAAAATGGCAATTTAGGCATCAATGTAACATTATTTCCATGTGT	1646		
RESULT 8		HSA400626	31705 bp	DNA	linear	PRI 02-APR-2001
LOCUS		Homo sapiens SIAH1 gene, exons 1-2.				
DEFINITION		AJ400626				
ACCESSION		AJ400626.1	GI:13539602			
VERSION		siah1 gene.				
KEYWORDS		Homo sapiens (human)				
SOURCE		Homo sapiens				
ORGANISM		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				
REFERENCE		1	Medhioub,M., Muchardt,C., Tubacher,E., Giudicelli,C., Hors-Cayla,M.C. and Thomas G. Down regulation of the TATA-less and GC-rich SIAH1 promoter by TP53 Unpublished			
AUTHORS		2	(bases 1 to 31705) Medhioub,M. Direct Submission			
JOURNAL		Submitted (11-APR-2000) Medhioub M., Fondation Jean DAUSSSET. CEPH, 27, rue Juliette Dodu, Paris 75010, FRANCE				
FEATURES		Location/Qualifiers				
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gene						
exon						
5'UTR						

	/gene="SIAH1"																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																											
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QY 241 LeuGluLeuAsnGlyHisArgArgLeuThrTrpGluAlaThrProArgSerIleHis 260
 Db 1734 CTTGAGCTAAATGGTTCATAGGCGACGATTGACTTTGGGAAGCGACTCCTCGATCTATTCAT 1793
 QY 261 GluGlyIleAlaThrAlaIleMetAsnSerAspCysLeuValPheAspThrSerIleAla 280
 Db 1794 GGAGGAATTGCAACAGCCATTATGATAGCGACTGTCGTAGTCTTTGACACCGACGATTGCA 1853
 QY 281 GlnLeuPheAlaGluAsnGlyAsnLeuGlyIleAsnValThrIleSerMetCys 298
 Db 1854 CAGCTTTTTCGAGAAAATGCAATTTAGGCATCAATGTAATCTATTTCCATGTGT 1907
 RESULT 13
 LOCUS AX780380 4090 bp DNA linear PAT 14-JUL-2003
 DEFINITION Sequence 2537 from Patent WO03039443.
 ACCESSION AX780380
 VERSION AX780380.1 GI:32697374
 KEYWORDS
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1
 AUTHORS Haferlach, T., Schoch, C., Kern, W., Kohlmann, A., Schnittger, S.,
 Dugas, M., Eils, R., Brors, B. and Mergenthaler, S.
 TITLE Novel genetic markers for leukemias
 JOURNAL Patent: WO 03039443-A 2537 15-MAY-2003;
 Deutsches Krebsforschungszentrum (DE);
 Ludwig-Maximilian-Universitaet Muenchen (DE); Haferlach, Torsten,
 PD Dr. Dr. (DE); Schoch, Claudia (DE); Kern, Wolfgang (DE)
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 Pred. No.: 6,09e-117 Length: 4090
 Score: 1565.00 Matches: 295
 Percent Similarity: 98.33% Conservative: 0
 Best Local Similarity: 98.33% Mismatches: 3
 Query Match: 97.14% Indels: 2
 DB: Gaps: 0
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 QY 21 ThrAlaThrAlaLeuProThrGlyThrSerLysCysProSerGlnArgValProAla 40
 Db 3278 ACTGCTACAGCATTAACCGGTACTCGAATGTGCCACCATCCAGAGGWTGCCCTGCC 3219
 QY 41 LeuThrGlyThrThrAlaSerAsnAsnAspLeuAlaSerLeuPheGluCysProValCys 60
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 QY 61 PheAspTyrValLeuProProIleLeuGlnCysGlnSerGlyHisLeuValCysSerAsn 80
 Db 3158 TTTGACTATGTGTATTCGCGCCCATTTCTCAATGTTCAGATGGCCATCTTGTGTAGCAAC 3099
 QY 81 CysArgProLysLeuThrCysCysProThrCysArgGlyProLeuGlySerIleArgAsn 100
 Db 3098 TGTGCGCCCAAGCTACATGTTGTCCAACTGCGCGGGCCCTTTGGGATCCATTCGCAAC 3039
 QY 101 LeuAlaMetGluLysValAlaAsnSerValLeuPheProCysLysTyrAlaSerSerGly 120
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 QY 121 CysGluIleThrLeuProHisThrGluLys-AlaAspHisGlu-GluLeuCysGluPheA 140

Db 2978 TGTGAATAACTCTGNCAACACAGAAAAAANGCAGACCACCATGAANANGCTCTGTGAGTTTA 2819
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 Db 2918 GGCCTTATTCCTGTCGTCGCCCTGGTGCTCTCTGTAATGGCAAGGCTCTCTGATGCTG 2859
 QY 160 alMerProHisLeuMetHisGlnHisLysSerIleThrThrLeuGlnGlyGluAspIlev 180
 Db 2858 TAATGCCCATCTGATGCATCAGCATAAGTCCATTACAACCCCTACAGGGAGAGATATAG 2799
 QY 180 alPheLeuAlaThrAspIleAsnLeuProGlyValaValAspTrpValMetMetGlnSerC 200
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 QY 200 yPheGlyPheHisPheMetLeuValLeuGluLysGlnGlyLysTyrAspGlyHisGlnG 220
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 AC105462
 LOCUS Rattus norvegicus clone CH230-145D2, WORKING DRAFT SEQUENCE.
 DEFINITION AC105462
 ACCESSION AC105462
 VERSION AC105462.7 GI:30521365
 KEYWORDS HTG; HTGS_PHASE2; HTGS_DRAFT; HTGS_FULLTOP.
 SOURCE Rattus norvegicus (Norway rat)
 ORGANISM Rattus norvegicus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
 Rattus.
 REFERENCE 1 (bases 1 to 220157)
 AUTHORS Muzny, D., Marie, Metzker, M., Lee, Abranzone, S., Adams, C., Alder, J.,
 Allen, C., Allen, H., Alsbrooks, S., Amin, A., Anguiano, D.,
 Anyalebechi, V., Aoyagi, A., Ayodeji, M., Baca, E., Baden, H.,
 Baldwin, D., Bandaranaike, D., Barber, M., Barnstead, M., Benahmed, F.,
 Biswal, K., Blair, J., Blankenburg, K., Blyth, P., Brown, M.,
 Bryant, N., Buhay, C., Burch, P., Burrell, K., Calderon, E.,
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 Delgado, O., Denson, S., Deramo, C., Ding, Y., Dinh, H., Divya, K.,
 Draper, H., Dugan-Rocha, S., Dunn, A., Durbin, K., Duval, B., Eaves, K.,
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 Gunaratne, P., Haaland, W., Hamil, C., Hamilton, C., Hamilton, K.,
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 Hernandez, R., Hines, S., Hladun, S.L., Hodgson, A., Hognes, M.,
 Hollins, B., Howells, S., Hulyk, S., Hume, J., Idlebird, D., Jackson, A.,
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* of the gaps between them are based on estimates that have
 * provided by the submitter.
 * This sequence will be replaced
 * by the finished sequence as soon as it is available and
 * the accession number will be preserved.
 * 1 220157: contig of 220157 bp in length.

FEATURES

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ORIGIN

Alignment Scores:
 Pred. No.: 6.31e-114 Length: 220157
 Score: 1553.50 Matches: 286
 Percent Similarity: 97.67% Conservative: 8
 Best Local Similarity: 95.02% Mismatches: 4
 Query Match: 96.43% Indels: 3
 Gaps: 1
 DB: 2

US-10-679-246-2 (1-298) x AC105462 (1-220157)

QY	1	MetValIleIleIlePheLeuLeuProProTyValPheIle-----SerGluMet	17
Db	118118	GTTATATTGTAACCTTCCCTGCTCTCTTTATTTCTTTCTTTACAGAGATG	118177
QY	18	SerArgGlnThrAlaThrAlaLeuProThrGlyThrSerLysCysProSerGlnArg	37
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QY	38	ValProAlaLeuThrGlyThrAlaSerAsnAspLeuAlaSerLeuPheGluCys	57
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QY	58	ProValCysPheAspTyrrValLeuProProIleLeuGlnCysGlnSerGlyHisLeuVal	77
Db	118298	CCTGCTCTGCTTGTGACTATGTATTGCCACCTATTTCTCAGTGTCCAGAGTGCCCATCTTGT	118357
QY	78	CysSerAsnCysArgProLysLeuThrCysCysProThrCysArgGlyProLeuGlySer	97
Db	118358	TGTAGCACTGTGCGCCCAACTTACATGTTGTCCACCTGCGGGGCCCGTTGGATCC	118417
QY	98	IleArgAsnLeuAlaMetGluLysValAlaAsnSerValLeuPheProCysLysTyrrAla	117
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QY	118	SerSerGlyCysGluIleThrLeuProHisThrGluLysAlaAspHisGluGluLeuCys	137
Db	118478	TCTTCTGGATGTGAGATAACTCTGCGGCACACCGAAAGCGAGACGAGGAGCTCTGT	118537
QY	138	GluPheArgProTyrrSerCysProCysProGlyAlaSerCysLysTyrrGlnGlySerLeu	157
Db	118538	GAGTTGAGGCTTACTTCTGCGCCCTGCTGCTGCTTCTCTGTAAGTGGCAAGGCTCTTGT	118597
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QY	178	AspIleValPheLeuAlaThrAspIleAsnLeuProGlyValaValaAspTrpValMetMet	197
Db	118658	GATATAGTTTCTTGTCTACAGACATTAACTTCTTCTGTTGCTGTTGCTGTTGCTGTTG	118717
QY	198	GlnSerCysPheGlyPheHisPheMetLeuValLeuGluLysGlnGluLysTyrrAspGly	217

Maheshwari, M., Mahindartne, M., Mahmoud, M., Malloy, K., Mangum, A., Mangum, B., Mapua, P., Martin, K., Martin, R., Martinez, E., Mahoney, S., McLeod, M.P., McNeill, T.Z., Meenen, E., Milosavljevic, A., Miner, G., Minja, E., Montemayor, J., Moore, S., Morgan, M., Morris, K., Morris, S., Munidasa, M., Murphy, M., Nair, L., Nankervis, C., Neal, D., Newton, N., Nguyen, N., Norris, S., Parks, K., Nwaokemele, O., Okunolu, G., Olarnpunsagoon, A., Pal, S., Parks, K., Pasternak, S., Paul, H., Perez, A., Perez, L., Pfannkuch, C., Plopper, F., Poindexter, A., Popovic, D., Primus, E., Pu, L.-L., Puazo, M., Quiroz, J., Rachlin, E., Reeves, K., Regier, M.A., Reigh, R., Reilly, B., Reilly, M., Ren, Y., Reuter, M., Richards, S., Riggs, F., Rives, C., Rodkey, T., Rojas, A., Rose, M., Rose, R., Ruiz, S.J., Sanders, W., Savary, G., Scherer, S., Scott, G., Shatsman, S., Shen, H., Shetty, J., Shvartsbeyn, A., Sisson, I., Sitter, C.D., Smajls, D., Sneed, A., Sodergren, E., Song, X.-Z., Sorelle, R., Sosa, J., Steimle, M., Strong, R., Sutton, A., Svatek, A., Tabor, P., Taylor, C., Taylor, T., Thomas, N., Thomas, S., Tingey, A., Trejos, Z., Usmani, K., Valas, R., Vera, V., Villasana, D., Waldron, L., Walker, B., Wang, J., Wang, Q., Wang, S., Warren, J., Warren, R., Wei, X., White, F., Williams, G., Willson, R., Wiczzyk, R., Wooden, H., Worley, K., Wright, D., Wright, R., Wu, J., Yakub, S., Yen, J., Yoon, L., Yoon, V., Yu, F., Zhang, J., Zhou, J., Zhou, X., Zhao, S., Dunn, D., von Niederhausern, A., Weiss, R., Smith, D.R., Holt, R.A., Smith, H.O., Weinstock, G. and Gibbs, R.A.

TITLE
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COMMENT

Submitted (09-JAN-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
 3 (bases 1 to 220157)
 Rat Genome Sequencing Consortium.
 Direct Submission
 Submitted (10-MAY-2003) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
 On May 10, 2003 this sequence version replaced gi:25008590.
 The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas (<http://www.hgsc.bcm.tmc.edu/projects/rat/>). Each contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence may extend beyond the ends of the clone and there may be sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence only contigs will be indicated in the feature table.

----- Genome Center
 Center: Baylor College of Medicine
 Center code: BCM
 Web site: <http://www.hgsc.bcm.tmc.edu/>
 Contact: hgsc-help@bcm.tmc.edu
 ----- Project Information
 Center project name: GHPM
 Center clone name: CH230-145D2
 ----- Summary Statistics
 Assembly program: Atlas 3.0;
 Consensus quality: 215295 bases at least Q40
 Consensus quality: 216317 bases at least Q30
 Consensus quality: 217167 bases at least Q20
 Estimated insert size: 223095; sum-of-contigs estimation
 Quality coverage: 9x in Q20 bases; sum-of-contigs estimation

 * NOTE: Estimated insert size may differ from sequence length
 * (see http://www.hgsc.bcm.tmc.edu/docs/genbank_draft_data.html).
 * NOTE: This is a 'working draft' sequence. It currently
 * consists of 1 contigs. Gaps between the contigs
 * are represented as runs of N. The order of the pieces
 * is believed to be correct as given, however the sizes

repeat_region 9203. .9293 /rpt_family="ERV1"
repeat_region 10285. .10327 /rpt_family="MIR"
repeat_region 10331. .10827 /rpt_family="MIR"
repeat_region 11815. .12024 /rpt_family="ERVK"
repeat_region 12030. .12203 /rpt_family="MaLR"
repeat_region 12320. .12669 /rpt_family="B2"
repeat_region 12730. .12839 /rpt_family="MaLR"
repeat_region 12897. .13082 /rpt_family="Alu"
repeat_region 13526. .13593 /rpt_family="MaLR"
repeat_region 13750. .13925 /rpt_family="MaLR"
repeat_region 13941. .14158 /rpt_family="B2"
repeat_region 14436. .14584 /rpt_family="L1"
repeat_region 15670. .15743 /rpt_family="ID"
repeat_region 16031. .16083 /rpt_family="MIR"
repeat_region 16332. .16525 /rpt_family="B4"
repeat_region 16578. .16719 /rpt_family="Alu"
repeat_region 16829. .17245 /rpt_family="L2"
repeat_region 17253. .17350 /rpt_family="B4"
repeat_region 17578. .17727 /rpt_family="L2"
repeat_region 17982. .18175 /rpt_family="B2"
repeat_region 18489. .18769 /rpt_family="ERVK"
repeat_region 18987. .19304 /rpt_family="MaLR"
repeat_region 19694. .19900 /rpt_family="B2"
repeat_region 20140. .20268 /rpt_family="Alu"
repeat_region 20369. .20579 /rpt_family="MaLR"
repeat_region 20599. .20725 /rpt_family="Alu"
repeat_region 21080. .21149 /rpt_family="ID"
repeat_region 21348. .21457 /rpt_family="Alu"
repeat_region 22354. .22573 /rpt_family="B2"
repeat_region 22986. .23157 /rpt_family="MaLR"
repeat_region 23168. .23278 /rpt_family="B4"
repeat_region 23456. .23520 /rpt_family="MaLR"
repeat_region 23996. .24325 /rpt_family="MaLR"
repeat_region 25121. .25290 /rpt_family="B4"
repeat_region 25402. .25492 /rpt_family="Alu"
repeat_region 25698. .25886 /rpt_family="L1"

repeat_region 26091. .26240 /rpt_family="L1"
repeat_region 26241. .26382 /rpt_family="Alu"
repeat_region 26383. .26516 /rpt_family="L1"

Alignment Scores:
Pred. No.: 4.11e-113 Length: 175636
Score: 1542.00 Matches: 286
Percent Similarity: 97.96% Conservativeness: 2
Best Local Similarity: 97.28% Mismatches: 4
Query Match: 95.72% Indels: 4
DB: 10 Gaps: 1

US-10-679-246-2 (1-298) x AC142211 (1-175636)

QY 5 IlePheLeuLeuProProTyTrValPheIleSerGluMetSerArgGlnThrAlaThrAla 24
Db 96935 ATTTTCTTTGTTT-----TTCTTTACAGATGAGCCGACACTGTACAGCA 96982

QY 25 LeuProThrGlyThrSerLysCysProProSerGlnArgValProAlaLeuThrGlyThr 44
Db 96983 TTACCACTGGCACCCTCAAGTGTCCACCATCCAGAGGGTACCTGCTTGACCGGCACA 97042

QY 45 ThrAlaSerAsnAsnAspLeuAlaSerLeuPheGluCysProValCysPheAspTyTrVal 64
Db 97043 ACTGCATCCAAACAATGACTTGGCGAGTCTTTTGTAGTGTCTGTCTTGTACTATGTG 97102

QY 65 LeuProProIleLeuGlnCysGlnSerGlyHisLeuValCysSerAsnCysArgProLys 84
Db 97103 TTGCCACCTATTCTTCAGTGTGAGAGTGGCCATCTTGTGTTGTAGCACTGTGCCCCCAA 97162

QY 85 LeuThrCysCysProThrCysArgGlyProLeuGlySerIleArgAsnLeuAlaMetGlu 104
Db 97163 CTTACATGTTGTCACCTTGGCGGGGCCCATTTGGGATCCATTGGCACTTGGCTATGGAG 97222

QY 105 LysValAlaAsnSerValLeuPheProCysLysTyTrAlaSerSerGlyCysGluLeuThr 124
Db 97223 AAAGTGGCCCACTCAGTACTCTTCTTGTAAATATGCTCTTCTGGATGGAATAACT 97282

QY 125 LeuProHisThrGluLysAlaAspHisGluGluLeuCysGluPheArgProTyTrSerCys 144
Db 97283 CTGCCACACACCCAAAGAGCAGACGAGAGACTCTGTAGTTCAGGCCTTACTCTGTC 97342

QY 145 ProCysProGlyAlaSerCysLysTrpGlnGlySerLeuAspAlaValMetProHisLeu 164
Db 97343 CCCTGCCCTGGTGTCTTCTGTAAAGTGGCAAGGCTCCTTGGATGCCCTCATGCCACCTG 97402

QY 165 MetHisGlnHisLysSerIleThrThrLeuGlnGlyGluAspIleValPheLeuAlaThr 184
Db 97403 ATGCATCAGCAAGTCCATTACCACTTCCGAAAGGAGAGATATAGTTTCTTGTCTACA 97462

QY 185 AspIleAsnLeuProGlyAlaValAspTrpValMetMetGlnSerCysPheGlyPheHis 204
Db 97463 GACATTAACCTTCTCTGGTGTCTGTGTAGTGGGTGATGATGACAGTCTTGTGTTTGGCTTCAT 97522

QY 205 PheMetLeuValLeuGluLysGlnGluLysTyTrAspGlyHisGlnGlnPhePheAlaIle 224
Db 97523 TTTTCATGTTAGTCTTGGAGAAACAAGAAAAATATGATGGTTCATCAGCAGTCTTTTTCGAAAT 97582

QY 225 ValGlnLeuIleGlyThrArgLysGlnAlaGluAsnPheAlaTyTrArgLeuGluLeuAsn 244
Db 97583 GTACAACTGATAGGAACACGCAAGCAAGCTGAAAAATTTTGCATATCGATTGAGCTAAAT 97642

QY 245 GlyHisArgArgLeuThrTrpGluAlaThrProArgSerIleHisGluGlyIleAla 264
Db 97643 GGTTCATAGCGCGGCAATTGACTTGGGAAGCGACTCTCTCGGTCTATTTCATGAGGAATTGCA 97702

QY 265 ThrAlaIleMetAsnSerAspCysLeuValPheAspThrSerIleAlaGlnLeuPheAla 284
Db 97703 ACAGCCATTATGAATAGTGTGACTGCTTGTAGTGTGTTTGCACACAGCAGATTGCAAGCTTTTGTCA 97762

Qy 285 GluAsnGlyAsnLeuGlyIleAsnValThrIleSerMetCys 298
Db 97763 GAAATGGCAATTAGGCATCAATGTAACTATTTCATGTGT 97804

Search completed: April 25, 2005, 08:26:52
Job time : 5084 secs

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GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: April 25, 2005, 06:39:19 ; Search time 614 Seconds
(without alignments)
2873.099 Million cell updates/sec

Title: US-10-679-246-2

Perfect score: 1611

Sequence: 1 MWIIIFLPPYVFISEMRQ.....IAQLFAENGLNINTISM 298

Scoring table: BLOSUM62

Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

-MODEL=framed_p2n.model -DEV=xlh
-O=/cqn2.1/USPTO.spool/US10679246/runat_22042005.185510.7675/app_query.fasta_1.455
-DB=N_Geneseq_16Dec04 -QFMT=fastap -SUFFIX=p2n.rng -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALLIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US10679246 @CQN 1 1 470 @runat_22042005.185510.7675 -NCPU=6 -ICPU=3
-NO MMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPELOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : N_Geneseq_16Dec04:*

1: Geneseqn1980s:*

2: Geneseqn1990s:*

3: Geneseqn2000s:*

4: Geneseqn2001as:*

5: Geneseqn2001bs:*

6: Geneseqn2002as:*

7: Geneseqn2002bs:*

8: Geneseqn2003as:*

9: Geneseqn2003bs:*

10: Geneseqn2003cs:*

11: Geneseqn2003ds:*

12: Geneseqn2004as:*

13: Geneseqn2004bs:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1611	100.0	1274	4 AAC67281	Aac67281 Human Siah
2	1611	100.0	2128	13 ADS34361	Ads34361 POSH prot
3	1611	100.0	2440	11 ADI31262	Adi31262 Human cdn
4	1611	100.0	2924	5 ABV28804	Abv28804 Human pro
5	1611	100.0	2924	5 ABV25468	Abv25468 Human pro

	6	1611	100.0	2924	5	ABV22970	Abv22970 Human pro
	7	1611	100.0	6107	4	AAL05382	Aal05382 Human rep
	8	1611	100.0	6107	4	ABL98246	Abi98246 Human tes
	9	1603	99.5	2829	11	ADM01584	Adm01584 Human cDN
	10	1603	99.5	2829	13	ADS34362	Ads34362 POSH prot
	11	1565	97.1	4090	10	ADF81981	Adf81981 Leukaemia
C	12	1540	95.6	1540	13	ADS34365	Ads34365 POSH prot
	13	1540	95.6	2048	13	ADS34360	Ads34360 POSH prot
	14	1537	95.4	2454	13	ADS34359	Ads34359 POSH prot
	15	1536	95.3	1968	6	ABI99429	Abi99429 Mouse isc
	16	1532	95.1	1886	13	ADS34363	Ads34363 POSH prot
	17	1527	94.8	2034	13	ADS34364	Ads34364 POSH prot
	18	1489	92.4	1884	2	AAT64820	Aat64820 Tumour su
C	19	1334.5	82.8	3128	10	ADI40343	Adi40343 Human pur
	20	1206	74.9	2502	8	ACC50293	Acc50293 Breast ca
	21	1199.5	74.5	2198	6	ABI99430	Abi99430 Mouse isc
	22	1199	74.4	975	13	ADR25256	Adr25256 Breast ca
	23	1198	74.4	2240	8	ACC50292	Acc50292 Breast ca
	24	1198	74.4	2240	12	ADP13401	Adp13401 Renal cel
	25	1198	74.4	2240	13	ADR14122	Adr14122 Human NF-
	26	1198	74.4	2240	13	ADP54830	Adp54830 Human PRO
	27	1153.5	71.6	4647	4	ABL15923	Abi15923 Drosophil
C	28	1153.5	71.6	8418	4	ABL15922	Abi15922 Drosophil
C	29	1153.5	71.6	12029	4	ABL15508	Abi15508 Drosophil
C	30	702.5	43.6	3349	4	ABL21784	Abi21784 Drosophil
C	31	530	32.9	1226	4	ABL21785	Abi21785 Drosophil
C	32	514.5	31.9	2363	4	ABL21782	Abi21782 Drosophil
	33	485.5	30.1	388	2	AAQ60440	Aaq60440 Human bra
	34	474	29.4	1535	3	AAC98856	Aac98856 Human pan
	35	447	27.7	1420	3	AAZ90582	Aaz90582 Maize SIN
	36	447	27.7	1428	3	AAC43673	Aac43673 Zea mays
	37	446	27.7	360	8	ABX44846	Abx44846 Bovine ES
	38	434.5	27.0	1599	3	AAC51542	Aac51542 Arabidops
	39	434.5	27.0	1601	3	AAC38735	Aac38735 Arabidops
	40	429	26.6	984	3	AAC43003	Aac43003 Arabidops
	41	429	26.6	984	6	ABZ12658	Abz12658 Arabidops
	42	426	26.4	257	10	ACAS5799	Acas5799 Human sig
	43	426	26.4	257	12	ADI55595	Adi55595 Human pol
	44	425	26.4	1080	10	ADB78903	Adb78903 Rice tran
	45	423	26.3	1264	3	AAC36352	Aac36352 Arabidops

ALIGNMENTS

RESULT 1
AAC67281
ID AAC67281 standard; cdna; 1274 BP.
XX
AC AAC67281;
XX
DT 09-APR-2001 (first entry)
XX
DE Human Siah-lalpa coding sequence SEQ ID NO: 1.
XX

Human; protein degradation; siah-mediated degradation protein; SNMP;
SCF-complex protein; SCP; siah-lalpa; siah-1 interacting protein; SIP;
Kw Skp1-associated F-box protein; SAF-1; SAF-2; SAD; cancer; cell division;
Kw Skp1-associated destruction-box protein; inflammatory disease; ss.
XX
OS Homo sapiens.
XX
PN WO200077207-A2.
XX
PD 21-DEC-2000.
XX
PF 09-JUN-2000; 2000WO-US015873.
XX
PR 11-JUN-1999; 99US-00330517.
XX
(BURN-) BURNHAM INST.
PI Reed JC, Matsuzawa S;
XX

DR WPI: 2001-071273/08.
 DR P-PSDB; AAB35157.
 XX Siah-Mediated Degradation Protein, useful for drug screening, for
 PT therapeutic applications and for functional genomics.
 XX
 PS
 PS Claim 5; Page 95-97; 121pp; English.
 XX
 CC The present invention provides the protein and coding sequences of
 CC several siah-mediated degradation proteins and SCF-complex proteins.
 CC These are designated Siah-1alpha, Siah-1 interacting protein (SIP), which
 CC encodes two proteins due to alternative splicing (SIP-L and SIP-S), Skp1-
 CC associated F-box protein-alpha and beta and -2 (SAF-1alpha, SAF-1beta
 CC and SAF-2) and Skp1-associated destruction-box protein (SAD). The
 CC proteins and their coding sequences are useful in the diagnosis and
 CC treatment of cancers, disorders where too little cell division occurs
 CC such as bone marrow aplasia, immunodeficiencies and inflammatory
 CC diseases including sepsis, fibrosis, arthritis and graft versus host
 CC disease
 XX
 SQ Sequence 1274 BP; 336 A; 273 C; 253 G; 412 T; 0 U; 0 Other;
 XX

Alignment Scores:
 Pred. No.: 1,046-138 Length: 1274
 Score: 1611.00 Matches: 298
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 4 Gaps: 0

US-10-679-246-2 (1-298) x AAC67281 (1-1274)

QY 1 MetValIleIleIlePheLeuLeuProProTyrValPheIleSerGluMetSerArgGln 20
 Db 274 ATGGTTATAATTATTTTCTCCGCTCTCTTATGATATTTATTTTCAGAAATGAGCGGTCA 333

QY 21 ThrAlaThrAlaLeuProThrGlyThrSerLysCysProSerGlnArgValProAla 40
 Db 334 ACTGCTACAGCAATACCTACCGGTACTCTCAATGTCACAGAGGTGCTGCTGCC 393

QY 41 LeuThrGlyThrThrAlaSerAsnAsnAspLeuAlaSerLeuPheGluCysProValCys 60
 Db 394 CTGACTGGCACTGATCACTCAATGATGCTTGGCGAGTCTTTTTCAGTGTCCAGTCTGC 453

QY 61 PheAspTyrValLeuProProIleLeuGlnCysGlnSerGlyHisLeuValCysSerAsn 80
 Db 454 TTTGACTATGTGTACCGCCCAATCTTCAATGTCAGAGTGGCCATCTTGTGTGACCAAC 513

QY 81 CysArgProLysLeuThrCysCysProThrCysArgGlyProLeuGlySerIleArgAsn 100
 Db 514 TGTGCGCCCAAGCTCACATGTTGTCCAACTTGGCGGGCCCTTGGGATCCATTCGCAAC 573

QY 101 LeuAlaMetGluLysValAlaAsnSerValLeuPheProCysLysTyrAlaSerSerGly 120
 Db 574 TTGGCTATGAGAAAGTGGCTAATTCAGTACTTTTCCCTGTAAATATGCGTCTCTGGA 633

QY 121 CysGluIleThrLeuProHisThrGluLysAlaAspHisGluLeuCysGluPheArg 140
 Db 634 TGTGAAATAAATCTGCGCACACACAGAAAGACAGACCATGAAGAGCTCTGTGAGTTAGG 693

QY 141 ProTyrSerCysProCysProGlyAlaSerCysLysTrpGlnGlySerLeuAspAlaVal 160
 Db 694 CCTATTTCCTGCTGCGTCCCTGGTGTCTTCTGTAATGGAAGGCTCTCTGGATGCTGTA 753

QY 161 MetProHisLeuMetHisGlnHisLysSerIleThrThrLeuGlnGlyGluAspIleVal 180
 Db 754 ATGCCCATCTGATGCATCAGCAATAGTCCATTAACCCCTACAGGAGGATATAGTT 813

QY 181 PheLeuAlaThrAspIleAsnLeuProGlyAlaValAspTrpValMetMetGlnSerCys 200
 Db 814 TTTCTTGCTACAGCAATTAATCTTCTCGTGTCTGTGACTGGGTGATGATGATGCTCTGT 873

QY 201 PheGlyPheHisPheMetLeuValLeuGluLysGlnGluLysTyrAspGlyHisGlnGln 220

Db 874 TTTGGCTTTTCATTTCAITTAGTCTTAGAGAAACAGGAAAAATACGATGTCACCGACG 933
 QY 221 PhePheAlaIleValGlnLeuIleGlyThrArgLysGlnAlaGluAsnPheAlaTyrArg 240
 Db 934 TTTCTTGGCAATCGTACAGCTGTAGAACACACGCAAGCAAGCTGAAATTTTGTCTTACCGA 993
 QY 241 LeuLeuLeuAsnGlyHisArgArgLeuThrTrpGluAlaThrProArgSerIleHis 260
 Db 994 CTTGAGCTAAATGTCATAGCGGACGATTCCTTGGGAAGGACTCTCGATCTATTTCAT 1053
 QY 261 GluGlyIleAlaThrAlaIleMetAsnSerAspCysLeuValPheAspThrSerIleAla 280
 Db 1054 GAGGAATTGCAACAGCCATTATGATAGCGACTGTCTAGTCTTTTGACACCGCAITTGCA 1113
 QY 281 GlnLeuPheAlaGluAsnGlyAsnLeuGlyIleAsnValThrIleSerMetCys 298
 Db 1114 CAGCTTTTTCAGAAATGCGCAATTTAGGCATCAATGTAATTTTCAITGTGT 1167

RESULT 2
 ADS34361/C
 ID ADS34361 standard; DNA; 2128 BP.
 XX
 AC ADS34361;
 XX
 DT 02-DEC-2004 (first entry)
 XX
 DE POSH protein associated DNA #115.
 XX
 KW ds; gene; cytostatic; nootropic; neuroprotective; antiparkinsonian;
 KW anticonvulsant; antiviral; neuroleptic; central nervous system;
 KW POSH polypeptide; POSH-associated protein; POSH-AP; HERPUD1;
 KW Ubiquitin ligase; anti-viral agent; anti-apoptotic agent;
 KW anti-cancer agent; secretory pathway trafficking inhibitor;
 KW neurological disorder progression disorder; Alzheimer's disease;
 KW Parkinson's disease; Huntington's disease; schizophrenia;
 KW Niemann-Pick's disease.
 XX
 OS Homo sapiens.
 XX
 PN WO2004078130-A2.
 XX
 PD 16-SEP-2004.
 XX
 XX 02-MAR-2004; 2004WO-US006308.
 XX
 XX 03-MAR-2003; 2003US-0451437P.
 XX 05-MAR-2003; 2003US-0452284P.
 XX 19-MAR-2003; 2003US-0455760P.
 XX 20-MAR-2003; 2003US-0456640P.
 XX 03-APR-2003; 2003US-0460526P.
 XX 04-APR-2003; 2003US-0460792P.
 XX 21-APR-2003; 2003US-0464285P.
 XX 09-MAY-2003; 2003US-0469462P.
 XX 15-MAY-2003; 2003US-0471378P.
 XX 20-MAY-2003; 2003US-0472327P.
 XX 30-MAY-2003; 2003US-0474706P.
 XX 03-JUN-2003; 2003US-0475825P.
 XX 17-JUN-2003; 2003US-0479317P.
 XX 19-JUN-2003; 2003US-0480215P.
 XX 19-JUN-2003; 2003US-0480376P.
 XX 08-AUG-2003; 2003US-0493860P.
 XX 28-AUG-2003; 2003US-0498634P.
 XX 16-SEP-2003; 2003US-0503931P.
 XX 10-NOV-2003; 2003WO-US035712.
 XX 05-FEB-2004; 2004WO-US003600.
 XX 02-MAR-2004; 2004US-0549896P.
 XX
 (PROT-) PROTEOLOGICS INC.
 XX
 XX Taglicht DN, Alroy I, Reiss Y, Yaar L, Ben-Avraham D, Tuvia S;
 XX Greener T;
 XX

DR WPI; 2004-662346/64.
XX Isolated, purified or recombinant complex, useful for identifying an
PT antiviral, anti-apoptotic or anti-cancer, comprising POSH polypeptide and
PT POSH-associated protein (POSH-AP).
XX
XX
XX Disclosure; SEQ ID NO 125; 374pp; English.
PS
CC The invention relates to an isolated, purified or recombinant complex (I)
CC comprising a POSH polypeptide and a POSH-associated protein (POSH-AP) (a)
CC or HRP21 and a ubiquitin ligase (b). Methods using (I), (a) or (b) are
CC useful for identifying an agent that modulates an activity of a POSH
CC polypeptide or POSH-AP, for identifying an antiviral agent, an anti-
CC apoptotic agent, an anti-cancer agent, an agent that inhibits trafficking
CC of a protein through the secretory pathway, an agent that inhibits the
CC progression of a neurological disorder, an agent that modulates a POSH
CC function, an agent that modulates a HRP21 function. The methods can be
CC used for treating a viral infection, for inhibiting an activity of a POSH
CC -AP in a cell, for treating a POSH-associated disease in a subject. The
CC POSH-associated disease is viral infection, POSH-associated cancer or
CC POSH-associated neurological disorder. The methods are useful for
CC treating or preventing POSH-associated neurological disorder in a subject
CC e.g. Alzheimer's disease, Parkinson's disease, Huntington's disease,
CC schizophrenia, Niemann-Pick's disease. This sequence corresponds to a
CC nucleic acid of the invention.
XX
SQ Sequence 2128 BP; 664 A; 400 C; 428 G; 636 T; 0 U; 0 Other;
Alignment Scores:
Pred. No.: 2,09e-138 Length: 2128
Score: 1611.00 Matches: 298
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 13 Gaps: 0
US-10-679-246-2 (1-298) x ADS34361 (1-2128)
QY 1 MetValIleIleIlePheLeuLeuProTrpValPheIleSerGluMetSerArgGln 20
Db 2025 ATGGTTATATATTTTCTCTGCTCTCTCTATGATATTTATTCAGAAATGAGCCCTCAG 1966
QY 21 ThrAlaThrAlaLeuProThrGlyThrSerLysCysProSerGlnArgValProAla 40
Db 1965 ACTGCTACAGCAATACCTACCGTACCTCGAAGTGTCCACCATCCAGAGGGTGCCTGCC 1906
QY 41 LeuThrGlyThrThrAlaSerIleAsnLeuLeuPheLeuSerIlePheGluCysProValCys 60
Db 1905 CTGACTGGCAGCACTGCATCCCAATGACTTGGCGAGTCTTTTGGAGTGTCCAGTCTGC 1846
QY 61 PheAspTyrValLeuProThrIleLeuGlnCysGlnSerGlyHisLeuValCysSerAsn 80
Db 1845 TTTGACTATGTGTACGGCCCATCTTCAATGTCAGATGGCCATCTTTGTTGTAGCAAC 1786
QY 81 CysArgProLysLeuThrCysCysProThrCysArgGlyProLeuGlySerIleArgAsn 100
Db 1785 TGTGCGCCCAAGCTACATGTTGTCCAACTTGGCGGGGCCCTTTGGCATCCATTCGCAAC 1726
QY 101 LeuAlaMetGluLysValAlaIleAsnSerValLeuPheProCysLysTyrAlaSerSerGly 120
Db 1725 TTTGGCTATGAGAAAGTGGCTAATTCAGTACTTTTCCCTGTAATAATGCGTCTTCTGGA 1666
QY 121 CysGluIleThrLeuProHisThrGluLysAlaAspHisGluLeuLeuValCysGluPheArg 140
Db 1665 TGTGAATTAATCTTGCACACACAGAAAGGACCATGAGAGCTCTGTGAGTTTAG 1606
QY 141 ProTyrSerCysProCysProGlyAlaSerCysLysTyrGlnGlySerLeuAspAlaVal 160
Db 1605 CCTTATCTCTGTCGGTCCCTGGTCTCTCTGTAATGCAAGGCTCTCTGGATGCTGA 1546
QY 161 MetProHisLeuMetHisGlnHisLysSerIleThrLeuGlnGluAspIleVal 180
Db 1545 ATGCCCCCATCTGATGATCAGCATAGTCCATTACAAACCTTACAGGAGGAGATAGTT 1486

QY 181 PheLeuAlaThrAspIleAsnLeuProGlyAlaValAspTrpValMetMetGlnSerCys 200
Db 1485 TTTCTTGCTACAGACATTAACTCTCTGCTGCTGTTGACTGGGTGATGATGCAGTCTCTGT 1426
QY 201 PheGlyPheHisPheMetLeuValLeuGluLysGlnGluLysTyrAspGlyHisGlnGln 220
Db 1425 TTTGGCTTTTCACTTCATGTTAGTCTTTAGAGAAACAGGAAAAATACGATGTCACACGAG 1366
QY 221 PhePheAlaIleValGlnLeuIleGlyThrArgLysGlnAlaGluAsnPheAlaTyrArg 240
Db 1365 TTTCTGCAATGTCAGCTGATAGGAAACAGGACAGCTGAAAATTTTGTCTTACCGA 1306
QY 241 LeuGluLeuAsnGlyHisArgArgLeuThrTrpGluAlaThrProArgSerIleHis 260
Db 1305 CTTGAGCTAAATGGTCATAGGCGAGCATTTGACTTTGGGAAGCGACTCTCTCATTTTCAT 1246
QY 261 GluGlyIleAlaThrAlaIleMetAsnSerAspCysLeuValPheAspThrSerIleAla 280
Db 1245 GAAGGAATTTGCAACAGCCATTATGATAGCGACTGTCTAGTCTTTGACACACGATTCGA 1186
QY 281 GlnLeuPheAlaGluAsnGlyAsnLeuGlyIleAsnValThrIleSerMetCys 298
Db 1185 CAGCTTTTTCGAGAAATGCGCAATTTAGGCAATCAATGTAATTTCCATGTGT 1132
RESULT 3
ADI31262
ID ADI31262 standard; cDNA; 2440 BP.
XX
AC ADI31262;
XX
DT 17-JUN-2004 (first entry)
XX
DE Human cDNA #598.
XX
KW Human; gene; ss; immunological response; immunopathological condition;
KW Crohn's disease; asthma; ulcerative colitis; hypersensitization;
KW irritable bowel syndrome; osteoarthritis; rheumatoid arthritis;
KW acute monocytic leukemia; antiinflammatory; antiasthmatic; antiulcer;
KW osteopathic; antiarthritic; antirheumatic; cytostatic.
XX
OS Homo sapiens.
XX
PN US6607879-B1.
XX
PD 19-AUG-2003.
XX
PF 09-FEB-1998; 98US-00023655.
XX
PR 09-FEB-1998; 98US-00023655.
XX
PA (INCY-) INCYTE CORP.
XX
PI Cocks BG, Stuart SG, Seilhamer JJ;
XX
DR WPI; 2003-895307/82.
XX
PT A composition comprising a plurality of cDNAs, useful for detecting
PT altered expression of genes in an immunological response or for
PT diagnosing and treating an immunopathology, e.g. Crohn's disease, asthma
PT or osteoarthritis.
XX
PS Claim 1; SEQ ID NO 588; 50pp; English.
XX
CC The invention relates to a composition comprising a plurality of cDNAs
CC for detecting the altered expression of genes in an immunological
CC response. The invention also relates to a method of diagnosing or
CC monitoring the treatment of an immunopathological condition in a sample,
CC comprising obtaining nucleic acids from a sample, contacting the nucleic
CC acids of the sample with an array comprising the plurality of cDNAs under
CC conditions to form one or more hybridisation complexes, detecting the
CC hybridisation complexes and comparing the levels of the detected
CC hybridisation complexes with the level of hybridisation complexes

XX	ABV25468;
AC	16-SEP-2002 (first entry)
DT	Human prostate expression marker cDNA 25459.
DE	Human; prostate cancer; cytostatic; carcinogen; pharmacodynamic marker;
XX	pharmacogenomic marker; gene; ss.
KW	Homo sapiens.
OS	WO200160860-A2.
XX	23-AUG-2001.
PN	20-FEB-2001; 2001WO-US005171.
XX	17-FEB-2000; 2000US-0183319P.
PR	16-MAR-2000; 2000US-0189862P.
PR	25-JUN-2000; 2000US-0207454P.
PR	09-JUN-2000; 2000US-0211314P.
PR	18-JUL-2000; 2000US-0219007P.
PR	13-DEC-2000; 2000US-0255281P.
XX	(MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
PA	Schlegel R, Endege WO, Monahan JE;
XX	WPI; 2001-662795/76.
DR	Novel isolated nucleic acid molecule associated with cancerous state of
XX	prostate cells and correlating with presence of prostate cancer, useful
PT	for detecting presence of prostate cancer, stage of prostate cancer.
PS	Claim 1; Page 5054-5055; 11750pp; English.
CC	The invention relates to an isolated nucleic acid molecule (I) comprising
CC	a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the
CC	specification or its complement (II) is useful for: (a) assessing whether
CC	a patient is afflicted with prostate cancer; (b) monitoring the efficacy
CC	of progression of prostate cancer in a patient; (c) assessing the efficacy
CC	of a test compound to inhibit prostate cancer in a patient; (d) assessing
CC	the efficacy of a therapy for inhibiting prostate cancer in a patient;
CC	(e) selecting a composition for inhibiting prostate cancer in a patient;
CC	(f) assessing the prostate cell carcinogenic potential of a compound; (g)
CC	determining whether prostate cancer has metastasized in a patient; (h)
CC	assessing the aggressiveness or indolence of prostate cancer in a patient
CC	; (I) is also useful as a pharmacodynamic or pharmacogenomic marker
XX	SQ Sequence 2924 BP; 871 A; 562 C; 562 G; 925 T; 0 U; 4 Other;
Alignment Scores:	
Pred. No.:	3,22e-138 Length: 2924
Score:	1611.00 Matches: 298
Percent Similarity:	100.00% Conservatives: 0
Best Local Similarity:	100.00% Mismatches: 0
Query Match:	100.00% Indels: 0
DB:	5 Gaps: 0
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QY 1 MetValIleIlePheLeuLeuProTyrValPheIleSerGluMetSerArgGln 20	
Db 753 ATGGTTATTAATTATTTCTTCCTGCCTCCTTAAGTATTTATTTTCAGAATAAGCGGTGAG 812	
QY 21 ThrAlaThrAlaLeuProThrGlyThrSerLysCysProProSerGlnArgValProAla 40	
Db 813 ACTGCTACAGCATTAACCTACCGGTACTCGAAGTGTCACCAATCCAGAGGGTGCTGCC 872	
QY 41 LeuThrGlyThrThrAlaSerAsnAspLeuAlaSerLeuPheGluCysProValCys 60	
Db 873 CTGACTGGCACAACTGCATCCACAATGACTTGGCGAGTCTTTTGAAGTGTCCAGTCTGC 932	
QY 61 PheAspTyrValLeuProPheLeuGlnCysGlnSerGlyHisLeuValCysSerAsn 80	
Db 933 TTGAGCATGTGTATCCGCCCATCTTCAATGTCCAGAGTGGCCATCTTGTGTAGCAAC 992	
QY 81 CysArgProLysLeuThrCysCysProThrCysArgGlyProLeuGlySerIleArgAsn 100	
Db 993 TGTCGCCCAAGCTCACATGTTGTCCAACTTGCCGGGGCCCTTTGGGATCCAATGCCAAC 1052	
QY 101 LeuAlaMetGluLysValAlaAsnSerValLeuPheProCysLysThrAlaSerSergly 120	
Db 1053 TTGGCTATGAGAAAAGTGCGTAATTCAGTACTTTTCCCCTGTAATATGCGTCTTCGGA 1112	
QY 121 CysGluIleThrLeuProHisThrGluLysAlaAspHisGluGluLeuCysGluPheArg 140	
Db 1113 TGTGAATAACTCTGCCACACACAGAAAAAGCAGACCACATGAAGAGCTCTGTGAGTTTAGG 1172	
QY 141 ProTyrSerCysProCysProGlyAlaSerCysLysTrpGlnGlySerLeuAspAlaVal 160	
Db 1173 CCTATTCTGTCCGTGCTTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGT 1232	
QY 161 MetProHisLeuMetHisGlnHisLysSerIleThrThrLeuGlnGlyCysAspIleVal 180	
Db 1233 ATGCCCCATCTGATGCATCAGCATAGTCCATTACAACTACAGGAGAGGATAGTAT 1292	
QY 181 PheLeuAlaThrAspIleAsnLeuProGlyAlaValAspTrpValMetMetGlnSerCys 200	
Db 1293 TTTCTTGTGTACAGACATTAATCTTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1352	
QY 201 PheGlyPheHisPheMetLeuValLeuGluLysGlnGluLysTyrAspGlyHisGlnGln 220	
Db 1353 TTTGGCTTTCATCTTCAATGATGCTTTAGAGAAACAGGAAATAATAGATGTTCCACGAG 1412	
QY 221 PhePheAlaIleValGlnLeuIleGlyThrArgLysGlnAlaGluAsnPheAlaTyrArg 240	
Db 1413 TTCTTCCGAATCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1472	
QY 241 LeuGluLeuAsnGlyHisArgArgArgLeuThrTrpGluAlaThrProArgSerIleHis 260	
Db 1473 CTTGAGCTAAATGGTGTATAGGCGACGATGAGCTTGGGAAGCGACTCTCTCGATATTTCAT 1532	
QY 261 GluGlyIleAlaThrAlaIleMetAsnSerAspCysLeuValPheAspThrSerIleAla 280	
Db 1533 GAAGGAATTTGCAACACCCATTATGAATAGCGACTGTCTAGTCTTTTGACACAGCATTCGA 1592	
QY 281 GlnLeuPheAlaGluAsnGlyAsnLeuGlyIleAsnValThrIleSerMetCys 298	
Db 1593 CAGCTTTTTGCAGAAAATGGCAATTTAGGCATCAATGTAATCTTTTCCATGTGT 1646	

RESULT 5
 ABV25468
 DD ABV25468 standard; cDNA; 2924 BP.


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QY 161 MetProHisLeuMetHisGlnHisLysSerIleThrThrlieuGlnGlyGluAspIleVal 180
Db 1233 ATCCCCATCTGATGATCAGCATAAGTCCATTACAACCCCTACAGGAGAGGATATAGTT 1292
QY 181 PheLeuAlaThrAspIleAsnLeuProGlyAlaValAspTyrValMetGlnSerCys 200
Db 1293 TTTCCTGCTACAGACATTAATCTTCTCTGGTCTGTTGACTGGGTGATGATGCAGTCTGT 1352
QY 201 PheGlyPheHisPheMetLeuValLeuGluLysGlnGlyLysTyrAspGlyHisGlnGln 220
Db 1353 TTTCGGCTTTCACCTTCATGTTAGTCTTAGAGAAACAGCAAAATACGATGTCACCAAGCAG 1412
QY 221 PhePheAlaIleValGlnLeuIleGlyThrArgLysGlnAlaGluAsnPheAlaTyrArg 240
Db 1413 TTCTTCGCATCATCTAGCTGATAGGAACACGCAAGCTGAAAAATTTTGCTTACCGA 1472
QY 241 LeuGluLeuAsnGlyHisArgArgLeuThrTyrGluAlaThrProArgSerIleHis 260
Db 1473 CTTCAGCTAAATGGTTCATAGGCGACGATTGACTTGGGAAGCGACTCTCGAICTATTCA 1532
QY 261 GluGlyIleAlaThrAlaIleMetAsnSerAspCysLeuValPheAspThrSerIleAla 280
Db 1533 GAAGGAATTGCAACGCCATTATGAATAGCAGCTGTAGTCTTTGCACACCAAGCATTGCA 1592
QY 281 GlnLeuPheAlaGluAsnGlyAsnLeuGlyIleAsnValThrIleSerMetCys 298
Db 1593 CAGCTTTTTCAGAAAAATGCAATTTAGGCATCAATGTAATCTATTTCCATGTGT 1646

RESULT 7
AAL05382
ID AAL05382 standard; DNA; 6107 BP.
XX
AC AAL05382;
DT
DE 21-NOV-2001 (first entry)
KW Human reproductive system related antigen DNA SEQ ID NO: 8070.
KW Human; reproductive system related antigen; reproductive system disorder;
KW cancer; gene therapy; ds.
OS Homo sapiens.
PN WO200155320-A2.
PD
PE 02-AUG-2001.
PF
XX 17-JAN-2001; 2001WO-US001339.
XX
PR 31-JAN-2000; 2000US-0179065P.
PR 04-FEB-2000; 2000US-0180628P.
PR 24-FEB-2000; 2000US-0184664P.
PR 02-MAR-2000; 2000US-0186350P.
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PN WO200155317-A2.
XX 02-AUG-2001.
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PR 11-DEC-2000; 2000US-0254097P.
PR 05-JAN-2001; 2001US-0259678P.
(HUMA-) HUMAN GENOME SCI INC.
Rosen CA, Barash SC, Ruben SM;
PI

XX WPI; 2001-483232/52.

XX Nucleic acids encoding 973 human testicular antigen polypeptides, useful

PT for preventing, diagnosing and/or treating testicular cancer.

XX Disclosure; SEQ ID NO 2898; 766pp; English.

XX The present invention provides the protein and coding sequences of 973

CC human testicular antigens, and fragments of their genomic sequences. The

CC sequences can be used in the treatment of cardiovascular, urinary system,

CC reproductive system, immune, respiratory, neurological and

CC gastrointestinal disorders, infections, and particularly cancer.

CC especially testicular cancers. The present sequence is a DNA encoding a

CC protein fragment of the invention

XX

XX Sequence 6107 BP; 1636 A; 1200 C; 1285 G; 1986 T; 0 U; 0 Other;

SQ

Alignment Scores:

Pred. No.: 8,79e-138 Length: 6107

Score: 1611.00 Matches: 298

Percent Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0

Query Match: 100.00% Indels: 0

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US-10-679-246-2 (1-298) x ABL98246 (1-6107)

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DB 3437 AUGTTATAATTATTTCTCCGCTCTCTTAIGTATTATTTCAGAAATGAGCGCTCAG 3496

QY 21 ThrAlaThrAlaLeuProThrGlyThrSerLysCysProSerGlnArgValProIla 40

DB 3497 ACTGCTACAGCATTAACCGGTACCTCGAAGTGTCCACCATCCAGAGGGTGGCTGCC 3556

QY 41 LeuThrGlyThrThrAlaSerAsnAspLeuAlaSerLeuPheGluCysProValCys 60

DB 3557 CTGACTGGCAACTGCAATCCAAATGACTTGGCGAGCTTTTTCAGTGTCAGTCTGC 3616

QY 61 PheAspTyrValLeuProIleLeuGlnCysGlnSerGlyHisLeuValCysSerAsn 80

DB 3617 TTTGACTATGTTTACCGCCCACTTCTCAATGTCAGAGTGGCCATCTTGTGTAGCAAC 3676

QY 81 CysArgProLysLeuThrCysCysProThrCysArgGlyProLeuGlySerIleArgAsn 100

DB 3677 TGTGCGCCAAAGCTCACATGTTGTCAACTTGGCGGGCCCTTTGGATCCATCCGAC 3736

QY 101 LeuAlaMetGluLysValAlaAsnSerValLeuPheProCysLysTyrAlaSerSergly 120

DB 3737 TTGGCTATGGAGAAAGTGGCTAATTCAGTACTTTTCCCTGTAAATATGCTTCTGGA 3796

QY 121 CysGluIleThrLeuProHisIleThrGluLysAlaAspHisGluLeuCysGluPheArg 140

DB 3797 TGTGAAATAACTCTGCCACACACAGAAAAAGCAGACCATGAAGAGCTCTGTGAGTTAGG 3856

QY 141 ProTyrSerCysProCysProGlyAlaSerCysLysTrpGlnGlySerLeuAspAlaVal 160

DB 3857 CCTTATTCCTGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCG 3916

QY 161 MetProHisLeuMetHisGlnHisLysSerIleThrThrLeuGlnGlyGluAspIleVal 180

DB 3917 ATGCCCATCTGATGATCAGCATTAAGTCCATTACAAACCCCTACAGGGAGAGGATATAGT 3976

QY 181 PheLeuAlaThrAspIleAsnLeuProGlyAlaValAspTrpValMetGlnSerCys 200

DB 3977 TTTCTTGTACAGACATTAAATCTTCCGTGGTCTGTGACTGGGTGATGATGAGTCTCTGT 4036

QY 201 PheGlyPheHisPheMetLeuValLeuGluLysGlnGlyLysTyrAspGlyHisGlnGln 220

DB 4037 TTTGGCTTTCCTCACTCACTCACTCACTCACTCACTCACTCACTCACTCACTCACTCA 4096

QY 221 PhePheAlaIleValGlnLeuIleGlyThrArgLysGlnAlaGluAsnPheAlaTyrArg 240

Db 4097 TTCTTCGAATCGTACAGCTGATAGGAACACGCAAGCTGAAATTTTGTTCACCGA 4156

QY 241 LeuGluLeuAsnGlyHisArgArgLeuThrTrpGluAlaThrProArgSerIleHis 260

Db 4157 CTTGAGCTAAATGCTCATAGCGAGCAATGACTTGGGAAGCGACTCTCGATCTTTTCAT 4216

QY 261 GluGlyIleAlaThrAlaIleMetAsnSerAspCysLeuValPheAspThrSerIleAla 280

Db 4217 GAAGGAATTCGACAGCGCATTAATGAAATGAGGACTGTCTAGTCTTTGACACGACATTGCA 4276

QY 281 GlnLeuPheAlaGluAsnGlyAsnLeuGlyIleAsnValThrIleSerMetCys 298

Db 4277 CAGCTTTTTCAGAAATGCGCAATTAGGCATCAATGTAATTTCCATTTCCATGTGT 4330

RESULT 9

ADM01584

ID ADM01584 standard; cDNA; 2829 BP.

XX

AC ADM01584;

XX

DT 20-MAY-2004 (first entry)

XX

DE Human cDNA of the invention SEQ ID NO:269.

XX

KW ss; gene; human; gene therapy; diagnostic marker; pharmaceutical.

XX

OS Homo sapiens.

XX

PN EPI347046-A1.

XX

PD 24-SEP-2003.

XX

PF 12-APR-2002; 2002EP-00008400.

XX

PR 22-MAR-2002; 2002JP-00137785.

XX

PA (REAS-) RES ASSOC BIOTECHNOLOGY.

XX

PI Isogai T, Sugiyama T, Otsuki T, Wakamatsu A, Sato H, Ishii S;

PI Yamamoto J, Isono Y, Hio Y, Otsuka K, Nagai K, Irie R, Tamechika I;

PI Seki N, Yoshikawa T, Otsuka M, Nagahari K, Masuho Y;

XX

WIPI; 2003-723558/69.

DR

P-PSDB; ADM04027.

XX

PT New polynucleotides and polypeptides are useful in gene therapy, for

PT developing a diagnostic marker or medicines for regulating their

PT expression and activity, or as a target of gene therapy.

XX

PS Claim 1; SEQ ID NO 269; 305pp; English.

XX

CC The invention relates to a novel human polynucleotide and the encoded

CC polypeptide. A polynucleotide of the invention may have a use in gene

CC therapy. An oligonucleotide of the invention ADM06202-ADM06773 is useful

CC as a primer for synthesizing the polynucleotide or as a probe for

CC detecting the polynucleotide. The polynucleotides ADM01316-ADM03758 are

CC useful in gene therapy, for developing a diagnostic marker or medicines

CC for regulating their expression and activity, or as a target of gene

CC therapy. The proteins ADM03759-ADM06201 encoded by the polynucleotides

CC are useful as pharmaceutical agents. The present sequence represents a

CC cDNA sequence of the invention.

XX

SQ Sequence 2829 BP; 756 A; 566 C; 553 G; 954 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 1.68e-137 Length: 2829

Score: 1603.00 Matches: 297

Percent Similarity: 99.66% Conservative: 0

Best Local Similarity: 99.66% Mismatches: 1

Query Match: 99.50% Indels: 0

DB: 11 Gaps: 0

US-10-679-246-2 (1-298) x ADM01584 (1-2829)

QY 1 MetValIleIleIleIlePheLeuLeuProTyrValPheIleSerGluMetSerArgGln 20
Db 1407 ATGGTTATATATATTTCTCTGCTCCCTATGATATATTTTACAGAAATGAGCCGTCAG 1466
QY 21 ThrAlaThrAlaLeuProThrGlyThrSerLysCysProProSerGlnArgValProAla 40
Db 1467 ACTGCTACAGCATTACTACCGGTACTCTGAAGTGTCCACCATCCAGAGGGTGCCTGCC 1526
QY 41 LeuThrGlyThrThrAlaSerAsnAsnAspLeuAlaSerLeuPheGluCysProValCys 60
Db 1527 CTGACTGGCACAACATGCATCAACATGACTTGGCGAGTCTTTTGGAGTGTCCAGTCTGC 1586
QY 61 PheAspTyrValLeuProProIleLeuGlnCysGlnSerGlyHisLeuValCysSerAsn 80
Db 1587 TTTGACTATGTGTACCGCCCATCTTCAATGTCCAGATGGCCATCTTGTGTAGCAAC 1646
QY 81 CysArgProLysLeuThrCysCysProThrCysArgGlyProLeuGlySerIleArgAsn 100
Db 1647 TGTGCGCCAAAGCTCACAATGTGTGCAACTTGGCGGGGCCCTTTGGGATCCATTCGCAAC 1706
QY 101 LeuAlaMetGluLysValAlaAsnSerValLeuPheProCysLysTyrAlaSerSerGly 120
Db 1707 TTGGCTATGAGAAAGTGGCTAATTCAGTACTTTTCCCTGTGAATATGCGTCTTCTGGA 1766
QY 121 CysGluIleThrLeuProHisThrGluLysAlaAspHisGluGluLeuCysGluPheArg 140
Db 1767 TGTGAATAAATCTGCCACACACAGAAAGAGAGACCATGAGAGCTCTGTGAGTTTAGG 1826
QY 141 ProTyrSerCysProCysProGlyAlaSerCysLysTyrGlnGlySerLeuAspAlaVal 160
Db 1827 CCTATTCTCTGTCGCGCCCTGTGTCTTCTGTAAATGGCAAGGCTCTCTGGATGCTGTA 1886
QY 161 MetProHisLeuMetHisGlnHisLysSerIleThrThrLeuGlnGlyGluAspIleVal 180
Db 1887 ATGCCCCATCTGATGATCAGCATAGTTCATTAACCCCTACAGGAGGAGATATAGTT 1946
QY 181 PheLeuAlaThrAspIleAsnLeuProGlyAlaValAspTyrValMetGlnSerCys 200
Db 1947 TTTCTTGCTACAGACATTAATCTTCTGCTGCTGTTGACTGGGTGATGATGACGCTCTGT 2006
QY 201 PheGlyPheHisPheMetLeuValLeuGluLysGlnGluLysTyrAspGlyHisGlnGln 220
Db 2007 TTTGGCTTTTCACTTCATGTAGTCTTAGAGAAACAGAGAAATACGATGCTCACCAGCAG 2066
QY 221 PhePheAlaIleValGlnLeuIleGlyThrArgLysGlnAlaGluAsnPheAlaTyrArg 240
Db 2067 TTCTTCGCAATCTGACGCTGATAGAACACGACGACGCAAGCTGAAATTTTGTCTTACCGA 2126
QY 241 LeuGluLeuAsnGlyHisArgArgLeuThrTrpGluAlaThrProArgSerIleHis 260
Db 2127 CTTGACCTAAATGCTCATAGGCGACGATGACTTGGAGAGGACTCTCTGATCTATTCAT 2186
QY 261 GluGlyIleAlaThrAlaIleMetAsnSerAspCysLeuValPheAspThrSerIleAla 280
Db 2187 GAAGGAATTCGAACGCCATATGATAGTAGCGTCTAGTCTTTCGCCACGACGATTGCA 2246
QY 281 GlnLeuPheAlaGluAsnGlyAsnLeuGlyIleAsnValThrIleSerMetCys 298
Db 2247 CAGCTTTTTCGAGAAATGGCAATTTAGGATCAATGTAATATTTTCCATGTGT 2300

RESULT 10

ADS34362

ID ADS34362 standard; DNA; 2829 BP.

XX AC ADS34362;

XX DT 02-DEC-2004 (first entry)

XX DE POSH protein associated DNA #116.

XX KW ds; gene; cytostatic; nootropic; neuroprotective; antiparkinsonian;

KW anticonvulsant; antiviral; neuroleptic; central nervous system;
KW POSH polypeptide; POSH-associated protein; POSH-AP; HERPUDI;
KW Ubiquitin ligase; antiviral agent; anti-apoptotic agent;
KW anti-cancer agent; secretory pathway trafficking inhibitor;
KW neurological disorder progression disorder; Alzheimer's disease;
KW Parkinson's disease; Huntington's disease; schizophrenia;
KW Niemann-Pick's disease.
XX Homo sapiens.
XX WO2004078130-A2.
XX 16-SEP-2004.
XX 02-MAR-2004; 2004WO-US006308.
XX 03-MAR-2003; 2003US-0451437P.
XX 05-MAR-2003; 2003US-0452284P.
XX 19-MAR-2003; 2003US-0455760P.
XX 20-MAR-2003; 2003US-0456640P.
XX 03-APR-2003; 2003US-0460526P.
XX 04-APR-2003; 2003US-0460792P.
XX 21-APR-2003; 2003US-0464285P.
XX 09-MAY-2003; 2003US-0469462P.
XX 15-MAY-2003; 2003US-0471378P.
XX 20-MAY-2003; 2003US-0472327P.
XX 30-MAY-2003; 2003US-0474706P.
XX 03-JUN-2003; 2003US-0475825P.
XX 17-JUN-2003; 2003US-0479317P.
XX 19-JUN-2003; 2003US-0480215P.
XX 19-JUN-2003; 2003US-0480376P.
XX 08-AUG-2003; 2003US-0493860P.
XX 28-AUG-2003; 2003US-0498634P.
XX 16-SEP-2003; 2003US-0503931P.
XX 10-NOV-2003; 2003WO-US035712.
XX 05-FEB-2004; 2004WO-US003600.
XX 02-MAR-2004; 2004US-0549896P.
XX (PROT-) PROTEOLOGICS INC.
XX Taglicht DN, Alroy I, Reiss Y, Yaar L, Ben-Avraham D, Tuvia S;
XX Greener T;
XX WPI; 2004-662346/64.
XX Isolated, purified or recombinant complex, useful for identifying an
XX antiviral, anti-apoptotic or anti-cancer, comprising POSH polypeptide and
XX POSH-associated protein (POSH-AP).
XX Disclosure; SEQ ID NO 126; 374pp; English.
XX The invention relates to an isolated, purified or recombinant complex (I)
XX comprising a POSH polypeptide and a POSH-associated protein (POSH-AP) (a)
XX or HERPUDI and a ubiquitin ligase (b). Methods using (I), (a) or (b) are
XX useful for identifying an agent that modulates an activity of a POSH
XX polypeptide or POSH-AP, for identifying an antiviral agent, an anti-
XX apoptotic agent, an anti-cancer agent, an agent that inhibits trafficking
XX of a protein through the secretory pathway, an agent that inhibits the
XX progression of a neurological disorder, an agent that modulates a POSH
XX function, an agent that modulates a HERPUDI function. The methods can be
XX used for treating a viral infection, for inhibiting an activity of a POSH
XX -AP in a cell, for treating a POSH-associated disease in a subject. The
XX POSH-associated disease is viral infection, POSH-associated cancer or
XX POSH-associated neurological disorder. The methods are useful for
XX treating or preventing POSH-associated neurological disorder in a subject
XX e.g. Alzheimer's disease, Parkinson's disease, Huntington's disease,
XX schizophrenia, Niemann-Pick's disease. This sequence corresponds to a
XX nucleic acid of the invention.
XX Sequence 2829 BP; 756 A; 566 C; 553 G; 954 T; 0 U; 0 Other;
SQ

Alignment Scores:

Pred. No.: 1.68e-137 Length: 2829

Score: 1603.00		Matches: 297
Percent Similarity: 99.66%		Conservative: 0
Best Local Similarity: 99.66%		Mismatches: 1
Query Match: 99.50%		Indels: 0
DB: 13		Gaps: 0
US-10-679-246-2 (1-298) x ADS34362 (1-2829)		
QY	1 MetValIleIleIlePheLeuLeuProProTyrValPheIleSerGluMetSerArgGln 20	
DB	1407 ATGGTTATTAATTAATTTCTCTGCTCTCTATGTAATTTATTTACAGAAATGAGCGTCTGAG 1466	
QY	21 ThrAlaThrAlaLeuProThrGlyThrSerIysCysProSerGlnArgValProAla 40	
DB	1467 ACTGCTACAGCATTACTACCGGTACCTCGAAAGTGTCCACCATCCAGAGGTGCTCTGCC 1526	
QY	41 LeuThrGlyThrAlaSerAsnAspLeuAlaSerLeuPheGluCysProValCys 60	
DB	1527 CTGACTGGCACAACCTGCATCCCAATGACTTGGCGAGTCTTTTGGAGTGTCAGTCTGC 1586	
QY	61 PheAspTyrValLeuProProIleLeuGlnCysGlnSerGlyHisLeuValCysSerAsn 80	
DB	1587 TTTGACTATGTGTACCGCCCATCTTCAATGTCAAGTGTGAGTGGCCATCTTTTGTAGCAAC 1646	
QY	81 CysArgProIysLeuThrCysCysProThrCysArgGlyProLeuGlySerIleArgAsn 100	
DB	1647 TGTGCGCCCAAGCTCATGTGTGTCCAACTTGCGGGGGCCCTTTGGGATCCCATTCGCAC 1706	
QY	101 LeuAlaMetGluLysValAlaAsnSerValLeuPheProCysLysTyrAlaSerSerGly 120	
DB	1707 TTGCGTATGAGAAAGTGGCTAATTCAGTACTTTTCCCTGTAATATATCGCTTCTGGA 1766	
QY	121 CysGluIleThrLeuProIleThrGluLysAlaAspHisGluLeuLeuCysGluPheArg 140	
DB	1767 TGTGAATAACTCTGCCACACACAGAAAAAGCAGACCATGAAGAGCTCTGTGAGTTAGG 1826	
QY	141 ProTyrSerCysProCysProGlyAlaSerCysLysTyrGlnGlySerLeuAspAlaVal 160	
DB	1827 CCTATTCTCCGTCCGTCCTGCTGCTCTCTGTAATGTCAGAGCTCTCTGGATGCTGTA 1886	
QY	161 MetProHisLeuMetHisGlnHisLysSerIleThrThrLeuGlnGlyGluAspIleVal 180	
DB	1887 ATGCCCATCTGATGCATCAGCATAAGTCCATTAACAACCTACAGGAGAGGATATAGTT 1946	
QY	181 PheLeuAlaThrAspIleAsnLeuProGlyAlaValAspTyrValMetGlnSerCys 200	
DB	1947 TTTCTTGTCTACAGACATTAATCTTCTGGTGTCTGTGACTGGGATGATGATGCTCTGT 2006	
QY	201 PheGlyPheHisPheMetLeuValLeuGluLysGlnGluLysTyrAspGlyHisGlnGln 220	
DB	2007 TTTGGCTTTTCATCTCATGTGTAGTCTTAGAGAAACAGGAAAAATACGATGTCACACGAC 2066	
QY	221 PhePheAlaIleValGlnLeuIleGlyThrArgLysGlnAlaGlnAsnPheAlaTyrArg 240	
DB	2067 TTCTTCGCAATCGTACAGCTGATAGGAACACGCAAGCAAGCTGAAAAATTTTGTCTACCGA 2126	
QY	241 LeuGluLeuAsnGlyHisArgArgArgLeuThrTyrGluAlaThrProArgSerIleHis 260	
DB	2127 CTTGAGTAAATGTGTATAGCGGACGATGACTTGGAGAGGACTCTCTCATCTATTCAT 2186	
QY	261 GluGlyIleAlaThrAlaIleMetAsnSerAspCysLeuValPheAspThrSerIleAla 280	
DB	2187 GAAGGAATGCAACAGCAGCATTTATGAATAGCGACTGTCTAGTCTTTGACCACGACGATTGCA 2246	
QY	281 GlnLeuPheAlaGluAsnGlyAsnLeuGlyIleAsnValThrIleSerMetCys 298	
DB	2247 CAGCTTTTTCAGAAAAATGGCAATTTAGGCAATCAATGTAACTATTTCCATGTGT 2300	
RESULT 11		
ADF81981/C		
ID ADF81981 standard; DNA; 4090 BP.		
XX		
AC ADF81981;		
XX	26-FEB-2004 (first entry)	
DT	Leukaemia-related DNA sequence #2537.	
DE	Cytostatic; Gene therapy; leukaemia; ss.	
XX	Unidentified.	
XX	WO2003039443-A2.	
XX	15-MAY-2003.	
XX	04-NOV-2002; 2002WO-EP012303.	
PF	05-NOV-2001; 2001EP-00126244.	
XX	30-APR-2002; 2002EP-00009758.	
PR	(DEKR-) DEUT KREBSFORSCHUNGSZENTRUM.	
XX	(UYLU-) UNIV LUDWIG MAXIMILIANS.	
PA	(HAPE/) HAERLACH T.	
PA	(SCHO/) SCHOCH C.	
PA	(KERN/) KERN W.	
XX	Haerlach T, Schoch C, Kern W, Kohlmann A, Schnittger S, Dugas M;	
PI	Ellis R, Broers B, Mergenthaler S;	
XX	WPI; 2003-505037/47.	
DR	Determining the subtype of leukemia cells and whether a patient sample	
XX	contains leukemia cells or other cells, useful for treating leukemia, a	
PT	comprises determining the expression profile of a group of markers in a	
PT	patient sample.	
PS	Disclosure; SEQ ID NO 2537; 2938pp; English.	
XX	The present invention relates to a method (M1) for determining the	
CC	subtype of leukaemia cells and whether a patient sample contains	
CC	leukaemia cells. The method comprises determining the expression profile	
CC	of a group of markers in a patient sample. The method is useful for	
CC	determining the presence of leukaemia cells, its types or subtypes, and	
CC	for the preparation of a medicament for treating leukaemia.	
XX	Sequence 4090 BP; 1233 A; 840 C; 768 G; 1189 T; 0 U; 60 Other;	
Alignment Scores:		
Pred. No.:	8.89e-134	Length: 4090
Score:	1565.00	Matches: 295
Percent Similarity:	98.33%	Conservative: 0
Best Local Similarity:	98.33%	Mismatches: 3
Query Match:	97.14%	Indels: 2
DB:	10	Gaps: 0
US-10-679-246-2 (1-298) x ADF81981 (1-4090)		
QY	1 MetValIleIleIlePheLeuLeuProProTyrValPheIleSerGluMetSerArgGln 20	
DB	3338 ATGGTTATTAATTAATTTCTCTGCTCTCTATGTAATTTATTTACAGAAATGAGCGTCTGAG 3279	
QY	21 ThrAlaThrAlaLeuProThrGlyThrSerLysCysProSerGlnArgValProAla 40	
DB	3278 ACTGCTACAGCATTACTACCGGTACCTCGAAAGTGTCCACCATCCAGAGGNTGCTCTGCC 3219	
QY	41 LeuThrGlyThrAlaSerAsnAspLeuAlaSerLeuPheGluCysProValCys 60	
DB	3218 CTGACTGGCACAACCTGCATCCCAATGACTTGGCGAGTCTTTTGGAGTGTCAGTCTGC 3159	
QY	61 PheAspTyrValLeuProProIleLeuGlnCysGlnSerGlyHisLeuValCysSerAsn 80	
DB	3158 TTTGACTATGTGTTCAGGCAATTTAGGCAATCAATGTAACTATTTCCATGTGT 3099	
QY	81 CysArgProIysLeuThrCysCysProThrCysArgGlyProLeuGlySerIleArgAsn 100	


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Db 3098 TGTGCGCCAAAGCTCACATGTTGTCTCAACTGTCGCCGGGGCCCTTTGGGATCCATTCGCAAC 3039
QY 101 LeuAlaMetGluLysValAlaAsnSerValLeuPheProCysLysTyrAlaSerSerGly 120
Db 3038 TTGGCTATGAGAAAGTGCTTAATTCAGTACTTTTCCCTCTAAATATGCGTCTCTGGA 2979
QY 121 CysGluLeuThrLeuProHisThrGluLys-AlaAspHisGlu-GluLeuCysGluPheA 140
Db 2978 TGTGAATAAATCTGNCACACACAGAAAAANGCAGACCATGAANANGCTCTGTGAGCTTTA 2919
QY 140 igProTyrSerCysProCysProGlyValaserCysLysTyrGlnGlySerLeuAspAlav 160
Db 2918 GGCCTTATTCCTGCTGCTGCCCTGGTCTCTCTGTAATGGCAAGCTCTCTGGATGCTG 2859
QY 160 alMetProHisLeuMetHisGlnHisLysSerIleThrThrLeuGlnGlyGluAspIleV 180
Db 2858 TAATGCCCATCTGATGATCATCAGCATAGTCCATTACAAACCTTACAGGAGGAGATATAG 2799
QY 180 alPheLeuAlaThrAspIleAsnLeuProGlyAlaValAspTrpValMetMetGlnSerC 200
Db 2798 TTTTCTTCTGCTACAGACATTAATCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2739
QY 200 YspHegGlyPheHisPheMetLeuValLeuGluLysGlnGluLysTyrAspGlyHisGlnG 220
Db 2738 GTTTTGGCTTTTCACTTCATGTTAGTCTTAGAGAAACAGGAAATAACGATGGTCCACG 2679
QY 220 lnPhePheAlaIleValGlnLeuIleGlyThrArgLysGlnAlaGluAsnPheAlaTyrA 240
Db 2678 AGTCTCTGCAATCGTACAGCTGATAGGACACGCAAGCAAGCTGAATTTTGTCTACC 2619
QY 240 rgLeuGluLeuAsnGlyHisArgArgLeuThrTrpGluAlaThrProArgSerIleH 260
Db 2618 GACTTGGAGCTAAATGCTATAGCGCAGATTGACTTGGGAAGCGCACTCTCGATCTATT 2559
QY 260 inGluGlyIleAlaThrAlaIleMetAsnSerAspCysLeuValPheAspThrSerIleA 280
Db 2558 ATGAAGGAATTGCAAGCACTTATGAATAGGCACTGTCTAGTCTTTTGACACAGCATTTG 2499
QY 280 laGlnLeuPheAlaGluAsnGlyAsnLeuGlyIleAsnValThrIleSerMetCys 298
Db 2498 CACAGCTTTTTCAGAAATGCAATTTAGGCATCAATGTAACTATTTCATGTGT 2443
RESULT 12
ADS34365
ID ADS34365 standard; DNA; 1540 BP.
XX
AC ADS34365;
XX
DT 02-DEC-2004 (first entry)
XX
DE POSH protein associated DNA #119.
XX
KW ds; gene; cytostatic; nootropic; neuroprotective; antiparkinsonian;
KW anticonvulsant; antiviral; neuroleptic; central nervous system;
KW POSH polypeptide; POSH-associated protein; POSH-AP; HERPUDI;
KW Ubiquitin ligase; antiviral agent; anti-apoptotic agent;
KW anti-cancer agent; secretory pathway trafficking inhibitor;
KW neurological disorder progression disorder; Alzheimer's disease;
KW Parkinson's disease; Huntington's disease; schizophrenia;
KW Niemann-Pick's disease.
XX
OS Homo sapiens.
XX
PN WO2004078130-A2.
XX
PD 16-SEP-2004.
XX
PF 02-MAR-2004; 2004WO-US0006308.
XX
PR 03-MAR-2003; 2003US-0451437P.
PR 05-MAR-2003; 2003US-0452284P.
PR 19-MAR-2003; 2003US-0455760P.
PR 20-MAR-2003; 2003US-0456640P.
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PR 03-APR-2003; 2003US-0460526P.
PR 04-APR-2003; 2003US-0460792P.
PR 21-APR-2003; 2003US-0464285P.
PR 09-MAY-2003; 2003US-0469462P.
PR 15-MAY-2003; 2003US-0471378P.
PR 20-MAY-2003; 2003US-0472327P.
PR 30-MAY-2003; 2003US-0474706P.
PR 03-JUN-2003; 2003US-0475825P.
PR 17-JUN-2003; 2003US-0479317P.
PR 19-JUN-2003; 2003US-0480215P.
PR 19-JUN-2003; 2003US-0480376P.
PR 08-AUG-2003; 2003US-0493860P.
PR 28-AUG-2003; 2003US-0498634P.
PR 16-SEP-2003; 2003US-0503931P.
PR 10-NOV-2003; 2003WO-US0357112.
PR 05-FEB-2004; 2004WO-US003600.
PR 02-MAR-2004; 2004US-0549896P.
XX
XX (PROT-) PROTEOLOGICS INC.
XX
PI Taglicht DN, Alroy I, Reiss Y, Yaar L, Ben-Avraham D, Tuvia S;
Greener T;
XX
XX WPI; 2004-662346/64.
XX
PT Isolated, purified or recombinant complex, useful for identifying an
PT antiviral, anti-apoptotic or anti-cancer, comprising POSH polypeptide and
PT POSH-associated protein (POSH-AP).
XX
XX Disclosure; SEQ ID NO 129; 374pp; English.
XX
CC The invention relates to an isolated, purified or recombinant complex (I)
CC comprising a POSH polypeptide and a POSH-associated protein (POSH-AP) (a)
CC or HERPUDI and a ubiquitin ligase (b). Methods using (I). (a) or (b) are
CC useful for identifying an agent that modulates an activity of a POSH
CC polypeptide or POSH-AP, for identifying an antiviral agent, an anti-
CC apoptotic agent, an anti-cancer agent, an agent that inhibits trafficking
CC of a protein through the secretory pathway, an agent that inhibits the
CC progression of a neurological disorder, an agent that modulates a POSH
CC function, an agent that modulates a HERPUDI function. The methods can be
CC used for treating a viral infection, for inhibiting an activity of a POSH
CC -AP in a cell, for treating a POSH-associated disease in a subject. The
CC POSH-associated disease is viral infection, POSH-associated cancer or
CC POSH-associated neurological disorder. The methods are useful for
CC treating or preventing POSH-associated neurological disorder in a subject
CC e.g. Alzheimer's disease, Parkinson's disease, Huntington's disease,
CC schizophrenia, Niemann-Pick's disease. This sequence corresponds to a
CC nucleic acid of the invention.
XX
SQ Sequence 1540 BP; 428 A; 313 C; 352 G; 447 T; 0 U; 0 Other;
```

Alignment Scores:

Pred. No.:	4,748-132	Length:	1540
Score:	1540.00	Matches:	285
Percent Similarity:	98.62%	Conservative:	1
Best Local Similarity:	98.28%	Mismatches:	0
Query Match:	95.59%	Indels:	4
DB:	13	Gaps:	1

US-10-679-246-2 (1-298) x ADS34365 (1-1540)

QY	9	ProProTyrValPheIleSerGluMetSerArgGlnThrAlaThrAlaLeuProThrGly	28
Db	106	CGCCCC-----ACAGAAATGAGCCGCTCAGACTGCTACAGCATTTACCTACCGGT	153
QY	29	ThrSerLysCysProProSerGlnArgValProAlaLeuThrGlyThrThrAlaSerAsn	48
Db	154	ACCTCGAAGTGTCCACCATCCAGAGGGTGCCTGCGCTGACTGGCACAACATGCAAC	213
QY	49	AsnAspLeuAlaSerLeuPheGluCysProValCysPheAspTyrValLeuProProfile	68
Db	214	AATGACTTGGCGAGTCTTTTGTGAGTGTCCAGTCTGCTGTTGACTGTGTGTACCGCCATT	273

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DB 274 CTTCAATGTACAGTGGCCATCTTCTTTGTAGCAACTGTGCCCCAAAGCTCACATGTTGT 333
QY 89 ProThrCysArgGlyProLeuGlySerIleArgAsnLeuAlaMetGluLysValAlaAsn 108
DB 334 CCAACTTGGCGGGGCCCTTTGGATCCATTCACACTTGGCTATGGAGAAAGTGGCTAAT 393
QY 109 SerValLeuPheProCysLysTyrAlaSerSerGlyCysGluIleThrLeuProHisThr 128
DB 394 TCAGTACTTTTCCCTGTAATATGCGTCTTCGTGATGTGAATAAATCTCTGCCACACACA 453
QY 129 GluLysAlaAspHisGluLeuCysGluPheArgProTyrSerCysProCysProGly 148
DB 454 GAAAAGCAGACCATGAGAGCTGTGTAGTTTAGGCCCTTATCTCTCCGGGCCCTGGT 513
QY 149 AlaSerCysLeuTyrGlnGlySerLeuAspAlaValMetProHisLeuMetHisGlnHis 168
DB 514 GCTTCTCTGAATGGCAAGCTCTCTGGATGCTGTAAATGCCCATCTGATGCATCAGCAT 573
QY 169 LysSerIleThrThrLeuGlnGlyGluAspIleValPheLeuAlaThrAspIleAsnLeu 188
DB 574 AAGTCCATTACACCTCAGGAGAGGATATAGTCTTTCTTGCTACACACATTAATCTT 633
QY 189 ProGlyAlaValAspTrpValMetMetGlnSerCysPheGlyPheHisPheMetLeuVal 208
DB 634 CTTGTTGCTGTGACTGGGTGATGATGATGATGATGATGATGATGATGATGATGATGAT 693
QY 209 LeuGluLysGlnGluLysTyrAspGlyHisGlnGlnPhePheAlaIleValGlnLeuIle 228
DB 694 TTAGAGAAACAGGAAATACGATGTCACAGCAGTCTTTCGCAATCGTACAGCTGATA 753
QY 229 GlyThrArgLysGlnAlaGluAsnPheAlaTyrArgLeuGluLeuAsnGlyHisArgArg 248
DB 754 GGAACACGCAAGCAAGCTGAAATTTTGTCTACCGACTTGAGCTAAATGCTATAGCGCA 813
QY 249 ArgLeuThrTrpGluAlaThrProArgSerIleHisGluGlyIleAlaThrAlaIleMet 268
DB 814 CGATTGACTTGGAGAGGACTCTCTCATCTATTTCATGAAGGAATTCACAGCAATTATG 873
QY 269 AsnSerAspCysLeuValPheAspThrSerIleAlaGlnLeuPheAlaGluAsnGlyAsn 288
DB 874 AATAGGCACTGTCTAGTCTTTGACACAGCATTCGACAGCTTTTTCAGAAAAATGGCAAT 933
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XX ds; gene; cytostatic; nootropic; neuroprotective; antiparkinsonian;
XX anticonvulsant; antiviral; neuroleptic; central nervous system;
XX POSH polypeptide; POSH-associated protein; POSH-AP; HERPUDI;
XX Ubiquitin ligase; antiviral agent; anti-apoptotic agent;
XX anti-cancer agent; secretory pathway trafficking inhibitor;
XX neurological disorder progression disorder; Alzheimer's disease;
XX Parkinson's disease; Huntington's disease; schizophrenia;
XX Niemann-Pick's disease.
XX Homo sapiens.
XX WO2004078130-A2.
XX 16-SEP-2004.
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PF 02-MAR-2004; 2004WO-US006308.
XX 03-MAR-2003; 2003US-0451437P.
PR 05-MAR-2003; 2003US-0452284P.
PR 19-MAR-2003; 2003US-0455760P.
PR 20-MAR-2003; 2003US-0456640P.
PR 03-APR-2003; 2003US-0460526P.
PR 04-APR-2003; 2003US-0460792P.
PR 21-APR-2003; 2003US-0464285P.
PR 09-MAY-2003; 2003US-0469482P.
PR 15-MAY-2003; 2003US-0471378P.
PR 20-MAY-2003; 2003US-0472327P.
PR 30-MAY-2003; 2003US-0474706P.
PR 03-JUN-2003; 2003US-0475825P.
PR 17-JUN-2003; 2003US-0479317P.
PR 19-JUN-2003; 2003US-0480215P.
PR 19-JUN-2003; 2003US-0480376P.
PR 08-AUG-2003; 2003US-0493860P.
PR 28-AUG-2003; 2003US-0498634P.
PR 16-SEP-2003; 2003US-0503931P.
PR 10-NOV-2003; 2003WO-US035712.
PR 05-FEB-2004; 2004WO-US003600.
PR 02-MAR-2004; 2004US-0549896P.
XX (PROT-) PROTEOLOGICS INC.
XX Taglicht DN, Alroy I, Reiss Y, Yaar L, Ben-Avraham D, Tuvia S;
PI Greener T;
XX WPI; 2004-662346/64.
XX Isolated, purified or recombinant complex, useful for identifying an
PT antiviral, anti-apoptotic or anti-cancer, comprising POSH polypeptide and
PT POSH-associated protein (POSH-AP).
XX Disclosure; SEQ ID NO 124; 374pp; English.
XX The invention relates to an isolated, purified or recombinant complex (I)
CC comprising a POSH polypeptide and a POSH-associated protein (POSH-AP) (a)
CC or HERPUDI and a Ubiquitin ligase (b). Methods using (I), (a) or (b) are
CC useful for identifying an agent that modulates an activity of a POSH
CC polypeptide or POSH-AP, for identifying an antiviral agent, an anti-
CC apoptotic agent, an anti-cancer agent, an agent that inhibits trafficking
CC of a protein through the secretory pathway, an agent that inhibits the
CC progression of a neurological disorder, an agent that modulates a POSH
CC function, an agent that modulates a HERPUDI function. The methods can be
CC used for treating a viral infection, for inhibiting an activity of a POSH
CC -AP in a cell, for treating a POSH-associated disease in a subject. The
CC POSH-associated disease is viral infection, POSH-associated cancer or
CC POSH-associated neurological disorder. The methods are useful for
CC treating or preventing POSH-associated neurological disorder in a subject
CC e.g. Alzheimer's disease, Parkinson's disease, Huntington's disease,
CC schizophrenia, Niemann-Pick's disease. This sequence corresponds to a
CC nucleic acid of the invention.
XX SQ Sequence 2048 BP; 537 A; 403 C; 463 G; 645 T; 0 U; 0 Other;
Alignment Scores:
Pred. No.: 6,99e-132 Length: 2048
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Percent Similarity: 98.62% Conservatative: 1
Best Local Similarity: 98.28% Mismatches: 0
Query Match: 95.59% Indels: 4
DB: 13 Gaps: 1
US-10-679-246-2 (1-298) x ADS34360 (1-2048)
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Db 223 ACCTCGAAGTGTCCACCATCCAGAGGGTGCCTGCCCTGACTGGCACAACTGCATCCAAC 282
QY 49 AsnAspLeuAlaSerLeuPheGluCysProValCysPheAspTyrValLeuProPhe 68
Db 283 AATGACTTGGCGAGTCTTTTGGAGTCCAGTCTGCTTTGACTATGTGTGTACCGCCCAAT 342
QY 69 LeuGlnCysGlnSerGlyHisLeuValCysSerAsnCysArgProIysLeuThrCysCys 88
Db 343 CTTCAATGTCCAGAGTGGCCATCTTGTGTAGCAACTGTGCCCAAGCTCAGATGTGT 402
QY 89 ProThrCysArgGlyProLeuGlySerIleArgAsnLeuAlaMetGluLysValAlaAsn 108
Db 403 CCAACTTGGCGGGCCCTTTGGGATCCATTCGCAACTTGGCTATGGAGAAGTGGCTAAT 462
QY 109 SerValLeuPheProCysLysTyrAlaSerSerGlyCysGluIleThrLeuProHisThr 128
Db 463 TCAGTACTTTTCCCTGTAAATATGCTCTCTGGATGTGAATAACTCTGCCACACACA 522
QY 129 GluLysAlaAspHisGluGluLeuCysGluPheArgProTyrSerCysProCysProGly 148
Db 523 GAAAAAGCAGACCATGAAGAGCTCTGTGAGTTTAGGCTTTATTCCTGTCGTCCTGGT 582
QY 149 AlaSerCysLysTrpGlnGlySerLeuAspAlaValMetProHisLeuMetHisGlnHis 168
Db 583 GCTTCTCTGAATGGCAGGCTCTCTGGATGCTGTATGCCCCATCTGATGCATCAGCAT 642
QY 169 LysSerIleThrThrLeuGlnGlyGluAspIleValPheLeuAlaThrAspIleAsnLeu 188
Db 643 AAGTCCATTACAACTTACAGGAGGAGGATATAGTTTTCTTCTGCTACAGACATTAATCT 702
QY 189 ProGlyAlaValAspTrpValMetMetGlnSerCysPheGlyPheHisPheMetLeuVal 208
Db 703 CCTGGTGTCTGTGACTGGGTGATGATGCAGTCTGTTTGGCTTTTCACTTCATGTGTAGTC 762
QY 209 LeuGluLysGlnGluLysTyrAspGlyHisGlnGlnPhePheAlaIleValGlnLeuIle 228
Db 763 TTAGAGAAACAGAAATAACATGATGTTCACACAGATTTCTTCCATTCGTACAGCTGATA 822
QY 229 GlyThrArgLysGlnAlaGluAsnPheAlaTyrArgLeuGluLeuAsnGlyHisArgArg 248
Db 823 GGAACACGCAAGCAAGCTGAAATTTTGTCTTACCGACTTGAGCTAAATGCTATAGCGCA 882
QY 249 ArgLeuThrTrpGluAlaThrProArgSerIleHisGluGlyIleAlaThrAlaIleMet 268
Db 883 CGATTGACTTGGGAAGCAGCTCTCGATCTATTTCATGAAGGAATTCACAGCACTTATG 942
QY 269 AsnSerAspCysLeuValPheAspThrSerIleAlaGlnLeuPheAlaGluAsnGlyAsn 288
Db 943 AATAGGAGTGTCTAGTCTTTGACACAGCATTCACAGCTTTTTCGAGAAAATGGCAAT 1002
QY 289 LeuGlyIleAsnValThrIleSerMetCys 298
Db 1003 TTAGGATCAATGTAATCTATTTCATGTGT 1032
RESULT 14
ID ADS34359
XX ADS34359 standard; DNA; 2454 BP.
AC ADS34359;
XX
DT 02-DEC-2004 (first entry)
DE POSH protein associated DNA #113.
KW ds; gene; cytostatic; nootropic; neuroprotective; antiparkinsonian;
KW anticonvulsant; antiviral; neuroleptic; central nervous system;
KW POSH polypeptide; POSH-associated protein; POSH-AP; HERPUDI;
KW Ubiquitin ligase; antiviral agent; anti-apoptotic agent;
KW anti-cancer agent; secretory pathway trafficking inhibitor;
KW neurological disorder progression disorder; Alzheimer's disease;
KW Parkinson's disease; Huntington's disease; schizophrenia;
KW Niemann-Pick's disease.
XX
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OS Homo sapiens.
XX WO2004078130-A2.
XX
XX PD 16-SEP-2004.
XX
XX PF 02-MAR-2004; 2004WO-US006308.
XX
XX PR 03-MAR-2003; 2003US-0451437P.
XX PR 05-MAR-2003; 2003US-0452284P.
XX PR 19-MAR-2003; 2003US-0455760P.
XX PR 20-MAR-2003; 2003US-0456640P.
XX PR 03-APR-2003; 2003US-0460526P.
XX PR 04-APR-2003; 2003US-0460792P.
XX PR 21-APR-2003; 2003US-0464285P.
XX PR 09-MAY-2003; 2003US-0469462P.
XX PR 15-MAY-2003; 2003US-0471378P.
XX PR 20-MAY-2003; 2003US-0472327P.
XX PR 30-MAY-2003; 2003US-0474706P.
XX PR 03-JUN-2003; 2003US-0475825P.
XX PR 17-JUN-2003; 2003US-0479317P.
XX PR 19-JUN-2003; 2003US-0480215P.
XX PR 19-JUN-2003; 2003US-0480376P.
XX PR 08-AUG-2003; 2003US-0493860P.
XX PR 28-AUG-2003; 2003US-0498634P.
XX PR 16-SEP-2003; 2003US-0503931P.
XX PR 10-NOV-2003; 2003WO-US035712.
XX PR 05-FEB-2004; 2004WO-US003600.
XX PR 02-MAR-2004; 2004US-0549896P.
XX
XX (PROT-) PROTEOLOGICS INC.
XX
XX Taglicht DN, Alroy I, Reiss Y, Yaar L, Ben-Avraham D, Tuvia S;
PI Greener T;
XX
XX WPI; 2004-662346/64.
XX
XX Isolated, purified or recombinant complex, useful for identifying an
PT antiviral, anti-apoptotic or anti-cancer, comprising POSH polypeptide and
PT POSH-associated protein (POSH-AP).
XX
XX Disclosure; SEQ ID NO 123; 374pp; English.
XX
XX The invention relates to an isolated, purified or recombinant complex (1)
CC comprising a POSH polypeptide and a POSH-associated protein (POSH-AP) (a)
CC or HERPUDI and a ubiquitin ligase (b). Methods using (1), (a) or (b) are
CC useful for identifying an agent that modulates an activity of a POSH
CC polypeptide or POSH-AP, for identifying an antiviral agent, an anti-
CC apoptotic agent, an anti-cancer agent, an agent that inhibits trafficking
CC of a protein through the secretory pathway, an agent that inhibits the
CC progression of a neurological disorder, an agent that modulates a POSH
CC function, an agent that modulates a HERPUDI function. The methods can be
CC used for treating a viral infection, for inhibiting an activity of a POSH
CC -AP in a cell, for treating a POSH-associated disease in a subject. The
CC POSH-associated disease is viral infection, POSH-associated cancer or
CC POSH-associated neurological disorder. The methods are useful for
CC treating or preventing POSH-associated neurological disorder in a subject
CC e.g. Alzheimer's disease, Parkinson's disease, Huntington's disease,
CC schizophrenia, Niemann-Pick's disease. This sequence corresponds to a
CC nucleic acid of the invention.
XX
XX Sequence 2454 BP; 743 A; 456 C; 510 G; 745 T; 0 U; 0 Other;
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Alignment Scores:
Pred. No.: 1-69e-131 Length: 2454
Score: 1537.00 Matches: 283
Percent Similarity: 100.00% Conservatives: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 95.41% Indels: 0
DB: 13 Gaps: 0
US-10-679-246-2 (1-298) x ADS34359 (1-2454)
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169	LysSerIleThrThrLeuGlnGlyGluAspIleValPheLeuAlaThrAspIleAsnLeu	188	
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189	ProGlyAlaValAspTrpValMetMetGlnSerCysPheGlyPheHisPheMetLeuVal	208	
637	CCTGGTGTCTTGACTGGGTGATGATGCAGCTTCTGTTTGGCTTTTCATTTCATGTATGTC	696	
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697	TTGAGAAACAAGAAAAAATATGATGGTCATCAGCAGTTCTTTTGCAATTGTACAAC	756	
229	GlyThrArgLysGlnAlaGluAsnPheAlaTyrArgLeuGluLeuAsnGlyHisArgArg	248	
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249	ArgLeuThrTrpGluAlaThrProArgSerIleHisGluGlyLeuAlaThrAlaIleMet	268	
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877	AATAGTGACTGCTAGTGTGTTGACACCAAGCATTTGCACAGCTTTTTCGAGAAATGCGCAAT	936	
289	LeuGlyIleAsnValThrIleSerMetCys	298	
937	TTAGGCATCAATGTAACTATTTCATGTGT	966	

Search completed: April 25, 2005, 07:02:25
Job time : 639 secs

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GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: April 25, 2005, 06:43:10 ; Search time 3685 Seconds
(without alignments)
3078.196 Million cell updates/sec

Title: US-10-679-246-2

Perfect score: 1611

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Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
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Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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2: gb_est2:
3: gb_hic:
4: gb_est3:
5: gb_est4:
6: gb_est5:
7: gb_est6:
8: gb_gsal:
9: gb_gsal2:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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3	1537	95.4	1857	3 CR614925	CR614925 full-length
4	1532	95.1	849	9 AY402255	AY402255 Homo sapi
5	1528	94.8	849	9 AY402257	AY402257 Mus muscu
6	1521	94.4	849	9 AY402256	AY402256 Pan trogl
7	1465.5	91.0	859	5 BX366404	BX366404
8	1427	88.6	1287	3 CR598465	CR598465 full-length
9	1412	87.6	1180	7 CK025134	CK025134 AGENCOURT

10	1360	84.4	848	5	BU614872	BU614872 UI-M-EV0-
11	1325	82.2	824	4	BG619351	BG619351 602619484
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13	1285	79.8	872	5	BX448317	BX448317 BX448317
14	1269	78.8	716	5	BU260826	BU260826 603504644
15	1247	77.4	779	1	AI936347	AI936347 w081b11.x
16	1247	77.4	852	5	BX463976	BX463976 BX463976
17	1229	76.3	890	7	CF551876	CF551876 AGENCOURT
18	1209	75.0	806	7	CF752915	CF752915 om_C001.5
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33	1129	70.1	621	7	CN677231	CN677231 A0993D06-
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ALIGNMENTS

RESULT 1

LOCUS--

U70056

U70056

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/lab host="DH10B (ampicillin resistant)"
/clone lib="Soares infant brain INIB"
/note="organ: whole brain; Vector: Lfamid BA; Site 1: Not
1; Site 2: Hind III; 1st strand cDNA was primed with a Not
I - oligo (dT) primer [5',
AACTGGAGAAATTCGGCCGCGAGAAATTTTTTTTTTTTTTTT 3'];
double-stranded cDNA was ligated to Hind III adaptors
(Pharmacia), digested with Not I and directionally cloned
into the Not I and Hind III sites of the Lfamid BA vector.
Library went through one round of normalization. Library
constructed by Bento Soares and M.Fatima Bonaldo."

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ORIGIN

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Alignment Scores:
Pred. No.: 1,16e-144 Length: 1221
Score: 1611.00 Matches: 298
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 7 Gaps: 0

US-10-679-246-2 (1-298) x U70056 (1-1221)

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DB 62 ATGGTTTAAATATTTTCTCGCTCTCTTATGATTTATTTTTCAGAAATGAGCGTCAG 121
QY 21 ThrAlaThrAlaLeuProThrGlyThrSerLysCysProSerGlnArgValProAla 40
DB 122 ACTGCTACAGCATTAACCTACCGGTACCTCGAAGTGTCCACCATCCAGAGGTGCGTGC 181
QY 41 LeuThrGlyThrThrAlaSerAsnAspLeuAlaSerIleuPheGluCysProValCys 60
DB 182 CTGACTGGCAACTGCATCCAAATGACTTGGCCAGTCTTTTGGAGTGCAGTCTGC 241
QY 61 PheAspTyrValLeuProPheLeuGlnCysGlnSerGlyHisLeuValCysSerAsn 80
DB 242 TTTGACTATGTGTACCGCCCATCTTCATGTCAGAGTGGCCATCTTGTGTAGCAAC 301
QY 81 CysArgProLysLeuThrCysCysProThrCysArgGlyProLeuGlySerIleArgAsn 100
DB 302 TGTGCGCCAAAGCTCACAATGTTGTCACACTTGGCGGGGCTTTGGGATCCATTCGCAAC 361
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DB 482 CCTATTTCCTGCTCGCTCGCTCGCTCGCTCGCTCGCTCGCTCGCTCGCTCGCTCGCT 541
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QY 181 PheLeuAlaThrAspIleAsnLeuProGlyAlaValAspTrpValMetMetGlnSerCys 200
DB 602 TTTCTTGCTACAGACATTAATCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 661
QY 201 PheGlyPheHisPheMetLeuValLeuGluLysGlnGluLysTyrAspGlyHisGlnGln 220
DB 662 TTTGGCTTTTCACTTCATGTTAGTCTTAGAGAAACAGGAAATAACGATGTCACAGCAG 721
QY 221 PhePheAlaIleValGlnLeuIleGlyThrArgLysGlnAlaGluAsnPheAlaTyrArg 240
DB 722 TTTCTGCAATCGTACAGCTCATAGGAACACGCAAGCAAGCTGAAATTTTGTCTTACCGA 781
QY 241 LeuGluLeuAsnGlyHisArgArgLeuThrTrpGluAlaThrProArgSerIleHis 260

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DB 782 CTTGAGCTAAATGTCATAGCGAGCAGATTGACTTGGGAGCGGACTCTCTCGATCTATTTCAT 841
QY 261 GluGlyIleAlaThrAlaIleMetAsnSerAspCysLeuValPheAspThrSerIleAla 280
DB 842 GAGGAATTCACAGCAGCATTAATGAGGACTGTCTAGTCTTTGACACAGCATTCGCA 901
QY 281 GlnLeuPheAlaGluAsnGlyAsnLeuGlyIleAsnValThrIleSerMetCys 298
DB 902 CAGCTTTTTCAGAAAATGCAATTAGGATCATCATGTAATCTTTCATTTTCATGTGT 955
RESULT 2
LOCUS CR607323 1360 bp mRNA linear HTC 21-JUL-2004
DEFINITION full-length cDNA clone CS0DC023YH14 of Neuroblastoma Cot
25-normalized of Homo sapiens (human).
ACCESSION CR607323
VERSION CR607323.1 GI:50488130
KEYWORDS HTC; cDNA; cDNA.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1. (bases 1 to 1360)
Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
Full-length cDNA libraries and normalization
Unpublished
Contact : Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ InvitroGen Corporation 1600
Faraday Avenue
2 (bases 1 to 1360)
Genoscope.
Direct Submission
Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :
BP 191 91006 Evry cedex - FRANCE (E-mail : segref@genoscope.cns.fr)
- Web : www.genoscope.cns.fr)
1st strand cDNA was primed with a NotI-oligo (dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR I sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen.
FEATURES
Location/Qualifiers
source
1..1360
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0DC023YH14"
/tissue_type="Neuroblastoma Cot 25-normalized"
/plasmid="pCMVSPORT_6"
ORIGIN
Alignment Scores:
Pred. No.: 1,91e-137 Length: 1360
Score: 1537.00 Matches: 283
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 95.41% Indels: 0
DB: 3 Gaps: 0
US-10-679-246-2 (1-298) x CR607323 (1-1360)
QY 16 GluMetSerArgGlnThrAlaLeuProThrGlyThrSerLysCysProSer 35
DB 3 GAAATGAGCGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 62
QY 36 GlnArgValProAlaLeuThrGlyThrThrAlaSerAsnAspLeuAlaSerLeuPhe 55
DB 63 CAGAGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 122
QY 56 GluCysProValCysPheAspTyrValLeuProIleuGlnCysGlnSerGlyHis 75
DB 123 GAGTGTCCAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 182
QY 76 LeuValCysSerAsnCysArgProLysLeuThrCysCysProThrCysArgGlyProLeu 95

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Db 183 CTGTGTTGAGGACCTGTCGCCAAAGCTCACATGTTGTCACACTTGCCTGGGCGCCCTTTG 242
Qy 96 GlySerIleArgAsnLeuAlaMetGluLysValAlaAsnSerValLeuPheProCysLys 115
Db 243 GGATCCATTCGCACTTGGCTATGGAGAAAGTGCTAATTCAGTACTTTTCCCTGTAA 302
Qy 116 TyrAlaSerSerGlyCysGluLeuThrLeuProHisThrGluLysAlaAspHisGluGlu 135
Db 303 TATGCGCTCTCTGGATGTGAATAAATCTGCCACACAGAAAAGCAGACCATGAAGAG 362
Qy 136 LeuCysGluPheArgProTyrSerCysProCysProGlyValaSerCysLysTrpGlnGly 155
Db 363 CTCTGTAGTTAGGCTTATCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 422
Qy 156 SerLeuAspAlaValMetProHisLeuMetHisGlnHisLysSerIleThrThrLeuGln 175
Db 423 TCTCTGGATGCTGTAATGCCGATCTGATGCATCAGCAATAAGTCCATTACACCCCTACAG 482
Qy 176 GlyGluAspIleValPheLeuAlaThrAspIleAsnLeuProGlyAlaValaAspTrpVal 195
Db 483 GGAGAGGATATAGTTTCTTGTGTAAGCAATTAATCTTCTGCTGCTGCTGCTGCTGCTG 542
Qy 196 MetMetGlnSerCysPheGlyPheHisGlnHisLysSerIleThrThrLeuGln 215
Db 543 ATGATGCACTGCTGTTTGGCTTCTTCACTTCATGTTAGTCTTAGAGAAACAGGAAAATAC 602
Qy 216 AspGlyHisGlnGlnPheAlaIleValGlnLeuIleGlyThrArgLysGlnAlaGlu 235
Db 603 GATGTCACCAAGCTTCTTCCGATCTGATAGTATAGGAAACAGCAGCAGCAGCTGAA 662
Qy 236 AsnPheAlaTyrArgLeuGluLeuAsnGlyHisArgArgLeuThrTrpGluAlaThr 255
Db 663 AATTTTGTCTACGACTTGTGCAATGCTGATAGTATAGGAAACAGCAGCAGCTGCTG 722
Qy 256 ProArgSerIleHisGluGlyLeuAlaThrAlaIleMetAsnSerAspCysLeuValPhe 275
Db 723 CCTCGATCTATTATGAGGAATTTGCAAGCATTATGAAATAGGCACTGCTAGTCTTT 782
Qy 276 AspThrSerIleAlaGlnLeuPheAlaGluAsnGlyAsnLeuGlyIleAsnValThrIle 295
Db 783 GACACGAGATTGCACAGCTTTTGGAGAAATGGCAATTTAGGCATCAATGTAATATT 842
Qy 296 SerMetCys 298
Db 843 TCCATGTGT 851
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RESULT 3

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CR614925
LOCUS full-length cDNA clone CS0DK012Y120 of HeLa cells Cot 25-normalized 21-JUL-2004
DEFINITION of Homo sapiens (human).
ACCESSION CR614925
VERSION CR614925.1 GI:50495732
KEYWORDS HTC; CNSLT; CDNA.
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 1857)
AUTHORS Li, W.B., Gruber, C., Jessee, J. and Palayes, D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished
REMARK Contact : Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
Faraday Avenue
Genoscope.
2 (bases 1 to 1857)
REFERENCE 2
AUTHORS Direct Submission
TITLE Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :
JOURNAL BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr)
- Web : www.genoscope.cns.fr)
COMMENT 1st strand cDNA was primed with a NotI-oligo (dT) primer. Five prime
```

end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen.

FEATURES

source
1..1857
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0DK012Y120"
/tissue_type="HeLa cells Cot 25-normalized"
/plasmid="pCMVSPORT_6"

ORIGIN

Alignment Scores:
Pred. No.: 3,06e-137 Length: 1857
Score: 1537.00 Matches: 283
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 95.41% Indels: 0
DB: 3 Gaps: 0
US-10-679-246-2 (1-298) x CR614925 (1-1857)
Qy 16 GluMetSerArgGlnThrAlaThrAlaLeuProThrGlyThrSerLysCysProProSer 35
Db 3 GAAATGAGCGCTGACACTGCTACAGCATTTACCTACCGGTACCTCGAAGTGTCCACCATCC 62
Qy 36 GlnArgValProAlaLeuThrGlyThrAlaSerAsnAsnAspLeuAlaSerLeuPhe 55
Db 63 CAGAGGTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 122
Qy 56 GluCysProValCysPheAspTyrValLeuProProIleLeuGlnCysGlnSerGlyHis 75
Db 123 GAGTGTCCAGTCTGCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 182
Qy 76 LeuValCysSerAsnCysArgProLysLeuThrCysCysProThrCysArgGlyProLeu 95
Db 183 CTTGTTTGTAGCAACTGTGCGCCAAAGCTCAGATGTTGTCCAACTTGTCCGGGCGCCCTTG 242
Qy 96 GlySerIleArgAsnLeuAlaMetGluLysValAlaAsnSerValLeuPheProCysLys 115
Db 243 GGATCCATTCGCACTTGGCTATGGAGAAAGTGCTAATTCAGTACTTTTCCCTGTAA 302
Qy 116 TyrAlaSerSerGlyCysGluLeuThrLeuProHisThrGluLysAlaAspHisGluGlu 135
Db 303 TATGCGCTCTCTGGATGTGAATAAATCTGCTACAGCATTAATCTCTGCTGCTGCTGCTG 362
Qy 136 LeuCysGluPheArgProTyrSerCysProCysProGlyValaSerCysLysTrpGlnGly 155
Db 363 CTCTGTAGTTAGGCTTATCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 422
Qy 156 SerLeuAspAlaValMetProHisLeuMetHisGlnHisLysSerIleThrThrLeuGln 175
Db 423 TCTCTGGATGCTGTAATGCCGATCTGATGCATCAGCAATAAGTCCATTACACCCCTACAG 482
Qy 176 GlyGluAspIleValPheLeuAlaThrAspIleAsnLeuProGlyAlaValaAspTrpVal 195
Db 483 GGAGAGGATATAGTTTCTTGTGTAAGCAATTAATCTTCTGCTGCTGCTGCTGCTGCTG 542
Qy 196 MetMetGlnSerCysPheGlyPheHisGlnHisLysSerIleThrThrLeuGln 215
Db 543 ATGATGCACTGCTGTTTGGCTTCTTCACTTCATGTTAGTCTTAGAGAAACAGCAGCAG 602
Qy 216 AspGlyHisGlnGlnPheAlaIleValGlnLeuIleGlyThrArgLysGlnAlaGlu 235
Db 603 GATGTCACCAAGCTTCTTCCGATCTGATAGTATAGGAAACAGCAGCAGCAGCTGAA 662
Qy 236 AsnPheAlaTyrArgLeuGluLeuAsnGlyHisArgArgLeuThrTrpGluAlaThr 255
Db 663 AATTTTGTCTACGACTTGTGCAATGCTGATAGTATAGGAAACAGCAGCAGCTGCTG 722
Qy 256 ProArgSerIleHisGluGlyLeuAlaThrAlaIleMetAsnSerAspCysLeuValPhe 275

Ferreira, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J.,
Adams, M.D. and Cargill, M.

TITLE
JOURNAL

Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
Rockville, MD 20850, USA

This sequence was made by sequencing genomic exons and ordering
them based on alignment

FEATURES
source

Location/Qualifiers
1..849
/organism="Mus musculus"
/mol_type="genomic DNA"
/db_xref="taxon:10090"
<1..849
/gene="Slah1"
/locus_tag="HCM1163"

ORIGIN

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Score: 1528.00 Matches: 281
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Best Local Similarity: 99.65% Mismatches: 0
Query Match: 94.85% Indels: 0
DB: 9 Gaps: 0

US-10-679-246-2 (1-298) x AY402257 (1-849)

Qy 17 MetSerArgGlnThrAlaThrAlaLeuProThrGlyThrSerLysCysProSerGln 36
Db 1 ATGAGCGCGCAGCTGCTACGATTAACCACTGGCAGCTCAAGTGTCCACCATCCAG 60
Qy 37 ArgValProAlaLeuThrGlyThrThrAlaSerAsnAspLeuAlaSerLeuPheGlu 56
Db 61 AGGGTACCTGCTGACCGGCACTGCAATGCAATGCAATGCAATGCAATGCAATGCA 120
Qy 57 CysProValCysPheAspTyrValLeuProThrLeuGlnCysGlnSerGlyHisLeu 76
Db 121 TGTCTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 180
Qy 77 ValCysSerAsnCysArgProLysLeuThrCysProThrCysArgGlyProLeuGly 96
Db 181 GTTGTAGCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 240
Qy 97 SerLeuArgAsnLeuAlaMetGluLysValAlaAsnSerValLeuPheProCysLysTyr 116
Db 241 TCCATTCGCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 300
Qy 117 AlaSerSerGlyCysGluLeuThrLeuProHisThrGluLysAlaAspHisGluGluLeu 136
Db 301 GCCTCTTCTGGATGTGAATAAATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 360
Qy 137 CysGluPheArgProTyrSerCysProCysProGlyValSerCysLysTyrGlnGlySer 156
Db 361 TGTGAGTTCAGCGCTTACTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 420
Qy 157 LeuAspAlaValMetProHisLeuMetHisGlnHisLysSerIleThrThrLeuGlnGly 176
Db 421 TTGGATGCGCTGATGCGCCCACTGATGATGATGATGATGATGATGATGATGATGAT 480
Qy 177 GluAspIleValPheLeuAlaThrAspIleAsnLeuProGlyValAlaAspTrpValMet 196
Db 481 GAAGATATATAGTTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 540
Qy 197 MetGlnSerCysPheGlyPheHisPheMetLeuValLeuGluLysGlnGluLysTyrAsp 216
Db 541 ATGAGCTCTGTGTTGGCTTTTCAATTCATGTTAGTCTTGGAGAACACAGAAATATGAT 600
Qy 217 GlyHisGlnGlnPhePheAlaIleValGlnLeuIleGlyThrArgLysGlnAlaGluAsn 236
Db 601 GGTTCATCAGCAGTCTTTTGCATTTGTACAACTGATAGGAACACGCAAGCACTGA 660
Qy 237 PheAlaTyrArgLeuGluLeuAsnGlyHisArgArgLeuThrTrpGluAlaThrPro 256

Db 661 TTGTGATATCGACTGTGAGTAAATGGTCTATAGCGCGGAGTACTTGGAGAGCATCTCT 720
Qy 257 ArgSerIleHisGluGlyIleAlaThrAlaIleMetAsnSerAspCysLeuValPheAsp 276
Db 721 CGGTCTATTTCATGAGGAAATGCAACAGCAATTTATGAATAGTACTGCTAGTGTGAC 780
Qy 277 ThrSerIleAlaGlnLeuPheAlaGluAsnGlyAsnLeuGlyIleAsnValThrIleSer 296
Db 781 ACCAGCATTCACAGCTTTTGTGAGAAATGCAATTTAGGCATCAATTAATCTATTC 840
Qy 297 MetCys 298
Db 841 ATGTGT 846

RESULT 6
AY402256 849 bp DNA linear GSS 15-DEC-2003
LOCUS
DEFINITION
Pan troglodytes Slah1 gene, VIRTUAL TRANSCRIPT, partial sequence,
genomic survey sequence.
ACCESSION
AY402256
VERSION
AY402256.1 GI:39758242
KEYWORDS
GSS.
SOURCE
Pan troglodytes (chimpanzee)
ORGANISM
Pan troglodytes

REFERENCE
AUTHORS
1 (bases 1 to 849)
Clark, A.G., Tanenbaum, D.M., Civeille, D.R., Lu, F., Murphy, B.,
Todd, M.A., Tanenbaum, D.M., Civeille, D.R., Lu, F., Murphy, B.,
Ferreira, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J.,
Adams, M.D. and Cargill, M.

TITLE
Inferring nonneutral evolution from human-chimp-mouse orthologous
gene trios
JOURNAL
Science 302 (5652), 1960-1963 (2003)
PUBMED
14671302

REFERENCE
AUTHORS
2 (bases 1 to 849)
Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejarawal, A.,
Todd, M.A., Tanenbaum, D.M., Civeille, D.R., Lu, F., Murphy, B.,
Ferreira, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J.,
Adams, M.D. and Cargill, M.

TITLE
JOURNAL
Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
Rockville, MD 20850, USA
COMMENT
This sequence was made by sequencing genomic exons and ordering
them based on alignment.

FEATURES
source

1..849
/organism="Pan troglodytes"
/mol_type="genomic DNA"
/db_xref="taxon:9598"
<1..849
/gene="Slah1"
/locus_tag="HCM1163"

gene

ORIGIN

Alignment Scores:
Pred. No.: 3,3e-136 Length: 849
Score: 1521.00 Matches: 281
Percent Similarity: 99.65% Conservative: 0
Best Local Similarity: 99.65% Mismatches: 1
Query Match: 94.41% Indels: 0
DB: 9 Gaps: 0

US-10-679-246-2 (1-298) x AY402256 (1-849)

Qy 17 MetSerArgGlnThrAlaThrAlaLeuProThrGlyThrSerLysCysProSerGln 36
Db 1 ATGAGCGCGCAGCTGCTACGATTAACCACTGGCAGCTCAAGTGTCCACCATCCAG 60
Qy 37 ArgValProAlaLeuThrGlyThrThrAlaSerAsnAspLeuAlaSerLeuPheGlu 56
Db 61 AGGGTACCTGCTGACCGGCACTGCAATGCAATGCAATGCAATGCAATGCAATGCA 120

Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Wen Zon, Harvard
cDNA Library Preparation: Open Biosystems
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone Distribution: ZGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM14819 row: h column: 07
High quality sequence stop: 877.
Location/Qualifiers
1. .1180
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/mol_type="mRNA"
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/clone="IMAGE:7049721"
/tissue_type="whole body"
/lab_host="DH10B"
/clone_lib="NIH ZGC 10"
/note="Vector: pExpress1; Site 1: NotI; Site 2: EcoRV;
Bulk tissue was collected from a whole adult individual
from the Tuebingen strain. 1st strand cDNA was primed with
a Not I - oligo(dT) primer, double-stranded cDNA was
cloned into the Not I and EcoRV sites of pExpress-1.
Library was size-selected for >1 kb fragments. A
normalized version of this library is also available
(NIH ZGC 7). Library was constructed by Open Biosystems
(Huntsville, AL)."

FEATURES source

ORIGIN

Alignment Scores:		1.82e-125	Length:	1180
Pred. No.:	Score:	1412.00	Matches:	257
Percent Similarity:		99.62%	Conservative:	6
Best Local Similarity:		97.35%	Mismatches:	1
Query Match:		87.65%	Indels:	0
DB:		7	Gaps:	0

US-10-679-246-2 (1-298) x CK025134 (1-1180)	
Qy	35 SerGlnArgValProAlaLeuThrGlyThrThrAlaSerAsnAsnAspLeuAlaSerLeu 54
Db	3 TCTCAGCGCGTTTCCAACTTTGTGGGCACCAACATCCACAGCTGACCTGCCAGCCTG 62
Qy	55 PheGluCysProValCysPheAspTyrValLeuProPheLeuGlnCysGlnSerGly 74
Db	63 TTTGAGTGC CGCGTCTGTTTCGACTATGTGTGGCGCCCATCTCTGCAGTGCAGAGCGCG 122
Qy	75 HisLeuValCysSerAsnCysArgProLysLeuThrCysCysProThrCysArgGlyPro 94
Db	123 CATTTGGTGTAGCACTCGCGCCTAAACTCACTTCCTGCTGCCCCACCTGCAGAGGCGCG 182
Qy	95 LeuGlySerIleArgAsnLeuAlaMetGluLysValAlaAsnSerValLeuPheProCys 114
Db	183 CTTGGGTGCA TCCGTAATTTGGCAATGAGAAAGTGGCACTCACTAGTGTCTTTCCCTTCG 242
Qy	115 LysTyrAlaSerSerGlyCysGluIleThrLeuProHisThrGluLysAlaAspHisGlu 134
Db	243 AAGTACGCCTCATCGGGCTGCGAAGTCACTCTACCGCACACAGACAAAGCTGAACACAG 302
Qy	135 GluLeuCysGluPheArgProTyrSerCysProCysProGlyAlaSerCysLysTrpGln 154
Db	303 GAGCTTTGTGAATTTCCGCCCATCTCTTGCCCCCTGTCTCTGGCGCTCTCTGC AAGTGGCAG 362
Qy	155 GlySerLeuAspAlaValMetProHisLeuMetHisGlnHisLysSerIleThrThrLeu 174
Db	363 GGATCTCTCGAGCGCGTTTATGCCCCACTTGCTGCACACGACACAAGTCCATAACCACTTA 422
Qy	175 GlnGlyGluAspIleValPheLeuAlaThrAspIleAsnLeuProGlyValaValAspTrp 194
Db	423 CAAGGTGAGGATATAGTCTTCTCGGCCACAGACATCACTTCCTCGCTGGAGCATGTGACTGG 482
Qy	195 ValMetMetGlnSerCysPheGlyPheHisPheMetLeuValLeuGluLysGlnGluLys 214

tail, is GTGCTGGAA. This library was created for the University of Iowa Mouse Brain Molecular Anatomy Project (BMAP): 'Gene Discovery in the Developing Mouse Nervous System', supported by National Institutes of Mental Health (NIMH), Hemin Chin, Ph.D., program coordinator."

ORIGIN

Alignment Scores:

Pred. No.: 1-166-120 Length: 848
Score: 1368.00 Matches: 254
Percent Similarity: 96.97% Conservatives: 2
Best Local Similarity: 96.21% Mismatches: 4
Query Match: 84.42% Indels: 5
DB: 5 Gaps: 1

US-10-679-246-2 (1-298) x BU614872 (1-848)

QY 9 ProProTyrrValPheIleSerGluMetSerArgGlnThrAlaThrAlaLeuProThrGly 28
DB 70 CCGCCC-----ACAGAGATGAGCGGCAGACTGCTACAGATTACCACTGGC 117
QY 29 ThrSerLysCysProSerGlnArgValProAlaLeuThrGlyThrAlaSerAsn 48
DB 118 ACCTCAAGTGTCCACATCCAGAGGTACCTGCTTGACCGGCACACTGCATCAAC 177
QY 49 AsnAspLeuAlaSerLeuPheGluCysProAlaCysPheAspTyrValLeuProPhe 68
DB 178 AATGACTTGGCGAGTCTTTTGAGTGTCTGTGCTTGTGACTATGTGTGCGACCTATT 237
QY 69 LeuGlnCysGlnSerGlyHisLeuValCysSerArgCysArgProLysLeuThrCysCys 88
DB 238 CTTCACTGTGAGTGTGCGCATCTTTGTGTGAGCACTGTGCGCCCAACATTACATTTGT 297
QY 89 ProThrCysArgGlyProLeuGlySerIleArgAsnLeuAlaMetGluLysValAlaAsn 108
DB 298 CCCACTTGGCGGCCCATTTGGATTCATTCGCACTTGGCTATGAGAAAGTGGCCAC 357
QY 109 SerValLeuPheProCysLysTyrAlaSerSerGlyCysGluIleThrLeuProHisThr 128
DB 358 TCAGTACTCTTCCCTGTAAATATGCTCTCTCTGATGTGAATAACTCTGCCACACACC 417
QY 129 GluLysAlaAspHisGluGluLeuCysGluPheArgProTyrSerCysProCysProGly 148
DB 418 GAAAGCGAGACACAGAGAGCTCTGTGATTCAGGCCCTTACTCTGCCCTGCCCTGGT 477
QY 149 AlaSerCysLysTyrGlnGlySerLeuAspAlaValMetProHisLeuMetHisGlnHis 168
DB 478 GCTTCTGTAAAGTGGCAAGGCTCTTGGATGCGCTCATGCCCCACCTGATCATCAGCAC 537
QY 169 LysSerIleThrThrLeuGlnGlyGluAspIleValPheLeuAlaThrAspIleAsnLeu 188
DB 538 AAGTCCATTACCACTGCAAGGAGAGATATAGTTTCTTGCTACAGACATTAACTTT 599
QY 189 ProGlyAlaValAspTyrValMetMetGlnSerCysPheGlyPheHisPheMetLeuVal 208
DB 598 CCTGGTGTCTGTGACTGGGTGATGATGATGATGATGATGATGATGATGATGATGATG 657
QY 209 LeuGluLysGlnGluLysTyrAspGlyHisGlnGlnPhePheAlaIleValGlnLeuIle 228
DB 658 TTGGAGAAACAGANAAATATGATGTGTCATGTCATGTCATGTCATGTCATGTCATGTC 717
QY 229 GlyThrArgLysGlnAlaGluAsnPheAlaTyrArgLeuGluLeuAsnGlyHisArgArg 248
DB 718 GGNACAGCAAGCAAGCTGAAATTTTGCATATCGACTTGAGCTTAATGGTCATATGCGG 777
QY 249 ArgLeuThrTyrGluAlaThrProArgSerIleHisGluGlyIleAlaThrAlaIleMet 268
DB 778 CGATTGACTTGGAGCGACTCTCGGTCTATTTCATGAGGAATTGC-ACAGCCCATATG 836
QY 269 AsnSerAspCys 272
DB 837 AATAGTACTGTC 848

RESULT 11

BG619351

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

BG619351 824 bp mRNA linear EST 18-APR-2001
602619484F1 NIH MGC 79 Homo sapiens CDNA clone IMAGE:4733228 5',
mRNA sequence.
BG619351
BG619351.1 GI:13670722
EST.
Homo sapiens (human)
Homo sapiens
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 824)
NIH-MGC <http://mgi.mci.nih.gov/>.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgabs-r@mail.nih.gov
Tissue Procurement: CLONTECH Laboratories, Inc.
CDNA Library Preparation: CLONTECH Laboratories, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Inyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: LLC1594 row: 9 column: 21
High quality sequence stop: 748.

FEATURES

Location/Qualifiers

1..824

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/lab_host="DH10B (T1 phage-resistant)"

/clone_lib="NIH MGC 38"

/note="Organ: Placenta; Vector: pDNR-LIB (Clontech);

Site 1: Sfii (ggcgctggcc); Site 2: Sfii

(ggccatgatggcc); 5' and 3' adaptors were used in cloning

as follows: 5' adaptor sequence: 5'-CACGGCCATTATGCC-3'

and 3' adaptor sequence:

5'-ATTCTAGAGCGCGGCGCCACATG-dT(30)BN-3' (where B = A,

C, or G and N = A, C, G, or T). Average insert size 1.3

kb (range 0.5-4.0 kb). 15/15 colonies contained inserts

by PCR. This library was enriched for full-length clones

and was constructed by Clontech Laboratories (Palo Alto,

CA). Note: this is a NIH_MGC Library."

ORIGIN

Alignment Scores:

Pred. No.: 2,666-117 Length: 824

Score: 1325.00 Matches: 251

Percent Similarity: 98.44% Conservatives: 2

Best Local Similarity: 97.67% Mismatches: 2

Query Match: 82.25% Indels: 3

DB: 4 Gaps: 0

US-10-679-246-2 (1-298) x BG619351 (1-824)

QY 43 GlyThrThrAlaSerAsnAsnAspLeuAlaSerLeuPheGluCysProValCysPheAsp 62
DB 1 GGCACAACTGCATCCCAACATGACTTGGCGAGTCTTTTGGAGTGTCCAGTCTCTTGGAC 60
QY 63 TyrValLeuProPheLeuGlnCysGlnSerGlyHisLeuValCysSerAsnCysArg 82
DB 61 TATGTGTACCCGCCATCTTCAATGTGAGTGGCCATCTTGTGTGACCACTGTCCG 120
QY 83 ProLysLeuThrCysCysProThrCysArgGlyProLeuGlySerIleArgAsnLeuAla 102
DB 121 CCAAGCTCACATGTTGTCCAACTTGGCGGGCCCTTTGGGATCCATTCCCAACTTGGCT 180
QY 103 MetGluLysValAlaAsnSerValLeuPheProCysLysTyrAlaSerSerGlyCysGlu 122
DB 181 ATGGAGAAAGTGGCTAAATTCAGTACTTTTTCCCTGTAAATATGCGTCTTCTGATGTGAA 240

/clone lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/note="1st strand cDNA was primed with a NotI-oligo (at)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized."

ORIGIN

Alignment Scores:
Pred. No.: 1.2e-116 Length: 921
Score: 1319.00 Matches: 245
Percent Similarity: 93.51% Conservative: 0
Best Local Similarity: 93.51% Mismatches: 17
Query Match: 81.87% Indels: 0
Gaps: 0
DB: 5

US-10-679-246-2 (1-298) x BX355841 (1-921)

QY 123 IleThrLeuProHisThrGluValAlaSerHisGluGluLeuCysGluPheArgProTyr 142
DB 241 ATAACCTGTGCCACACAGAAACACAGACCATGAAGAGCTCTGTGATTTAGGCTTAT 300
QY 143 SerCysProCysProGluValAlaSerCysValysTyrGlnGlySerLeuAlaValMetPro 162
DB 301 TCTGTCCGTGCGCTGTGCTCTCTGTAAAGGCAAGGCTCTGTGATGCTGTATGCC 360
QY 163 HisLeuMetHisGlnHisLysSerIleThrThrLeuGlnGlyGluAspIleValPheLeu 182
DB 361 CATCTGATGCATCAGCATAGTCCATTACAACCCATACAGGAGAGATAGATTTTCTT 420
QY 183 AlaThrAspIleAsnLeuProGlyAlaValAlaSerProValMetGlnSerCysPheGly 202
DB 421 GCTACAGACATTAATCTCTCTGTGCTGTGTGATGGTGATGATGATGCTGTATGGC 480
QY 203 PheHisPheMetLeuValLeuGluLysGlnGlyLysTyrAspGlyHisGlnGlnPhePhe 222
DB 481 TTTCACCTTCATGTAGCTTTAGAGAACAGAGAAATATGATGGTCACCGAGTCTTTC 540
QY 223 AlaIleValGlnLeuIleGlyThrArgLysGlnAlaGluAsnPheAlaTyrArgLeuGlu 242
DB 541 GCAATCGTACAGCTGATAGGAACACGCAAGCAAGCTGTAATTTTGTCTTACCGACTGAG 600
QY 243 LeuAsnGlyHisArgArgLeuThrTyrGluAlaThrProArgSerIleHisGluGly 262
DB 601 CTAAATGGTCATAGGCGAGATTGACTTGGGAAGCACTCTTCGATCTATTATCATGAGGA 660
QY 263 IleAlaThrAlaIle-MetAsnSerAspCys-LeuValPheAspThrSerIleAlaGlnL 282
DB 661 ATTGCAACAGCCATTTCATGAATAGGACTGTGTAGCTTTTGACACAGCAATTGCACAGC 720
QY 282 euPheAlaGluAnGlyAsnLeuGlyIleAsnValThrIleSerMet 297
DB 721 T-TTTCAGAAAATGCAATTTAGGCTCACTGAATATATATCCAG 766

RESULT 12

BX355841 921 bp mRNA linear EST 08-APR-2004
LOCUS BX355841 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA
DEFINITION clone CS0DI004YF12 5-PRIME, mRNA sequence.

ACCESSION BX355841

VERSION BX355841.2 GI:46288391

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1. (bases 1 to 921)
Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
Full-length cDNA libraries and normalization

Unpublished (2001)

On May 5, 2003 this sequence version replaced gi:30369970.

Contact: Genoscope

Genoscope - Centre National de Sequencage

2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE

Email: seqref@genoscope.cns.fr, Web: www.genoscope.cns.fr

1st strand cDNA was primed with a NotI-oligo (at) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen. This sequence belongs to sequence cluster
8104.1

For more information about this cluster, see

http://www.genoscope.cns.fr/cdna?s=CS0DI004DC06QPL&c=8104.1.

FEATURES

source

1. .921
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0DI004YF12"
/tissue_type="PLACENTA COT 25-NORMALIZED"

EcoRI; Site 2: NotI; This normalized library was constructed from 1 million independent clones. cDNA synthesis was initiated using an oligo(dT) primer, using methylated C in the first strand synthesis reaction. Following this first strand reaction, double-stranded cDNA was blunt-ended, ligated to NotI adapters, digested with EcoRI, size-selected, and cloned into the NotI and EcoRI compatible sites of a custom modified MCS of the pBlueScript (KS+) vector. The library was normalized in 2 rounds using conditions adapted from Soares et al., PNAS (1994) 91: 9228-9232 and Bonaldo et al., Genome Research 6 (1996) 791, except that a significantly longer reannealing hybridization was used."

ORIGIN

Alignment Scores:
 Pred. No.: 5,51e-112 Length: 716
 Score: 1269.00 Matches: 232
 Percent Similarity: 99.15% Conservativeness: 0
 Best Local Similarity: 99.15% Mismatches: 2
 Query Match: 78.77% Indels: 0
 DB: 5 Gaps: 0

US-10-679-246-2 (1-298) x BU260B26 (1-716)

QY	16	GluMetSerArgGlnThrAlaThrAlaLeuProThrGlyThrSerLysCysProSer	35
DB	11	GAATGAGCGCTGACACTCTACAGCACTACTACAGGTACTTCAAGTGTACGCCATCA	70
QY	36	GlnArgValProAlaLeuThrGlyThrAlaSerAsnAspLeuAlaSerLeuPhe	55
DB	71	CAGAGGTCCTGCGCTGAGCGGCCTACAGCTTCCAAATGACTTGGCTAGTCTCTTT	130
QY	56	GluCysProValCysPheAspTyrValLeuProIleLeuGlnCysGlnSerGlyHis	75
DB	131	GAGTGTCTCTGTTTTCATGTATGTCTGCCACCAATTTCTTCAGTGTACAGTGGCCAC	190
QY	76	LeuValCysSerAsnCysArgProLysLeuThrCysCysProThrCysArgGlyProLeu	95
DB	191	CTTGCTGTAGCAACTGTGCGCCCAACTTACGTCTGTCCAACTGCGCAGCGCGCTG	250
QY	96	GlySerIleArgAsnLeuAlaMetGluLysValAlaAsnSerValLeuPheProCysLys	115
DB	251	GGCTCCATTGTAACCTGCTATGAGAGAAAGTTGCCAATTTCTGTACTGTTCCTCATGTA	310
QY	116	TyrAlaSerSerGlyCysGluLeuThrLeuProHisThrGluLysAlaAspHisGluGlu	135
DB	311	TATGCTCTTCTGGATGTGAGATAATCTGCCACACACAGAAAACAGACCATGAGGAG	370
QY	136	LeuCysGluPheArgProTyrSerCysProCysProGlyValaSerCysLysTyrGlnGly	155
DB	371	CTATGTGAGTTTAGGCTTATCTCTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	430
QY	156	SerLeuAspAlaValMetProHisLeuMetHisGlnHisLysSerIleThrThrLeuGln	175
DB	431	TCCTGATGCTCTGTAATGCCACATCTGATGCAATCAACATAAGTCAATTAACACACTTCAG	490
QY	176	GlyGluAspIleValPheLeuAlaThrAspIleAsnLeuProGlyValaValaAspTyrVal	195
DB	491	GGAGAGATATAGTGTCTTGGCAGACATTAATCTTCTGCTGCTGCTGCTGCTGCTGCTGCT	550
QY	196	MetMetGlnSerCysPheGlyPheHisPheMetLeuValLeuGluLysGlnGluLysTyr	215
DB	551	ATGATGAGTCTGTTTGGCTTTCATTTTCATGTAGTATTGGAGAAACAGGAAAAATAT	610
QY	216	AspGlyHisGlnGlnPhePheAlaIleValGlnLeuLeuGlyThrArgLysGlnAlaGlu	235
DB	611	GATGGTCAACAGAGTCTTCTTGGCATTTGATAGTGTATAGTGTATAGTGTATAGTGTAT	670
QY	236	AsnPheAlaTyrArgLeuGluLeuAsnGlyHisArgArgArg	249
DB	671	AACTTTCTTATCGACTTGAGTTAATGGTCATAGGCGGCA	712

RESULT 15

AI936347 779 bp mRNA linear EST 08-MAR-2000
 w081b1.x1 NCI CGAP Kid11 Homo sapiens cDNA clone IMAGE:2461725 3',
 similar to TR:043289.043269 HSI4H1.; mRNA sequence.
 ACCESSION AI936347
 VERSION AI936347.1 GI:5675217
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 779)
 NCI CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
 AUTHORS National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
 Tumor Gene Index
 JOURNAL Unpublished (1997)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-roman@nih.gov
 Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
 Emmert-Buck, M.D., Ph.D.
 cDNA Library Preparation: M. Bento Soares, Ph.D.
 DNA Sequencing by: Greg Lennon, Ph.D.
 Cloning Distribution: Washington University Genome Sequencing Center
 found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
 Insert Length: 1411 Std Error: 0.00
 Seq primer: -40UP from Gubco
 High quality sequence stop: 444.
 Location/Qualifiers
 1. 779
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:2461725"
 /lab_host="DH10B"
 /clone_lib="NCI CGAP Kid11"
 /note="Organ: kidney; Vector: p773D-Pac (Pharmacia) with
 a modified polylinker. Site 1: Not I; Site 2: Eco RI;
 plasmid DNA from the normalized library NCI CGAP Kid3 was
 prepared, and ss circles were made in vitro. Following HAP
 purification, this DNA was used as tracer in a subtractive
 hybridization reaction. The driver was PCR-amplified cDNAs
 from a pool of 5,000 clones made from the same library
 (clone IDs 132376-132391, 1456007-1456775, and
 1500552-1502855). Subtraction by Bento Soares and M.
 Fatima Bonaldo."

FEATURES

source

ORIGIN

Alignment Scores:
 Pred. No.: 8,33e-110 Length: 779
 Score: 1247.00 Matches: 229
 Percent Similarity: 97.46% Conservativeness: 1
 Best Local Similarity: 97.03% Mismatches: 6
 Query Match: 77.41% Indels: 0
 DB: 1 Gaps: 0

US-10-679-246-2 (1-298) x AI936347 (1-779)

QY	1	MetValIleIleIlePheLeuLeuProTyrValPheIleSerGluMetSerArgGln	20
DB	72	ATGGTTATTAATATATTTTCTCTGCTCTCTATATATTTTTCAGAAATGAGCGCTCAG	131
QY	21	ThrAlaThrAlaLeuProThrGlyThrSerLysCysProSerGlnArgValProAla	40
DB	132	ACTGCTACAGCATTACCTACCGGTACTCGAAGTGTCCACCATCCAGAGGGTGCCTGCC	191
QY	41	LeuThrGlyThrThrAlaSerAsnAspLeuAlaSerLeuPheGluCysProValCys	60
DB	192	CTGACTGGCACAACATGCTCAACATGACTTGGCGAGTCTTTTTCAGTGTCCAGTCTGC	251
QY	61	PheAspTyrValLeuProIleLeuGlnCysGlnSerGlyHisLeuValCysSerAsn	80

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Db      252  TTTGACTATGTGTTACCGCCCATCTTCAATGTCAGAGTGGCCATCTTGTGTTAGCAAC 311
Qy      81   CysArgProLysLeuThrCysCysProThrCysArgGlyProLeuGlySerIleArgAsn 100
Db     312  TGTGGCCCAAGCTACATGTTGTCCAACTTGCGCGGGCCCTTTGGGATCCATTGCAAC 371
Qy     101  LeuAlaMetGluLysValAlaAsnSerValLeuPheProCysLysTyrAlaSerSerGly 120
Db     372  TTGGCTATCGAGAAAGTGGCTAATTCAGTACTTTTCCCTGTAAATATGCGTCTTCTGGA 431
Qy     121  CysGluIleThrLeuProHisThrGluLysAlaAspHisGluLysCysGluPheArg 140
Db     432  TGTGAATAACTCTGCCACACACAGAAAAGCAGACCATGAAGAGCTCTGTGAGTTAGG 491
Qy     141  ProTyrSerCysProCysProGlyAlaSerCysLysTyrPheGlnGlySerLeuAspAlaVal 160
Db     492  CCTTATTCTGTCGCGCTGCTGCTCTCTGTAAATGGCAGGCTCTCTGGATGCTGTA 551
Qy     161  MetProHisLeuMetHisGlnHisLysSerIleThrThrLeuGlnGlyGluAspIleVal 180
Db     552  ATGCCCCATCTGATGCATCAGCATAGTCCATTACAAACCTACAGGAGAGGATATAGTT 611
Qy     181  PheLeuAlaThrAspIleAsnLeuProGlyAlaValAspTyrValMetMetGlnSerCys 200
Db     612  NNTCTTGCTACAGACATTAACTTCTGCTGCTGTTGACTGGGTGATGATGAGTCCTGT 671
Qy     201  PheGlyPheHisPheMetLeuValLeuGluLysGlnGluLysTyrAspGlyHisGlnGln 220
Db     672  TTTGGCTTTCACTTTTCATGCTAGTCTAGAGAANCAGAAAAATACGATGTCACCCAGAG 731
Qy     221  PhePheAlaIleValGlnLeuIleGlyThrArgLysGlnAlaGluAsn 236
Db     732  TTCTTTTCGCATCGTACAGCTGATAGGAACACGTCAGCAAGCTGAAAAAT 779
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Search completed: April 25, 2005, 09:25:45
Job time : 3698 secs

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GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: April 25, 2005, 06:45:00 ; Search time 204 Seconds
(without alignments)
2390.247 Million cell updates/sec

Title: US-10-679-246-2

Perfect score: 1611

Sequence: 1 MWIIIFLLPPYVFISEMSRQ.....IAQLFAENGILGINTWISM 298

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:

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-O=/cgn2_1/USPTO_spool/US10679246/runat_22042005_185511_7719/app_query.fasta_1.455
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-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALLIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15
-MODES=LOCAL -OUTFMT=p2o -NORM=ext -HEAPSIZ=500 -MINLEN=0 -MAXLEN=2000000000
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-NO MMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSBLOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

Issued Patents NA:
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5: /cgn2_6/prodata/1/ina/6C_COMB.seq:
6: /cgn2_6/prodata/1/ina/6D_COMB.seq:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1611	100.0	1274	4	US-09-591-694-1
2	1611	100.0	2440	4	US-09-023-655-588
3	1489	92.4	1884	4	US-09-544-618-11
4	447	27.7	1420	3	US-09-362-506-1
5	436	26.4	257	4	US-09-016-434-397
6	336	20.2	1036	3	US-09-325-932A-39
7	325	20.2	1425	3	US-09-325-932A-200
8	217	13.5	8050	3	US-09-491-362-11
9	217	13.5	8050	3	US-09-874-562-11
10	130.5	8.1	2327	4	US-09-270-767-13738
11	128.5	8.0	2308	4	US-09-270-767-29760
12	121	7.5	1463	4	US-09-620-312D-23

13	112.5	7.0	2854	2	US-08-724-394A-17	Sequence 17, Appl
14	111	6.9	1260	4	US-09-949-016-1949	Sequence 1949, Ap
15	108.5	6.7	2248	1	US-08-639-237-1	Sequence 1, Appl
16	108.5	6.7	2248	1	US-08-975-405-1	Sequence 1, Appl
17	108.5	6.7	2264	3	US-09-167-109-6	Sequence 6, Appl
18	108	6.7	1029	4	US-09-270-767-13746	Sequence 13746, A
19	107.5	6.7	563	3	US-09-325-932A-40	Sequence 40, Appl
20	106	6.6	1335	4	US-09-774-528-33	Sequence 33, Appl
21	104.5	6.5	1926	3	US-09-249-588A-2	Sequence 2, Appl
22	104.5	6.5	1926	3	US-09-410-399-3	Sequence 3, Appl
23	104.5	6.5	2580	3	US-09-050-863-2	Sequence 2, Appl
24	104.5	6.5	2580	3	US-09-359-081-2	Sequence 2, Appl
25	104.5	6.5	2943	3	US-09-221-017B-153	Sequence 153, App
26	104.5	6.5	5452	2	US-09-130-114-1	Sequence 1, Appl
27	104.5	6.5	8705	4	US-09-647-344A-14	Sequence 14, Appl
28	104.5	6.5	9600	3	US-09-910-647-1	Sequence 1, Appl
29	104.5	6.5	9600	3	US-09-620-925-1	Sequence 1, Appl
30	104.5	6.5	10596	1	US-07-884-811-15	Sequence 15, Appl
31	104.5	6.5	10596	1	US-07-885-971-15	Sequence 15, Appl
32	104.5	6.5	10596	1	US-08-087-783A-15	Sequence 15, Appl
33	104.5	6.5	10596	1	US-08-194-088B-15	Sequence 15, Appl
34	104.5	6.5	10596	2	US-08-194-087-15	Sequence 15, Appl
35	104.5	6.5	10596	5	PCT-US93-04648-15	Sequence 15, Appl
36	104.5	6.5	16080	4	US-09-724-566A-48	Sequence 48, Appl
37	104.5	6.5	16080	4	US-09-471-669A-48	Sequence 48, Appl
38	103.5	6.4	1329	4	US-09-270-767-13968	Sequence 13968, A
39	103.5	6.4	8572	4	US-09-949-016-13691	Sequence 13691, A
40	103	6.4	1023	4	US-09-902-540-3824	Sequence 3824, Ap
41	103	6.4	13807	3	US-09-052-469-5	Sequence 5, Appl
42	103	6.4	13807	4	US-08-422-582-5	Sequence 5, Appl
43	103	6.4	13807	4	US-09-052-262-5	Sequence 5, Appl
44	103	6.4	13941	4	US-09-799-451-341	Sequence 341, App
45	103	6.4	14060	3	US-08-658-136-4	Sequence 4, Appl

ALIGNMENTS

RESULT 1

US-09-591-694-1

; Sequence 1, Application US/09591694

; Patent No. 6638734

; GENERAL INFORMATION:

; APPLICANT: John C. Reed

; APPLICANT: Shu-ichi Matsuzawa

; TITLE OF INVENTION: Nucleic Acid Encoding Proteins Involved

; TITLE OF INVENTION: in Protein Degradation, Products and Methods Related Thereto

; FILE REFERENCE: P-LJ 4220

; CURRENT APPLICATION NUMBER: US/09/591,694

; CURRENT FILING DATE: 2000-06-09

; EARLIER FILING DATE: 1999-06-11

; NUMBER OF SEQ ID NOS: 49

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 1

; LENGTH: 1274

; TYPE: DNA

; ORGANISM: Homo sapien

; FEATURE:

; NAME/KEY: CDS

; LOCATION: (274)...(1167)

US-09-591-694-1

Alignment Scores:

Pred. No.: 1.45e-171 Length: 1274

Score: 1611.00 Matches: 298

Percent Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0

Query Match: 100.00% Indels: 0

DB: 4 Gaps: 0

US-10-679-246-2 (1-298) x US-09-591-694-1 (1-1274)

Qy 1 MetValIleIlePheLeuLeuProProTyValPheIleSerGluMetSerArgGln 20

```
Db 274 ATGGTTATATATATTTCTCTGCTCTCTATGATTTATTTTCAGAAATGAGCGCTCAG 333
Qy 21 ThrAlaThrAlaLeuProThrGlyThrSerLysCysProProSerGlnArgValProAla 40
Db 334 ATGCTTACAGCAATACCTACCGGTACTCGAAGTGTCCACCATCCAGAGGGTGCCTGCC 393
Qy 41 LeuThrGlyThrThrAlaSerAsnAspLeuAlaSerLeuPheGluCysProValCys 60
Db 394 CTGACTGGCACAACTGCATCCAAATGACTTGGGAGTCTTTTGAGTGTCCAGTCTGC 453
Qy 61 PheAspTyrValLeuProProLeuLeuGlnCysGlnSerGlyHisLeuValCysSerAsn 80
Db 454 TTTGACTATGTGTACCGGCCATCTTCAATGTCAGAGTGGCCATCTTTGTTGTAGCAAC 513
Qy 81 CysArgProLysLeuThrCysCysProThrCysArgGlyProLeuGlySerIleArgAsn 100
Db 514 TGTGCGCCAAAGCTCACATGTTGTCCAACTTGGCGGGGCCCTTTGGATCCATTCGCAAC 573
Qy 101 LeuAlaMetGluLysValAlaAsnSerValLeuPheProCysLysTyrAlaSerSerGly 120
Db 574 TTGGCTATGAGAAAGTGGTAAATTCAGTACTTTTCCCTGTAAATATCGCTCTTCTGA 633
Qy 121 CysGluIleThrLeuProHisThrGluLysAlaAspHisGluLeuLeuCysGluPheArg 140
Db 634 TGTGAATAACTCTGCCACACACAGAAAGACACCATGAGAGCTCTGTGAGTTAGG 693
Qy 141 ProTyrSerCysProCysProGlyAlaSerCysLysTyrGlnGlySerLeuAspAlaVal 160
Db 694 CCTTATCTCTGTCGTCGCTGTCTTCTGTAAATGGCAAGCTCTCTGGATGCTGTA 753
Qy 161 MetProHisLeuMetHisGlnHisLysSerIleThrThrLeuGlnGlyGluAspIleVal 180
Db 754 ATGCCCATCTGATGCATCAGCATAGTTCATTTACAACTTACAGGAGGAGGATATAGTT 813
Qy 181 PheLeuAlaThrAspIleAsnLeuProGlyValAlaValAspTyrValMetGlnSerCys 200
Db 814 TTTCTTGCTACAGCAATTAATCTTCTGGTGTCTTTGACTGGGTGATGATGCAGTCTGT 873
Qy 201 PheGlyPheHisPheMetLeuValLeuGluLysGlnGluLysTyrAspGlyHisGlnGln 220
Db 874 TTTGGCTTTTCATCTCATGTGTAGTCTTAGAGAAACAGAGAAATACGATGTCACACG 933
Qy 221 PhePheAlaIleValGlnLeuIleGlyThrArgLysGlnAlaGluAsnPheAlaTyrArg 240
Db 934 TTTCTTCCAACTGATACAGCTGATAGGAAACAGCAAGCAAGCTGAAATTTTGTACCGA 993
Qy 241 LeuGluLeuAsnGlyHisArgArgGlyLeuThrTyrGluAlaThrProArgSerIleHis 260
Db 994 CTTGAGCTAATGGTCATAGCGCAGATTGACTTTGGGAGCGACTCTCTCGATCTATTCT 1053
Qy 261 GluGlyIleAlaThrAlaIleMetAsnSerAspCysLeuValPheAspThrSerIleAla 280
Db 1054 GAAGGAATTCACACAGCCATTAATGAATAGCGACTGTCTAGTCTTTGACACACGATGCA 1113
Qy 281 GlnLeuPheAlaGluAsnGlyAsnLeuGlyIleAsnValThrIleSerMetCys 298
Db 1114 CAGCTTTTTCAGAAATATGCAATTTAGGCATCATATGACTATTTCATGTTGT 1167

RESULT 2
US-09-023-655-588
; Sequence 588, Application US/09023655
; Patent No. 6607879
; GENERAL INFORMATION:
; APPLICANT: Cocks, Benjamin G.
; APPLICANT: Susan G. Stuart
; APPLICANT: Jeffrey J. Seilhamer
; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL GENE
; TITLE OF INVENTION: EXPRESSION
; NUMBER OF SEQUENCES: 1508
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
; STREET: 3174 PORTER DRIVE
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; CITY: PALO ALTO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/023,655
; FILING DATE: HEREWITH
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Zeller, Karen J.
; REGISTRATION NUMBER: 37,071
; REFERENCE/DOCKET NUMBER: PA-0001 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 855-0555
; TELEFAX: (650) 845-4166
; INFORMATION FOR SEQ ID NO: 588:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2440 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: SPLNFET01
; CLONE: 29244
; US-09-023-655-588

Alignment Scores:
Pred. No.: 4,15e-171 Length: 2440
Score: 1611.00 Matches: 298
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: Gaps: 0

US-10-679-246-2 (1-298) x US-09-023-655-588 (1-2440)
Qy 1 MetValIleIleIlePheLeuLeuProProTyrValPheIleSerGluMetSerArgGln 20
Db 507 ATGGTTATATATATTTCTCTGCTCTCTATGATTTATTTTCAGAAATGAGCGCTCAG 566
Qy 21 ThrAlaThrAlaLeuProThrGlyThrSerLysCysProProSerGlnArgValProAla 40
Db 567 ACTGCTACAGCATTAACCTACCGGTACTCGAAGTGTCCACCATCCAGAGGGTGCCTGCC 626
Qy 41 LeuThrGlyThrThrAlaSerAsnAspLeuAlaSerLeuPheGluCysProValCys 60
Db 627 CTGACTGGCACAACTGCATCCAAATGACTTTGGCGAGTCTTTTGGAGTGTCCAGTCTGC 686
Qy 61 PheAspTyrValLeuProProIleLeuGlnCysGlnSerGlyHisLeuValCysSerAsn 80
Db 687 TTTGACTATGTGTACCGGCCATTTCTCAATGTGCAGATGGCCATCTTTGTTGTAGCAAC 746
Qy 81 CysArgProLysLeuThrCysCysProThrCysArgGlyProLeuGlySerIleArgAsn 100
Db 747 TGTGCGCCAAAGCTCACATGTTGTCCAACTTGGCGGGGCCCTTTGGGATCCATTCGCAAC 806
Qy 101 LeuAlaMetGluLysValAlaAsnSerValLeuPheProCysLysTyrAlaSerSerGly 120
Db 807 TTGGCTATGAGAAAGTGGTAAATTCAGTACTTTTCCCTGTAAATATGCGTCTTCTGGA 866
Qy 121 CysGluIleThrLeuProHisThrGluLysAlaAspHisGluLeuCysGluPheArg 140
Db 867 TGTGAATAACTCTGCCACACACAGAAAGACGACCATGAGAGCTCTGTGAGTTAGG 926
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QY 141 ProTyrSerCysProCysProGlyAlaSerCysLysTrpGlnGlySerLeuAspAlaVal 160
Db 927 CCTATTCTCTGTCGCGCCCTGCTGCTCTCTGTAATGGCAAGCTCTCTGGAATGCTGA 986
QY 161 MetProHisLeuMetHisGlnHisLysSerIleThrThrLeuGlnGlyGluAspIleVal 180
Db 987 ATGCCCCATCTGATGATCAGCATAGTCCATTAACCCCTACAGGAGAGGATATAGTT 1046
QY 181 PheLeuAlaThrAspIleAsnLeuProGlyAlaValAspTrpValMetMetGlnSerCys 200
Db 1047 TTTCTTGCTACAGACATTAATCTCTCTGCTGCTGTTGACTGGGTGATGATGCACTCTGT 1106
QY 201 PheGlyPheHisPheMetLeuValLeuGluLysGlnGlyLysTrpAspGlyHisGlnGln 220
Db 1107 TTTGGCTTTTCACTTCATGTTAGTCTTAGAGAAACAGGAAATAACGATGTCACCAAGCAG 1166
QY 221 PhePheAlaIleValGlnLeuIleGlyThrArgLysGlnAlaGluAsnPheAlaTyrArg 240
Db 1167 TTTCTTGGCAATCTGACAGCTGATAGGACACGCAAGCAAGCTGAAATTTTGTTCACCGA 1226
QY 241 LeuGluLeuAsnGlyHisArgArgArgLeuThrTrpGluAlaThrProArgSerIleHis 260
Db 1227 CTTGAGCTAAATGGTCATAGGCGCAGATTGACTTTGGGAAGCGACTCTCGATCTATTCTAT 1286
QY 261 GluGlyIleAlaThrAlaIleMetAsnSerAspCysLeuValPheAspThrSerIleAla 280
Db 1287 GAAGGAATTTGCAACAGCCATTATGAATAGCGACTGTCTAGTCTTTGACACCAAGCATTGCA 1346
QY 281 GlnLeuPheAlaGluAsnGlyAsnLeuGlyIleAsnValThrIleSerMetCys 298
Db 1347 CAGCTTTTTCAGAAAATGGCAATTTAGGCATCAATGTAATTAATTTTCAATGTGT 1400
RESULT 3
US-09-544-618-11
; Sequence 11, Application US/09544618
; Patent No. 6503502
; GENERAL INFORMATION:
; APPLICANT: Telerman, Adam
; APPLICANT: Amson, Robert
; APPLICANT: Cohen, Daniel
; TITLE OF INVENTION: NUCLEOTIDE SEQUENCES, PROTEINS, DRUGS AND DIAGNOSTIC
; FILE OF INVENTION: AGENTS OF USE IN TREATING CANCER
; FILE REFERENCE: 065691-0139
; CURRENT APPLICATION NUMBER: US/09/544,618
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 11
; LENGTH: 1884
; TYPE: DNA
; ORGANISM: TSAP 3
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(846)
US-09-544-618-11
Alignment Scores:
Pred. No.: 1.56e-157 Length: 1884
Score: 1489.00 Matches: 280
Percent Similarity: 99.29% Conservative: 1
Best Local Similarity: 98.94% Mismatches: 1
Query Match: 92.43% Indels: 2
DB: 4 Gaps: 0
US-10-679-246-2 (1-298) x US-09-544-618-11 (1-1884)
QY 17 MetSerArgGlnThrAlaThrAlaLeuProThrGlyThrSerLysCysProProSerGln 36
Db 1 ATGAGCGGTGACACTGCTACAGCATTAACCTACCGGTACCTCGAAGTGTCCACCATCCAG 60
QY 37 ArgValProAlaLeuThrGlyThrAlaSerAsnAspLeuAlaSerLeuPheGlu 56
Db 61 AGGGTGCCCTGACCTGGCACAACCTGCAATGCAATGACTTGGCGAGTCTTTTGTAG 120
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QY 57 CysProValCysPheAspTyrValLeuProIleLeuGlnCysGlnSerGlyHisLeu 76
Db 121 TGTCCAGTCTGCTTTGACTATGTGTACCGCCCATTTCTTCAATGTGAGAGTGCCATCTT 180
QY 77 ValCysSerAsnCysArgProLysLeuThrCysCysProThrCysArgGlyProLeuGly 96
Db 181 GTTTGTAGCACTGTGCGCCCAAGCTCAGTGTGTCCAACTTTGCGGGGCCCTTTGGGA 240
QY 97 SerIleArgAsnLeuAlaMetGluLysValAlaAsnSerValLeuPheProCysLysTyr 116
Db 241 TCCATTGCAACTTGGCTATGGAAAGTGGCTAATTCAGTACTTTTCCCTGTAAATAT 300
QY 117 AlaSerSerGlyCysGluLeuThrLeuProHisThrGluLysAlaAspHisGluGluLeu 136
Db 301 GCGTCTTCTGGATGTGAATAAATCTCTGCCACACACAGAAAAAGCAGACCATGAAGAGCTC 360
QY 137 CysGluPheArgProTyrSerCysProCysProGlyAlaSerCysLysTrpGlnGlySer 156
Db 361 TGTGAGTTTGTAGGCTTTATTCCTGTCGTCGCCCTGCTGCTTCTGTAAATGGCAAGCTCT 420
QY 157 LeuAspAlaValMetProHisLeuMetHisGlnHisLysSerIleThrThrLeuGlnGly 176
Db 421 CTGGATGCTGTAATGCCCATCTGATGCATCAGCATAAGTCCATTACACCCCTACAGGGA 480
QY 177 GluAspIleValPheLeuAlaThrAspIleAsnLeuProGlyAlaValAspTrpValMet 196
Db 481 GAGGATATAGTTTCTTCTGCTACAGACATTAATCTTCTGCTGCTGCTGCTGCTGCTGCTG 540
QY 197 MetGlnSerCysPheGlyPheHisPheMetLeuValLeuGluLysGlnGlyLysTyrAsp 216
Db 541 ATGCAGTCTCTGTTTGGCTTTTCACTTCATGTTAGTCTTAGAGAAACAGAGAAAAATACGAT 600
QY 217 GlyHisGlnGlnPhePheAlaIleValGlnLeuIleGlyThrArgLysGlnAlaGluAsn 236
Db 601 GGTCAACAGCAGTCTTCTGCAATCTGATAGCTGATAGGAAACAGCAGCAAGCTGAAAT 660
QY 237 PheAlaTyrArgLeuGluLeuAsnGlyHisArgArgArgLeuThrTrpGluAlaThrPro 256
Db 661 TTTGCTTACCGACTTGAGCTAAATGCTCATAGCGCAGATTGACTTGGGAAGCGACTCTCT 720
QY 257 ArgSerIleHisGluGlyIleAlaThrAlaIleMetAsnSerAspCysLeuValPheAsp 276
Db 721 CGATCTATTATGAAAGAAATGCAACAGCCATTATGAATAGCGACTGTCTAGTCTTTGAC 780
QY 277 ThrSerIleAlaGlnLeuPheAlaGluAsnGlyAsnLeuGlyIleAsnValThrIleSe 296
Db 781 CC-AGCATTCACAGCTTTTTCGACAAATGGCAATTTAGGCATCAATGTAATTAATTTTC 839
QY 296 rMetCys 298
Db 840 CATGTGT 846
RESULT 4
US-09-362-506-1
; Sequence 1, Application US/09362506
; Patent No. 6111167
; GENERAL INFORMATION:
; APPLICANT: Mahajan, Pramod B.
; TITLE OF INVENTION: Maize SINA Orthologue-1 and Uses Thereof
; FILE REFERENCE: 0936
; CURRENT APPLICATION NUMBER: US/09/362,506
; CURRENT FILING DATE: 1999-07-27
; EARLIER APPLICATION NUMBER: 60/100,258
; EARLIER FILING DATE: 1998-09-14
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 1420
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: CDS
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; LOCATION: (202)...(1140)
US-09-362-506-1

Alignment Scores:
Pred. No.: 3,128-40 Length: 1420
Score: 447.00 Matches: 103
Percent Similarity: 53.65% Conservative: 44
Best Local Similarity: 37.59% Mismatches: 101
Query Match: 27.75% Indels: 26
DB: 9 Gaps: 9

US-10-679-246-2 (1-298) x US-09-362-506-1 (1-1420)

QY 39 ProAlaLeuThrGlyThrAlaSerAsnAspLeuAlaSer----- 53
DB 316 CCGTGTCTACATCGCATCGCTAGCATGTTCATGTCGTCGTGTGCTTGAAT 375
QY 54 ---LeuPheGluCysProValCysPheAspTyrValLeuProPheLeuGlnCysGln 72
DB 376 GATTGCTCGAATGCCAGTGTGTACCAACTCGATCGCGCCACCTATCTCCAGTGCCTCA 435
QY 73 SerGlyHisLeuValCysSerAsnCysArgProLysLeu---ThrCysCysProThrCys 91
DB 436 AATGGCCACACGATCTCTCTAGTTCAGACAGGAGTAGAGAACCATTCGCCAACCTGT 495
QY 92 ArgGlyProLeuGlySerLeuArgAsnLeuAlaMetGluLysValAlaAsnSerValLeu 111
DB 496 CGCCAGAACTGGAAACATCATCAGGTCTCTCGAGAGGTGGCAGAGCACTCCAG 555
QY 112 PheProCysLysTyrAlaSerSerGlyCysGluLeuThrLeuProHisThrGluLysAla 131
DB 556 CTTCCGTGCAAGTACAGAGCAGCGAGATGCCAGAGATCCACCCATACAGCAAACTG 615
QY 132 AspHisGluGluLeuCysGluPheArgProTyrSerCysProCysProGlyAlaSerCys 151
DB 616 AAGCAGCAGAGCTCTGACGTTTCAGCGCTCAGCTGCGCGTACGACGAGTTCGAGTCC 675
QY 152 LysTrpGlnGlySerLeuAspAlaValMetProHisLeuMetHisGlnHisLysSerIle 171
DB 676 CTGATCGCAGCAGCGTCCGCTTCCTGTTGTTCCATCTCTATCAACACCATAG---GTG 732
QY 172 ThrThrLeuGlnGlyGluAspIleValPheLeuAlaThrAspIleAsnLeuProGlyAla 191
DB 733 GACTTGACAGGGCTGCACGTTCAACCCGCTACGTGAAGCCCAAC---CGTACGAG 789
QY 192 ValAsp-----TrpValMet---MetGlnSerCysPheGlyPheHisPheMetLeu 207
DB 790 GTGGAGAAATGCCAGTGTGATCTCACTGTCTTCAAGTGTTCGGGAGCAGCTTCTGCCCTG 849
QY 208 -----ValLeuGluLysGlnGluLysTyrAspGlyHisGlnGlnPhePhe 222
DB 850 CACTTCAGCGGCTGCTGCTGGGATGCGCGCGGTGTAC-----ATG 891
QY 223 AlaIleValGlnLeuIleGlyThrArgLysGlnAlaGluAsnPheAlaTyrArgLeuGlu 242
DB 892 GCGTTCCTGCGGTTTCATGGCGAGGAGAGCGAGCGCGGCGGTTCGGGTACAGCCTGGAG 951
QY 243 LeuAsnGlyHisArgArgLeuThrTrpGluAlaThrProArgSerIleHisGluGly 262
DB 952 GTGGCGCGGCGCGGCGGAGAGTACGTGGCAGGCGACGCGCGGAGCGGTACGAGGACAGC 1011
QY 263 IleAlaThrAlaIleMetAsnSerAspCysLeuValPheAspThrSerIleAlaGlnLeu 282
DB 1012 CACCGAAGGTGCGGACAGCTTCAGCGGCTCATCTCCACAGGAACATGGCGCTCTTC 1071
QY 283 PheAlaGluAsnGly-----AsnLeuGlyIleAsnValThr 294
DB 1072 TTCTCGGCGCGCGCAGCAGGAGCTCAAGTTCGCGGTCAAC 1113

RESULT 5
US-09-016-434-397
; Sequence 397, Application US/09016434
; Patent No. 6500938

GENERAL INFORMATION:
APPLICANT: Janice Au-Young
APPLICANT: Jeffrey J. Seilhamer
TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING
TITLE OF INVENTION: PATHWAY GENE EXPRESSION
NUMBER OF SEQUENCES: 1490
CORRESPONDENCE ADDRESS:
ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
STREET: 3174 PORTER DRIVE
CITY: PALO ALTO
STATE: CALIFORNIA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/016,434
FILING DATE: HEREWITH
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Zeller, Karen J.
REGISTRATION NUMBER: 37,071
REFERENCE/DOCKET NUMBER: PA-0002 US
TELEPHONE: (650) 855-0555
TELEFAX: (650) 845-4166
INFORMATION FOR SEQ ID NO: 397:
SEQUENCE CHARACTERISTICS:
LENGTH: 257 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: BRAITUT03
CLONE: 2113436
US-09-016-434-397

Alignment Scores:
Pred. No.: 4,588-39 Length: 257
Score: 426.00 Matches: 73
Percent Similarity: 92.94% Conservative: 6
Best Local Similarity: 85.88% Mismatches: 6
Query Match: 26.44% Indels: 0
DB: 4 Gaps: 0

US-10-679-246-2 (1-298) x US-09-016-434-397 (1-257)

QY 120 GlyCysGluIleThrLeuProHisThrGluLysAlaAspHisGluLeuCysGluPhe 139
DB 3 GCGTGTCTCCTGACCTCCATCGGAAACCCAGACATGACACATATGTGAATAC 62
QY 140 ArgProTyrSerCysProCysProGlyAlaSerCysLysTrpGlnGlySerLeuAspAla 159
DB 63 CGTCCCTACTCTCTGCCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 122
QY 160 ValMetProHisLeuMetHisGlnHisLysSerIleThrThrLeuGlnGlyGluAspIle 179
DB 123 GTGATGTCCCATCTCATGACGCCCAAGAGCAITACCACCTTCAGGAGAGACATC 182
QY 180 ValPheLeuAlaThrAspIleAsnLeuProGlyAlaValAspTrpValMetMetGlnSer 199
DB 183 GTCTTTCTAGCTACACACATTAACCTTCCAGGCGGCTGCTGCTGCTGCTGCTGCTGCTGCT 242
QY 200 CysPheGlyPheHis 204
DB 243 TGTTTGGCCATCAC 257

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Db	528	GCCTCCGAATGCAAGCTAGTTCGAGATATTCCTTTTGGTGGCTCATTTAAGACATGAT	587	TCGGCTAAGTTGTTGGATCTTGATGTTCTTGACGTCCGGTTTCTTCGAGCCGCTCACT	6451
Qy	168	HisLys-	173	ProPro-	67
Db	588	CACAAAGTTTATATGATCAATAATAGTTGCACCTTTTGATCATCGATATGTAAGTCAAATCCA	647	ATTCCTACCTTTCAGGTTATGTTTGAACCTGCAATGCAATTTATTTGTTTCATGTGACA	6511
Qy	174	LeuGlnGlyGluAspIleValPheLeuAlaThrAspIleAsnLeuProGlyAlaValAsp	193	TTTGAATTCGCTTTTGTAAATATTTTATTTAATACGGCTTTTGATTGTATCTCGTTTG	6571
Db	648	CTCAGGTTGAGAATGCTATTTGGATGCCAACTGTAATCAAT	689	-----IleLeuGlnCysGlnSerGlyHisLeuValCysSerAsnCysArgProIys	84
Qy	194	TrpValMetMetGlnSerCysPheGlyPheHisPheMetLeuValLeuGlnGlyGlnGlu	213	GTATATTATGCGTTTCAGTTCATGATGATGACATAGTTTGCATTTTGCATTTTGCCTCCAAA	6631
Db	690	-----TGTITTTGGCAATCTTTTGTCTACATTTGAA	728	85 LeuThr-----Cys---CysProThrCysArgGlyProLeuGlySerIleArgAsnLeu	101
Qy	214	LysTyrAspGlyHisGlnGlnPheAlaIleValGlnLeuLeuGlyThrArgIysGln	233	6632 GTGAGTAAACAGTCCCTCGTCTGGGTGATTTACCCATTTGTAATAACGCGATGCTTC	6691
Db	729	CTATTAGACATGCCCTCTATATATATAGCTTTCTGATTTTTCATGGAGATGATAATGAA	788	102 AlaMetGluIysValAlaAsnSerValLeuPheProCysLysTyrAlaSerSerGlyCys	121
Qy	234	AlaGluAsnPheAlaTyrArgLeuGluLeuAsnGlyHisArgArgLeuThrTrpGlu	253	6692 GCAATGGAGAGGGTTCTCGAATCAGCCTTTTCTCATGTCAAAATACTGAGTTTGGCTGC	6751
Db	789	GCTAAAAACTTATAGCTATTGCTCGAGACTGGAGGCAATGGTCGAAACTGATTTGGCAT	848	122 GluIleThrLeuProHisThrGluLysAlaAspHisGluGluLeuCysGluPheArgPro	141
Qy	254	AlaThrProArgSerIleHisGluGlyIleAlaThrAlaIleMetAsnSerAspCysLeu	273	6752 ACAAAAAGTGTCTTATGAAAAAGTGTCAAGTCACGAAAGGATGCAACTACTCT	6808
Db	849	GGGTTCTCTCGAAGCATCAGATTTCTACAGGAAAGTTTCATGACAGTAGTACGACGACTA	908	142 TyrSerCysProCysProGlyAlaSerCysLysTrpGlnGlySerLeuAspAlaValMet	161
Qy	274	ValPheAspThrSerIleAlaGlnLeuPheAlaGluAsnGlyAsnLeuGly	292	6809 ---CAATGCTTTGCCCTTAACCTCGAATGCAATTACACTGGCTCATATAACATCATCTAC	6865
Db	909	ATTATACAAAGAGATGCGCA---CTCTTTTCTCAGGTGGTGACATAAATGAATTGAAT	965	162 ProHisLeuMetHisGlnHisSerIleThrThrLeuGlnGlnGlyGluAspIleValPhe	181
Qy	293	ValThrIleSer	296	6866 GGTCACTTTATGCTGCGCATCTTTTACAATAGTAGCATCGTTTCTCCAAATGGGATAT	6925
Db	966	CTTAGATTGACA	977	182 LeuAlaThrAsp-----IleAsnLeuProGlyAlaValAspTrpValMetMetGlnSer	199
RESULT 8					6982
US-09-491-362-11					200
; Sequence 11, Application US/09491362					7030
; Patent No. 6281017					239
; GENERAL INFORMATION:					7090
; APPLICANT: Croteau, Rodney B					254
; TITLE OF INVENTION: 1-DEOXY-D-XYLULOSE-5-PHOSPHATE REDUCTOISOMERASE, AND					7135
; FILE REFERENCE: WSUR14977					
; CURRENT APPLICATION NUMBER: US/09/491,362					
; CURRENT FILING DATE: 2000-01-26					
; EARLIER APPLICATION NUMBER: 60/118,349					
; EARLIER FILING DATE: 1999-02-03					
; NUMBER OF SEQ ID NOS: 13					
; SOFTWARE: PatentIn Ver. 2.0					
; SEQ ID NO 11					
; LENGTH: 8050					
; TYPE: DNA					
; ORGANISM: Arabidopsis thaliana					
US-09-491-362-11					
Alignment Scores:					
Pred. No.:	4.46e-13	Length:	8050		
Score:	217.00	Matches:	65		
Percent Similarity:	40.07%	Conservative:	46		
Best Local Similarity:	23.47%	Mismatches:	108		
Query Match:	13.47%	Indels:	58		
DB:	3	Gaps:	10		
US-10-679-246-2 (1-298) x US-09-491-362-11 (1-8050)					
Qy	27	ThrGlyThrSerLysCysProSerGlnArgValProAlaLeuThrGlyThrThrAla	46	240 ArgLeu-----GluLeuAsnGlyHisArgArgLeuThrTrpGluAla	254
Db	6332	ACATCAAAAGAAAAAGCTCTCACCGCAAAAGAACGATATGAGAGATGAACACGA	6391	7091 CGTCTTCGTATAGTAGTACGCGACAT-----AATGTACTTACGAATCA	7135
Qy	47	SerAsnAspLeu---AlaSerLeuPheGluCysProValCysPheAspTyrValLeu	65		

Alignment Scores:

Pred. No.: 4,46e-13 Length: 8050
Score: 217.00 Matches: 65
Percent Similarity: 40.07% Conservative: 46
Best Local Similarity: 23.47% Mismatches: 108
Query Match: 13.47% Indels: 58
DB: 3 Gaps: 10

US-10-679-246-2 (1-298) x US-09-874-562-11 (1-8050)

QY 27 ThrGlyThrSerLysCysProSerGlnArgValProAlaLeuThrGlyThrAla 46
DB 6332 ACATCAAAAAGAAAGCTCTCCCGCAAAAGAACGATGGAGAAATGAACACGA 6391
QY 47 SerAsnAsnAspLeu---AlaSerLeuPheGluCysProValCysPheAspTyrValLeu 65
DB 6392 TCGGCTAAGTTGTTGGATCTTGATGTTCTTGACTGTCGGTTGCTTCGAGCGCTCACT 6451
QY 66 ProPro----- 67
DB 6452 ATTCCTACCTTTCCAGGTATGTTTGAACCTGCATGCAATTTATTTTGTTCATGTGACA 6511
QY 67 ----- 67
DB 6512 TTTTGATTCGCTTTTGTAAATTTATTTTGAATACGCGCTTTGATGTATCTCGTTTG 6571
QY 68 -----IleLeuGlnCysGlnSerGlyHisLeuValCysSerAsnCysArgProLys 84
DB 6572 GTATATATCGCTTTCAGTGTGATGGACATATAGTTTGCAATTTTGTTCGCAAA 6631
QY 85 LeuThr-----Cys---CysProThrCysArgGlyProLeuGlySerLeuArgAsnLeu 101
DB 6632 GTGAGTAACAAGTCCCTGGTCTGGTGTGATTTACCCATGCTAATAAGCGATGCTTC 6691
QY 102 AlaMetGluLysValAlaAsnSerValLeuPheProCysLysTyrAlaSerSerGlyCys 121
DB 6692 GCAATGAGAGGGTCTCGAATCAGCCTTGTGTTCCATGTCAAATACACTGAGTTTGCTGC 6751
QY 122 GluIleThrLeuProHisThrGluLysAlaAspHisGluGluLeuCysGluPheArgPro 141
DB 6752 ACNAAAAGTCTCTTATGAAAAGTGTCAAGTCACGAAAAGAAAGTCAACTACTCT--- 6808
QY 142 TyrSerCysProCysProGlyAlaSerCysLysTrpGlnGlySerLeuAspAlaValMet 161
DB 6809 ---CAATGCTCTTGCCTAACCTCGAATGCAATTACACTGGCTCATATAACATCATCTAC 6865
QY 162 ProHisLeuMetHisGlnHisLysSerIleThrThrLeuGlnGlyGluAspIleValPhe 181
DB 6866 GGTCACTTTATGCTGCGCCATCTTTACAATAGTACGATCGTTTCTCCAAATGGGGATAT 6925
QY 182 LeuAlaThrAsp-----IleAsnLeuProGlyAlaValAspTrpValMetGlnSer 199
DB 6926 TCCACTGTTGATGTTCTAATAAACATCAAGAAAAGTTTCA---GTTCTCTGGGAATCT 6982
QY 200 CysPheGlyPheHisPheMetLeuValLeuGluLysGlnGlnLysTyrAspGlyHisGln 219
DB 6983 CGTCAGAAAATTTGTTGTAGTTAGTGTGTTTCAAGGAGCGA-----CATGCT 7030
QY 220 GlnPhePheAlaIleValGlnLeuIleGlyThrArgLysGlnAlaGluAsnPheAlaTyr 239
DB 7031 GTTATGTTACTGTTAGACGCATCGCACCCACTGCTTCAGAATTCAGAAAGTTCTCGTAT 7090
QY 240 ArgLeu-----GluLeuAsnGlyHisArgGlyArgLeuThrTrpGluAla 254
DB 7091 CGTCTTCGTATAGTATCGACGACAT-----AATGTTACTTACGAATCA 7135

RESULT 10

US-09-270-767-13738
; Sequence 13738, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.

; TITLE OF INVENTION: Nucleic acids and proteins of *Drosophila melanogaster*
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 13738
; LENGTH: 2927
; TYPE: DNA
; ORGANISM: *Drosophila melanogaster*
US-09-270-767-13738

Alignment Scores:

Pred. No.: 0.000493 Length: 2927
Score: 130.50 Matches: 63
Percent Similarity: 32.38% Conservative: 39
Best Local Similarity: 20.00% Mismatches: 81
Query Match: 8.10% Indels: 133
DB: 4 Gaps: 16

US-10-679-246-2 (1-298) x US-09-270-767-13738 (1-2927)

QY 24 AlaLeuProThrGlyThrSerLysCys---ProProSerGlnArgVal----- 38
DB 1663 GCAGTCCAGATGGGCCATCTGA-TGTGCGCGCCCTGTTTCAGCATCTGCTGGCGGATG 1721
QY 39 -----ProAlaLeuThrGlyThrAlaSerAsn 48
DB 1722 GACGGTATGACCCACACTCTAGAAATAAAGTAAAGTCTTGCATGCGCCACCAAC 1781
QY 49 AsnAspLeuAlaSerLeuPheGluCysProValCysPheAsp----- 62
DB 1782 TCCAACTAACGAGTTCTGTTTACTGTCTCT---TAGCACCTTTTTCATCAATA 1835
QY 63 TyrValLeuProIleLeuGlnCysGlnSerGlyHisLeuValCysSerAsnCysArg 82
DB 1836 TATCTCTCCCTAGCTTG-----CGC 1856
QY 83 ProLysLeuThrCysCysProThrCysArgGlyProLeuGly-----SerIleArg 99
DB 1857 GATCAGATTGCCACGTGCCCCAATGCGCGTGGAAATTTCTAAGAGCACTGGCTCGCGC 1916
QY 100 AsnLeuAlaMetGluLysValAlaAsnSerValLeuPheProCysLysTyrAlaSerSer 119
DB 1917 AACTTGGCGGTGAGAGGCGCCTCAGAAATGCCCGAGGTGTCAATTC----- 1967
QY 120 GlyCysGluIleThrLeuProHisThrGluLysAlaAspHisGluGlu---LeuCysGlu 138
DB 1968 ---TGCAACAAGGAGTTCCCATACAAATCTCTCGAACGCCATGAACACACGAGTCCAG 2024
QY 139 PheArgProTyrSerCysProCysProGlyAlaSerCysLysTrpGlnGlySerLeuAsp 158
DB 2025 GAGCGCCCAACCAAGTGAATACCATCCATGCTGTCAGTGGCGGGAGCCCTACCAC 2084
QY 159 AlaValMetProHis-----LeuMetHisGlnHisLysSerIleThrThrLeuGln 175
DB 2085 GAGACCAACGAGCATGAGCGCAACTGCTTGTGATCCCGAGAAGTCT----- 2129
QY 176 GlyGluAspIleValPheLeuAlaThrAspIleAsnLeuProGlyAlaValAspTrpVal 195
DB 2129 ----- 2129
QY 196 MetMetGlnSerCysPheGlyPheHisPheMetLeuValLeuGlu----- 210
DB 2130 -----GGCTACGAGGTAAATGGCAGCCCTGGAGGCCCCACGACGATAGG 2171
QY 211 ---LysGlnGluLysTyrAspGlyHisGlnPheAlaIleValGlnLeuIleGly 229
DB 2172 ATCAAGGAGGAGAAG-----AAGATGTTTAAACACCTGATTGCTTGTCTAGC 2219
QY 230 ThrArgLys-----GlnAlaGluAsnPheAla 238
DB 2220 TACGAGAAGATCATATTCATGACCTCCAAATGAAACCCCTACCGCACGACGATGCTG 2279

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QY 239 TyrArgLeu-----241
Db 2280 CACAAGCTTTTATGAGAGCGCCGCTTCTCGGCTTCAATCAGCAGTGGTGGTGAAG 2339
QY 242 ----GluLeuAsn-----GlyHisArgArgLeuThrTrp 252
Db 2340 GCGCGCATCAACAACAGCAGCGCGATCGCATCAGTCCAGCAGCGGACCATCACTAT 2399
QY 253 Glu-----AlaThrProArgSerIleHis 260
Db 2400 CATCTGATCTCAAGACCAAGACAGCAGCGCCCATGAGCATACAT 2444

RESULT 11
US-09-270-767-29760
; Sequence 29760, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 29760
; LENGTH: 2308
; TYPE: DNA
; ORGANISM: Drosophila melanogaster
US-09-270-767-29760

Alignment Scores:
Pred. No.: 0.000564 Length: 2308
Score: 128.50 Matches: 54
Percent Similarity: 34.16% Conservative: 29
Best Local Similarity: 22.22% Mismatches: 72
Query Match: 7.98% Indels: 89
DB: 4 Gaps: 12

US-10-679-246-2 (1-298) x US-09-270-767-29760 (1-2308)

QY 24 AlaLeuProThrGlyThrSerIleCys---ProProSerGlnArgVal-----38
Db 1663 GCATGCCAGATGGCCATCTGA-TGTGCGCGCTGTTTCAGGCATCTGCTGGCGGATG 1721
QY 39 -----ProAlaLeuThrGlyThrThrAlaSerAsn 48
Db 1722 GACGGTATGAACCCACACTCTAGAAATAAATAAGATCTTGCATAATGCCACCACCAAC 1781
QY 49 AsnAspLeuAlaSerLeuPheGluCysProValCysPheAsp-----62
Db 1782 TCCAACTAAGAGTTCGTGTTACTGTCTCT-----TACGACCTTTTITTTTCAATA 1835
QY 63 TyrValLeuProPheLeuGlnCysGlnSerGlyHisLeuValCysSerAsnCysArg 82
Db 1836 TATTCCTCTCTAGCTTG-----CGC 1856
QY 83 ProlsLeuThrCysCysProThrCysArgGlyProLeuGly-----SerIleArg 99
Db 1857 GATCAGATTGCCACGTCGCCCAATTTGCGGTGGAATTTCTAAGACATCGCTGCGCG 1916
QY 100 AsnLeuAlaMetGluIleValAlaAsnSerValLeuPheProCysIleTyrAlaSerSer 119
Db 1917 AACTTGCGCGTGGAGAGCGGCTCAGAAATGCGCAGCGAGTGCTCAATC-----1967
QY 120 GlyCysGluIleThrLeuProHisThrGluIleAlaAspHisGluGlu----LeuCysGlu 138
Db 1968 ---TGCAACAAGAGATTCCCATACAAATCTCTCGAACGCCATGAACAACACGAGTGCCAG 2024
QY 139 PheArgProTyrSerCysProCysProGlyAlaSerCysIleTyrGlnGlySerLeuAsp 158
Db 2025 GAGCGCCCGACCAAGTGCATAATACCATCGCATTCGGTGTGATGGCGGGAGACCTTACCAC 2084
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QY 159 AlaValMetProHis-----LeuMetHisGlnHisIleSerIleThrThrLeuGln 175
Db 2085 GAGACCAACGAGCATGAGCGCACTGCTTGATCCCCAGAGTCT-----2129
QY 176 GlyGluAspIleValPheLeuAlaThrAspIleAsnLeuProGlyAlaValAspTyrVal 195
Db 2129 -----2129
QY 196 MetMetGlnSerCysPheGlyPheHisPheMetLeuValLeuGlu-----210
Db 2130 -----GGCTACGAGTAATGCGAGCCCTGGAGGCCACGACGATAGG 2171
QY 211 ---LysGlnGluIleTyrAspGlyHisGlnGlnPhePheAlaIleValGlnLeuIleGly 229
Db 2172 ATCAAGGAGGAGAAG-----AAGATGTTTAAACACCTGATTGCTTGTAGC 2219
QY 230 ThrArgIle 232
Db 2220 TACGAGAAG 2228

RESULT 12
US-09-620-312D-23
; Sequence 23, Application US/09620312D
; Patent No. 6569662
; GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom
; APPLICANT: Liu, Chenghua
; APPLICANT: Asundi, Vinod
; APPLICANT: Zhang, Jie
; APPLICANT: Ren, Feiyan
; APPLICANT: Chen, Rui-hong
; APPLICANT: Zhao, Qing A.
; APPLICANT: Wehrman, Tom
; APPLICANT: Xue, Aidong J.
; APPLICANT: Yang, Yonghong
; APPLICANT: Wang, Jian-Rui
; APPLICANT: Zhou, Ping
; APPLICANT: Ma, Yungqing
; APPLICANT: Wang, Dunrui
; APPLICANT: Wang, Zhiwei
; APPLICANT: John Tillinghast
; APPLICANT: Drmanac, Radojke T.
; TITLE OF INVENTION: No. 6569662el Nucleic Acids and
; TITLE OF INVENTION: Polypeptides
; FILE REFERENCE: 784CIP2B
; CURRENT APPLICATION NUMBER: US/09/620,312D
; CURRENT FILING DATE: 2000-07-19
; PRIOR APPLICATION NUMBER: 09/552,317
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: 09/488,725
; PRIOR FILING DATE: 2000-01-21
; NUMBER OF SEQ ID NOS: 1105
; SOFTWARE: pt_FL_genes Version 1.0
; SEQ ID NO 23
; LENGTH: 1463
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (178)..(1002)
US-09-620-312D-23

Alignment Scores:
Pred. No.: 0.00189 Length: 1463
Score: 121.00 Matches: 30
Percent Similarity: 39.64% Conservative: 14
Best Local Similarity: 27.03% Mismatches: 49
Query Match: 7.51% Indels: 18
DB: 4 Gaps: 4

US-10-679-246-2 (1-298) x US-09-620-312D-23 (1-1463)
QY 67 ProlLeuGlnCysGlnSerGlyHisLeuValCysSerAsnCys-----81
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; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1949
; LENGTH: 1260
; TYPE: DNA
; ORGANISM: Human
; US-09-949-016-1949

Alignment Scores:
Pred. No.: 0.0199 Length: 1260
Score: 111.00 Matches: 50
Percent Similarity: 42.86% Conservative: 10
Best Local Similarity: 35.71% Mismatches: 53
Query Match: 6.89% Indels: 29
DB: 8 Gaps: 4

US-10-679-246-2 (1-298) x US-09-949-016-1949 (1-1260)
QY 24 AlaLeuProThrGlyThrSerLysCysPro---ProSerGlnArg-----Val 38
Db 751 TCCCTGCTCTGGTACCTGAGCTGCCACACCCAGAGAGAGGTCAGTCTGAAAGTG 810
QY 39 ProAlaLeuThrGlyThrThrAlaSerAsnAsnAspLeuAlaSerLeuPheGlu----- 56
Db 811 CCCAGGAG-CCAGAGCCAGGGATGTGGAGGGCGACGCTGCGCGGCTGCAGGAGGAGG 869
QY 57 ---CysProValCysPheAspTyrValLeuProProIleLeuGlnCysGlnSerGlyHis 75
Db 870 ACGTGCAAGGTGTGCTTGCAGCCGCGCGTG---TCCATGTGCTTTGTGCGCGGCCAC 926
QY 76 LeuValCysSerAsnCysArgProLysLeuThrCysCysProThrCysArgGlyProLeu 95
Db 927 CTGGTCTGTGCTGAGTGTGCGCGCGCTGCAGCTGTGCCCTATCTGCAGAGCCCGCTC 986
QY 96 GlySerIleArgAsnLeuAlaMetGluLysValAlaAsnSerValLeuPheProCysLys 115
Db 987 CGCAGCGG-CGT-----GGCACCTTCTGCTAGGCCAGGTGCCATGGCCGCCGCGC 1039
QY 116 TyrAlaSer-SerGlyCysGluIleThrLeuProHisThrGluLysAlaAspHisGlu 135
Db 1040 TGGGCTGCAGATGGG-----CTCCCT-----GCCCG 1066
QY 135 uLeuCysGluPheArgProTyrSerCysProCysProGlyAlaSerCysLysTrpGln 154
Db 1067 TCTCTGCTCTTCTGGACTGTGTCTGGGCGCTGCTGAGGA-----TGGCAG 1112

RESULT 15
US-08-639-237-1
; Sequence 1, Application US/08639237
; Patent No. 5710013
; GENERAL INFORMATION:
; APPLICANT: Xiong, Jessie
; APPLICANT: Goeddel, David V.
; TITLE OF INVENTION: No. 5710013el Protein - TRAF6
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Flehr, Hohbach, Test, Albritton & Herbert
; STREET: 4 Embarcadero Center, Suite 3400
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111

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; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/639,237
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Brezner, David J
; REGISTRATION NUMBER: 24,7747
; REFERENCE/DOCKET NUMBER: T96-004/A63312
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 781-1989
; TELEFAX: (415) 398-3249
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2248 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 230..1795
; US-08-639-237-1

Alignment Scores:
Pred. No.: 0.0973 Length: 2248
Score: 108.50 Matches: 82
Percent Similarity: 31.40% Conservative: 48
Best Local Similarity: 19.81% Mismatches: 128
Query Match: 6.73% Indels: 157
DB: 1 Gaps: 19

US-10-679-246-2 (1-298) x US-08-639-237-1 (1-2248)
QY 5 IlePheLeuLeuProTyrValPheIleSerGluMetSerArgGlnThrAlaThrAla 24
Db 176 CTCCTGGTTGGCGCTCCCGCGGCACTAGAACGAGCAGTGAATCAAGTTACTATGAGT 235
QY 25 LeuProThrGlyThrSerLysCysProSerGln-----GlyThrThrAlaSerAsn 36
Db 236 CTGTAAACTGTGAAACAGACGTGTGGATCCAGCCAGTCTGAAAGTACTGCTGTGCGCC 295
QY 37 -----ArgValProAlaLeuThr-----GlyThrThrAlaSerAsn 48
Db 296 ATGGCCAGCTCTCTGTAGCGCTGTAACAAAGATGATGTGGTGGAACTGCCAGCAGC 355
QY 49 AsnAspLeuAlaSerLeuPhe-----GlyThrThrAlaSerLeuPhe 55
Db 356 GGGAACTCTCCAGCTCATTTATGGAGGAGATCCAGGAGATATGATGTAGAGTTGACCCA 415
QY 56 -----GluCysProValCysPheAspTyrValLeuProIleLeu 69
Db 416 CCCCTGGAAGCAAGTATGAATGCCCATCTCTCTG---ATGCGATTACGAGAGCAGTG 472
QY 70 GlnCysGlnSerGlyHisLeuValCysSerAsnCysArgProLysLeuThrCysCysPro 89
Db 473 CAACGCCATCGGCCCATAGGTTCTGCAAGAGCTGCATCATATAA-----LeuAlaMet 517
QY 90 ThrCysArgGlyProLeuGlySerIleArgAsn-----LeuAlaMet 103
Db 518 -----TCAATAGGGATGGAGGTCAACAAATGTCAGTTGACAT 556
QY 104 GluLysValAlaAsnSerValLeuPheProCysLysTyrAla----- 117
Db 557 GAAATACTCTGGAAATCAACTATTTCAGACAAATTTTGCAAAACGTCGAGATCTTTCT 616
QY 118 -----SerSerGlyCys-----GluIleThrLeuProHisThrGlu 129
Db 617 CTGATGGTGAATGTCCAATGAAGTTGTTTGCACAGATGGAATGAGCATCTTTGAG 676

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QY 130 LysAlaAspHisGluGluLeuCysGluPhe-----Arg 140
    |||||::: |||||
Db 677 -----GATCATCAAGCACATTGTGAGTTTGTCTTATGGATTGTCCCAATGCCAGCGT 730
QY 141 ProTyr-----142
    |||||
Db 731 CCCTTCCAAAATTCCATATTATATTCACATTCTGAAGGATTGTCCAAGGAGACAGGTT 790
QY 143 -----Ser 143
    :::
Db 791 TCTTGTGACAACTGTGTCATCGCATTTGAAGATAAAGAGATCCATGACCAGAAC 850
QY 144 CysProCysProGlyAlaSerCysLysTrpGlnGlySerLeuAspAlaValMetProHis 163
    |||||
Db 851 TGTCTCTTTGGCAAAATGTCATCTGTGAATACTGCAATACTATA-----CTCATCGAGAA 904
QY 164 LeuMetHisGlnHisLysSerIle-ThrThrLeuGlnGlyGluAspIleValPheLeuAl 183
    |||||
Db 905 CAGATGCTTAATCATATTATGATCTAGACTGCCCTACAGCCCAA-----TTCCATGC 955
QY 183 aThrAspIleAsnLeuProGlyAlaValAspTrpValMetMetGlnSerCysPheGlyPh 203
    |||||
Db 956 ACATTCAGTACTTTG-----GTTGCCATGAAAAGATGCAGAGGAAT 997
QY 203 eHisPheMetLeuValLeuGluLysGlnGlyLysTyrAspGlyHisGlnGlnPheAl 223
    |||||
Db 998 -CAC-----TTGGCAGCGCCACTACAGAGAAACACCCAGTCACACATGAGAATGTTGGC 1050
QY 223 a-----IleValGlnLeuIleGlyThrArgLysGlnAlaGluAs 236
    |||||
Db 1051 CCAGGCTGTTCAAGTTTGTAGCGTTATACCCGACTCTGGGTATATCTCAGAGGTCGGAA 1110
QY 236 nPheAlaTyr-----ArgLeuGluLeuAsnGlyHisArgArgAr 249
    |||||
Db 1111 TTTCCAGGAAACTATTCCAGCTTAGAGGGTGCCTTTGAAGACAGACCATCAATCCG 1170
QY 249 gLeuThrTrpGluAlaThrProArgSerIleHisGluGlyIleAlaThrAlaIleMetAs 269
    |||||
Db 1171 G-----GAGCTGACTGTCTAAATGGAACCTCAGAGTATGTATGTAAGTGAGTCAA 1221
QY 269 nSerAspCysLeuValPheAspThrSerIleAlaGlnLeuPheAlaGluAsn-----286
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Db 1222 ACGAACCATTCGAACCTTTGAGGACAAAGTTGCTGAATCGAAGCACAGCAGTGAATGG 1281
QY 287 -----GlyAsnLeuGlyIleAsnVal 293
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Db 1282 AATTATATTGGAGATTGGCAACTTTGGAATGCATTG 1321
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Search completed: April 25, 2005, 09:29:18
Job time : 219 secs

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GenCore version 5.1.6
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2766.320 Million cell updates/sec

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Perfect score: 1611
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Ygapop 10.0 , Ygapext 0.5
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Searched: 5633728 seqs, 3035525691 residues
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Listing first 45 summaries

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-THR MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0
-MAXLEN=2000000000 -WMAP=US10679246 @CGN 1.1 480 @runat 22042005 185512 7796
-NCPU=6 -ICPU=3 -NO MMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100
-LONGLOG -DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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1	1611	100.0	1274	18	US-10-679-246-1	Sequence 1, Appli
2	1611	100.0	2440	17	US-10-641-643-588	Sequence 588, App
3	1611	100.0	2924	18	US-10-357-930-22959	Sequence 22959, A
4	1611	100.0	2924	18	US-10-357-930-25457	Sequence 25457, A
5	1611	100.0	2924	18	US-10-357-930-28822	Sequence 28822, A
6	1611	100.0	6107	10	US-09-764-891-8070	Sequence 8070, Ap
7	1603	99.5	2829	17	US-10-108-260A-269	Sequence 269, App
8	1206	74.9	2502	15	US-10-177-293-426	Sequence 426, App
9	1199	74.4	975	17	US-10-172-118-1117	Sequence 1117, Ap
10	1199	74.4	975	17	US-10-342-887-1117	Sequence 1117, Ap
11	1198	74.4	2240	15	US-10-177-293-424	Sequence 424, App
12	1198	74.4	2240	18	US-10-177-597-137	Sequence 137, App
13	1198	74.4	2240	18	US-10-755-889-123	Sequence 123, App
14	474	29.4	1535	9	US-09-925-297-84	Sequence 84, Appl
15	462.5	28.7	1438	18	US-10-437-963-83416	Sequence 83416, A
16	447	27.7	1408	17	US-10-425-114-2756	Sequence 2756, Ap
17	446	27.7	360	9	US-09-960-352-10011	Sequence 10011, A
18	446	27.7	360	9	US-09-960-352-10011	Sequence 10011, A
19	429.5	26.7	1444	17	US-10-425-114-4151	Sequence 4151, Ap
20	429.5	26.7	1667	18	US-10-425-115-28950	Sequence 28950, A
21	429	26.6	984	9	US-09-938-842A-463	Sequence 463, App
22	429	26.6	984	11	US-09-938-842A-463	Sequence 463, App
23	426	26.4	257	17	US-10-305-720-397	Sequence 397, App
24	422	26.2	1448	18	US-10-437-963-84963	Sequence 84963, A
25	419	26.0	1398	17	US-10-424-599-98299	Sequence 98299, A
26	417.5	25.9	1383	18	US-10-324-120-4	Sequence 4, Appli
27	416	25.8	1526	17	US-10-424-599-21498	Sequence 21498, A
28	416	25.8	1683	18	US-10-425-115-27188	Sequence 27188, A
29	415	25.8	2542	18	US-10-437-963-9355	Sequence 9355, Ap
30	413.5	25.7	1540	17	US-10-424-599-18853	Sequence 18853, A
31	410.5	25.5	856	18	US-10-767-795-1843	Sequence 1843, Ap
32	405	25.1	1388	18	US-10-425-115-61385	Sequence 61385, A
33	405	25.1	1835	18	US-10-437-963-55834	Sequence 55834, A
34	404	25.1	1378	17	US-10-424-599-15841	Sequence 15841, A
35	398.5	24.7	1638	18	US-10-437-963-29521	Sequence 29521, A
36	397	24.6	1740	17	US-10-424-599-18852	Sequence 18852, A
37	358	22.2	2078	17	US-10-424-599-21496	Sequence 21496, A
38	338	21.0	1342	18	US-10-425-115-183094	Sequence 183094, A
39	332	20.6	777	18	US-10-767-701-3143	Sequence 3143, Ap
40	326	20.2	921	18	US-10-425-115-147280	Sequence 147280, A
41	326	20.2	1036	14	US-10-219-220-39	Sequence 39, Appl
42	326	20.2	1319	14	US-10-219-220-228	Sequence 228, App
43	325	20.2	1425	14	US-10-219-220-200	Sequence 200, App
44	324.5	20.1	832	18	US-10-425-115-32733	Sequence 32733, A
45	319.5	19.8	2142	17	US-10-108-260A-1336	Sequence 1336, Ap

ALIGNMENTS

RESULT 1
US-10-679-246-1
; Sequence 1, Application US/10679246
; Publication No. US20040163138A1
; GENERAL INFORMATION:
; APPLICANT: Reed, John C.
; APPLICANT: Matsuura, Shu-ichi
; TITLE OF INVENTION: Nucleic Acid Encoding Proteins Involved
; TITLE OF INVENTION: in Protein Degradation, Products and Methods Related Thereto
; FILE REFERENCE: 66821-235
; CURRENT APPLICATION NUMBER: US/10/679,246
; CURRENT FILING DATE: 2003-10-02
; PRIOR APPLICATION NUMBER: US 09/591,694
; PRIOR FILING DATE: 2000-06-09
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 1274
; TYPE: DNA
; ORGANISM: Homo sapien


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QY 61 PheAspTyrValLeuProPheLeuGlnCysGlnSerGlyHisLeuValCysSerAsn 80
Db 687 TTGACTATGTGTACCGCCCATCTTCAATGTCAGAGTGGCCATCTTGTGTAGCAAC 746
QY 81 CysArgProLysLeuThrCysCysProThrCysArgGlyProLeuGlySerIleArgAsn 100
Db 747 TGTGCGCCAAAGCTCACATGTTGTCCAACTTGCGGGGCCCTTTGGATCCATTCGCAC 806
QY 101 LeuAlaMetGluLysValAlaAsnSerValLeuPheProCysLysTyrAlaSerSerGly 120
Db 807 TTGGCTATGAGAAAGTGCGTAATTCAGTACTTTTCCCTGTAAATATGCGTCTTCTGGA 866
QY 121 CysGluLeuThrLeuProHisThrGluLysAlaAspHisGluGluLeuCysGluPheArg 140
Db 867 TGTGAATAAATCTGTCACACAGAAAAGCAGACCATGAAGAGCTCTGTGAGTTTAGG 926
QY 141 ProTyrSerCysProCysProGlyAlaSerCysLysTyrGlnGlySerLeuAspAlaVal 160
Db 927 CCTTATCTGTCGCGCCCTGGTGTCTTCTGTAAATGCAAGGCTCTCTGGATGCTGA 986
QY 161 MetProHisLeuMetHisGlnHisLysSerIleThrThrLeuGlnGlyGluAspIleVal 180
Db 987 ATGCCCATCTGATGCATCAGCATAGTCCATTACAACCTACAGGAGAGGATAGTT 1046
QY 181 PheLeuAlaThrAspIleAsnLeuProGlyAlaValAspTyrValMetGlnSerCys 200
Db 1047 TTTCTTGTACAGACATTAATCTTCTGTGTCTTGTGCTGTGATGATGAGTCTCTGT 1106
QY 201 PheGlyPheHisPheMetLeuValLeuGluLysGlnGlyLysTyrAspGlyHisGlnGln 220
Db 1107 TTTGGCTTTCATCTCATGTAGTCTTAGAGAAACAGGAAATATACGATGTCACGACG 1166
QY 221 PhePheAlaIleValGlnLeuIleGlyThrArgLysGlnAlaGluAsnPheAlaTyrArg 240
Db 1167 TTTCTTGCAGCAATCGTACAGCTGATAGGAACAGCAAGCAAGCTGAAATTTTGTACCGA 1226
QY 241 LeuGluLeuAsnGlyHisArgArgArgLeuThrTyrGluAlaThrProArgSerIleHis 260
Db 1227 CTTGAGCTAAATGGTTCATAGGCGACGATTGACTTGGGAAAGCGACTCTCGATCTATT 1286
QY 261 GluGlyIleAlaThrAlaIleMetAsnSerAspCysLeuValPheAspThrSerIleAla 280
Db 1287 GAAGGAATTCACAGCCCATTAATGATAGGACTGTCTAGTCTTTGACACCGAGATTGCA 1346
QY 281 GlnLeuPheAlaGluAsnGlyAsnLeuGlyIleAsnValThrIleSerMetCys 298
Db 1347 CAGCTTTTGCAGAAATGCAATTTAGGCATCAATGTAACATTTTCCATGTGT 1400
RESULT 3
US-10-357-930-22959
; Sequence 22959, Application US/10357930
; Publication No. US20040259086A1
; GENERAL INFORMATION:
; APPLICANT: Schlegel, Robert
; APPLICANT: Endege, Wilson
; APPLICANT: Monahan, John
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
; TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY OF
; TITLE OF INVENTION: HUMAN PROSTATE CANCER
; FILE REFERENCE: MRI-007ECN
; CURRENT APPLICATION NUMBER: US/10/357,930
; CURRENT FILING DATE: 2003-02-04
; PRIOR APPLICATION NUMBER: 09/785,276
; PRIOR FILING DATE: 2003-02-16
; PRIOR APPLICATION NUMBER: 60/183,319
; PRIOR FILING DATE: 2000-02-17
; PRIOR APPLICATION NUMBER: 60/189,862
; PRIOR FILING DATE: 2000-03-16
; PRIOR APPLICATION NUMBER: 60/207,454
; PRIOR FILING DATE: 2000-05-25
; PRIOR APPLICATION NUMBER: 60/211,314
; PRIOR FILING DATE: 2000-06-09
; PRIOR APPLICATION NUMBER: 60/219,007
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; PRIOR FILING DATE: 2000-07-19
; PRIOR APPLICATION NUMBER: 60/255,281
; PRIOR FILING DATE: 2000-12-13
; NUMBER OF SEQ ID NOS: 62232
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 22959
; LENGTH: 2924
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 1, 57, 2923, 2924
; OTHER INFORMATION: n = A,T,C or G
US-10-357-930-22959
Alignment Scores:
Pred. No.: 4,69e-189 Length: 2924
Score: 1611.00 Matches: 298
Percent Similarity: 100.00% Conservatives: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 18 Gaps: 0
US-10-679-246-2 (1-298) x US-10-357-930-22959 (1-2924)
QY 1 MetValIleIleIlePheLeuLeuProProTyrValPheIleSerGluMetSerArgGln 20
Db 753 ATGGTTATATAATTAATTTTCTCTGCTCCTTATGTATTTATTTTCAGAAATGAGCCGTCAG 812
QY 21 ThrAlaThrAlaLeuProThrGlyThrSerLysCysProSerGlnArgValProAla 40
Db 813 ACTGCTACAGCAATTAACCTACCGGTACCTCGAAGTGTCCACCATCCAGAGGGTGCCTGCC 872
QY 41 LeuThrGlyThrThrAlaSerAsnAsnAspLeuAlaSerLeuPheGluCysProValCys 60
Db 873 CTGACTGGCACAACTGCATCCAACTGACTTGGCGAGTCTTTTGGAGTGTCCAGTCTGC 932
QY 61 PheAspTyrValLeuProProIleLeuGlnCysGlnSerGlyHisLeuValCysSerAsn 80
Db 933 TTTGACTATGTGTACCGCCCATCTTCAATGTCAGAGTGGCCATCTTCTTTGTAGCAAC 992
QY 81 CysArgProLysLeuThrCysCysProThrCysArgGlyProLeuGlySerIleArgAsn 100
Db 993 TGTGCCCAAAAGCTCACATGTTGTCCAACTTCCCGGGGCCCTTTGGGATCCCATTCGCAAC 1052
QY 101 LeuAlaMetGluLysValAlaAsnSerValLeuPheProCysLysTyrAlaSerSerGly 120
Db 1053 TTGGCTATGGAGAAAGTGGCTAAATTCAGTACTTTTCCCTGTAAATATGCGTCTTCTGA 1112
QY 121 CysGluIleThrLeuProHisThrGluLysAlaAspHisGluLeuCysGluPheArg 140
Db 1113 TGTGAAATAAATCTGCCACACAGAAAAAGCAGACCATGAAGAGCTCTGTGAGTTTAGG 1172
QY 141 ProTyrSerCysProCysProGlyAlaSerCysLysTyrGlnGlySerLeuAspAlaVal 160
Db 1173 CTTTATCTCTGTCGCTGCTCTTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1232
QY 161 MetProHisLeuMetHisGlnHisLysSerIleThrThrLeuGlnGlyGluAspIleVal 180
Db 1233 ATGCCCCATCTGATGCATCAGCATTAAGTCCATTACACCTACAGGAGAGGATATAGTT 1292
QY 181 PheLeuAlaThrAspIleAsnLeuProGlyAlaValAspTyrValMetGlnSerCys 200
Db 1293 TTTCTTGTACAGACATTAATCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1352
QY 201 PheGlyPheHisPheMetLeuValLeuGluLysGlnGlyLysTyrAspGlyHisGlnGln 220
Db 1353 TTTGGCTTTCATCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1412
QY 221 PhePheAlaIleValGlnLeuIleGlyThrArgLysGlnAlaGluAsnPheAlaTyrArg 240
Db 1413 TTTCTTCCCAATCGTACAGCTGATAGAACACGCAAGCAGCTGAAATTTTCTTACCAG 1472
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QY 241 LeuGluLeuAsnGlyHisArgArgLeuThrTrpGluAlaThrProArgSerIleHis 260
Db 1473 CTTGAGCTAAATGGTCATAGGCGAGGATTGACTTGGGAAGGACCTCTCGATCTATTCAAT 1532
QY 261 GluGlyIleAlaThrAlaIleMetAsnSerAspCysLeuValPheAspThrSerIleAla 280
Db 1533 GAAGGAATTTGCAACGCAATTAATAGCAGCTGTCTAGTCTTTGACACCGAGCATTTGCA 1592
QY 281 GlnLeuPheAlaGluAsnGlyHisLeuGlyIleAsnValThrIleSerMetCys 298
Db 1593 CAGCTTTTTCAGAAAATGGCAATTTAGGCATCAATGTAACATTTTCCAATGTT 1646

RESULT 4
US-10-357-930-25457
; Sequence 25457, Application US/10357930
; Publication No. US20040259086A1
; GENERAL INFORMATION:
; APPLICANT: Schlegel, Robert
; APPLICANT: Endege, Wilson
; APPLICANT: Monahan, John
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
; TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY OF
; TITLE OF INVENTION: HUMAN PROSTATE CANCER
; FILE REFERENCE: MRI-007BCN
; CURRENT APPLICATION NUMBER: US/10/357,930
; PRIOR FILING DATE: 2003-02-04
; PRIOR APPLICATION NUMBER: 09/785,276
; PRIOR FILING DATE: 2003-02-16
; PRIOR APPLICATION NUMBER: 60/183,319
; PRIOR FILING DATE: 2000-02-17
; PRIOR APPLICATION NUMBER: 60/189,862
; PRIOR FILING DATE: 2000-03-16
; PRIOR APPLICATION NUMBER: 60/207,454
; PRIOR FILING DATE: 2000-05-25
; PRIOR APPLICATION NUMBER: 60/211,314
; PRIOR FILING DATE: 2000-06-09
; PRIOR APPLICATION NUMBER: 60/219,007
; PRIOR FILING DATE: 2000-07-18
; PRIOR APPLICATION NUMBER: 60/255,281
; PRIOR FILING DATE: 2000-12-13
; NUMBER OF SEQ ID NOS: 62232
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 25457
; LENGTH: 2924
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 1, 57, 2923, 2924
; OTHER INFORMATION: n = A,T,C or G
US-10-357-930-25457

Alignment Scores:
Pred. No.: 4,69e-189 Length: 2924
Score: 1611.00 Matches: 298
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 18 Gaps: 0

US-10-679-246-2 (1-298) x US-10-357-930-25457 (1-2924)
QY 1 MetValIleIlePheLeuLeuProProTyrValPheIleSerGluMetSerArgGln 20
Db 753 ATGGTTATTAATTTTCTCGCTCTCTTATGATTTATTTCAGAAATGAGCGGTGAG 812
QY 21 ThrAlaThrAlaLeuProThrGlyThrSerLysCysProProSerGlnArgValProAla 40
Db 813 ACTGCTACGATTAATCTACCGGTACCTCGAGTGTCCACCATCCAGAGGGTGCCTGCC 872
QY 41 LeuThrGlyThrThrAlaSerAsnAsnAspLeuAlaSerIlePheGluCysProValCys 60
Db 873 CTGACTGGCACAACTGCATCCCAATGACTTTGGCGAGTCTTTTGGAGTGTCCAGTCTGC 932
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QY 61 PheAspTyrValLeuProProIleLeuGlnCysGlnSerGlyHisLeuValCysSerAsn 80
Db 933 TTTGACTATGTGTATACCGCCCATCTTCAATGTACAGAGTGGCCATCTGTTTGTAGCAAC 992
QY 81 CysArgProLysLeuThrCysCysProThrCysArgGlyProLeuGlySerIleArgAsn 100
Db 993 TGTGCCCCAAAGCTCACATGTTGTCCAACTTGC CGGGGCCCTTTGGGATGCCATTGCCAAC 1052
QY 101 LeuAlaMetGluLysValAlaAsnSerValLeuPheProCysLysTyrAlaSerSerGly 120
Db 1053 TTTGGCTATGGAGAAAGTGGCTAAATTCAGTACTTTTCCCTGTAAATATGCGTCTTCTGGA 1112
QY 121 CysGluIleThrLeuProHisThrGluLysAlaAspHisGluGluLeuCysGluPheArg 140
Db 1113 TGTGAATAATTAATCTGCCCACACAGAAAAGCAGACCATGAAGACTCTGTGAGTTAGG 1172
QY 141 ProTyrSerCysProCysProGlyAlaSerCysLysTyrGlnGlySerIleAspAlaVal 160
Db 1173 CCTTATTCCTGTCCGCTGCTGCTTCTTCTGTAATGCAAGGCTCTCTGGATGCTGTA 1232
QY 161 MetProHisLeuMetHisGlnHisLysSerIleThrThrLeuGlnGlyGluAspIleVal 180
Db 1233 ATGCCCATCTGATGATCAGCATTAAGTCCATTACACCCCTACAGGAGAGGATATAGTT 1292
QY 181 PheLeuAlaThrAspIleAsnLeuProGlyAlaValAspTrpValMetMetGlnSerCys 200
Db 1293 TTTCTTGTCTACAGACATTAATCTTCTGCTGCTGTTGACTGGGTGATGATGCAGTCTGT 1352
QY 201 PheGlyPheHisPheMetLeuValLeuGluLysGlnGluLysTyrAspGlyHisGlnGln 220
Db 1353 TTTGGCTTTTCACTTCATGTTAGTCTTAGAGAAACAGGAAAAATACGATGGTCCACGACAG 1412
QY 221 PhePheAlaIleValGlnLeuIleGlyThrArgLysGlnAlaGluAsnPheAlaTyrArg 240
Db 1413 TTTCTTGGCAATCGTACAGCTGATAGAAACACCAAGCAAGCTGAAAAATTTTCTTACCGA 1472
QY 241 LeuGluLeuAsnGlyHisArgArgLeuThrTrpGluAlaThrProArgSerIleHis 260
Db 1473 CTTGAGCTAAATGGTCATAGGCGAGGATTGACTTGGGAAGGACCTCTCGATCTATTCAAT 1532
QY 261 GluGlyIleAlaThrAlaIleMetAsnSerAspCysLeuValPheAspThrSerIleAla 280
Db 1533 GAAGGAATTTGCAACGCAATTAATAGCAGCTGTCTAGTCTTTGACACCGAGCATTTGCA 1592
QY 281 GlnLeuPheAlaGluAsnGlyHisLeuGlyIleAsnValThrIleSerMetCys 298
Db 1593 CAGCTTTTTCAGAAAATGGCAATTTAGGCATCAATGTAACATTTTCCAATGTT 1646

RESULT 5
US-10-357-930-28822
; Sequence 28822, Application US/10357930
; Publication No. US20040259086A1
; GENERAL INFORMATION:
; APPLICANT: Schlegel, Robert
; APPLICANT: Endege, Wilson
; APPLICANT: Monahan, John
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
; TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY OF
; TITLE OF INVENTION: HUMAN PROSTATE CANCER
; FILE REFERENCE: MRI-007BCN
; CURRENT APPLICATION NUMBER: US/10/357,930
; PRIOR FILING DATE: 2003-02-04
; PRIOR APPLICATION NUMBER: 09/785,276
; PRIOR FILING DATE: 2003-02-16
; PRIOR APPLICATION NUMBER: 60/183,319
; PRIOR FILING DATE: 2000-02-17
; PRIOR APPLICATION NUMBER: 60/189,862
; PRIOR FILING DATE: 2000-03-16
; PRIOR APPLICATION NUMBER: 60/207,454
; PRIOR FILING DATE: 2000-05-25
; PRIOR APPLICATION NUMBER: 60/211,314
; PRIOR FILING DATE: 2000-06-09
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; PRIOR APPLICATION NUMBER: 60/219,007
; PRIOR FILING DATE: 2000-07-18
; PRIOR APPLICATION NUMBER: 60/255,281
; PRIOR FILING DATE: 2000-12-13
; NUMBER OF SEQ ID NOS: 62232
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 28822
; LENGTH: 2924
; TYPE: DNA
; ORGANISM: Homo sapiens
; NAME/KEY: misc feature
; LOCATION: 1, 57, 2923, 2924
; OTHER INFORMATION: n = A,T,C or G
US-10-357-930-28822

Alignment Scores:
Pred. No.: 4,69e-189 Length: 2924
Score: 1611.00 Matches: 298
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 18 Gaps: 0

US-10-679-246-2 (1-298) x US-10-357-930-28822 (1-2924)

QY 1 MetValIleIlePheLeuLeuProProTyrValPheIleSerGluMetSerArgGln 20
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Db 753 ATGGTTATAATTATTTCTCGCTCCTCTATGTATTTATTTTCAGAAATGAGCGCTCAG 812

QY 21 ThrAlaThrAlaLeuProThrGlyThrSerLysCysProProSerGlnArgValProAla 40
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|
|
Db 813 ACTGCTACAGCATTAACCTACCGTACCTCGAAGTGTCACCATCCAGAGGGTGCCTGCC 872

QY 41 LeuThrGlyThrThrAlaSerAsnAspLeuAlaSerLeuPheGluCysProValCys 60
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|
|
Db 873 CTGACTGGCACAACCTGCATCCACAATGACTTGGCGAGTCTTTTTCAGTGTCAGTCTGC 932

QY 61 PheAspTyrValLeuProProLeuLeuGlnCysGlnSerGlyHisLeuValCysSerAsn 80
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|
Db 933 TTTGACTATGTGTACCGCCCATTTCTCAATGTGCAGTGGCCATCTTGTGTAGCAAC 992

QY 81 CysArgProLysLeuThrCysCysProThrCysArgGlyProLeuGlySerIleArgAsn 100
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|
|
Db 993 TGTGCGCCCAAGCTCATGTGTGTCCAACTGTCGCGGGGCCCTTTTGGGATCCATTCGCAAC 1052

QY 101 LeuAlaMetGluLysValAlaAsnSerValLeuPheProCysLysTyrAlaSerSerGly 120
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|
Db 1053 TTGGCTATGGAGAAAGTGGCTAATTCAGTACTTTTCCCTGTAAATATGCGTCTTCTGGA 1112

QY 121 CysGluIleThrLeuProHisThrGluLysAlaAspHisGluLeuLeuCysGluPheArg 140
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|
Db 1113 TGTGAAATAACTCTGCCACACACAGAAAAAGCAGACCATGAAAGAGCTCTGTGAGTTAGG 1172

QY 141 ProTyrSerCysProCysProGlyAlaSerCysLysTyrGlnGlySerLeuAspAlaVal 160
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Db 1173 CCTTATTCTGTGCGGCCCTGTGTCTTCTGTAATGGCAAGGCTCTCTGGATGCTGTA 1232

QY 161 MetProHisLeuMetHisGlnHisLysSerIleThrLeuGlnGlyGluAspIleVal 180
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Db 1233 ATGCCCCATCTGATGATCAGCATAAGTCCATTTACAACCTTACAGGAGGAGGATATAGTT 1292

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Db 1293 TTTCTGTCTACAGACATTAATCTTCTGTGTGTGTGTGACTGGGTGATGATGAGTCTGT 1352

QY 201 PheGlyPheHisPheMetLeuValLeuGluLysGlnGlyTyrAspGlyHisGlnGln 220
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Db 1353 TTTTGGCTTTTCACTTCATGTAGTCTTAGAGAAACAGAAAAATACGATGCTCACCAGCAG 1412

QY 221 PhePheAlaIleValGlnLeuIleGlyThrArgLysGlnAlaGluAsnPheAlaTyrArg 240
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QY 241 LeuGluLeuAsnGlyHisArgArgLeuThrTrpGluAlaThrProArgSerIleHis 260
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Db 1473 CTTGAGCTAAATGGTTCATAGCGCAGCAATTGACTTGGAAAGCGACTCTCTCGATCTATTTCAT 1532

QY 261 GluGlyIleAlaThrAlaIleMetAsnSerAspCysLeuValPheAspThrSerIleAla 280
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|
Db 1533 GAAGGAATTGCAACAGCCATTATGATAGGACTGTCTAGTCTTTGACACCAACCATGCA 1592

QY 281 GlnLeuPheAlaGluAsnGlyAsnLeuGlyIleAsnValThrIleSerMetCys 298
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Db 1593 CAGCTTTTTCAGAAAAATGGCAATTTAGGCATCAATGTAACATTTTCCATGTGT 1646

RESULT 6
US-09-764-891-8070
; Sequence 8070, Application US/09764891
; Publication No. US20030077808A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PC006
; CURRENT APPLICATION NUMBER: US/09/764,891
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 10231
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 8070
; LENGTH: 6107
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-764-891-8070

Alignment Scores:
Pred. No.: 1.4e-188 Length: 6107
Score: 1611.00 Matches: 298
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 10 Gaps: 0

US-10-679-246-2 (1-298) x US-09-764-891-8070 (1-6107)
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QY 1 MetValIleIlePheLeuLeuProProTyrValPheIleSerGluMetSerArgGln 20
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Db 3437 ATGGTTATAATTATTTTCTCGCTCCTCTATGTATTTATTTTCAGAAATGAGCGCTCAG 3496

QY 21 ThrAlaThrAlaLeuProThrGlyThrSerLysCysProProSerGlnArgValProAla 40
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|
|
Db 3497 ACTGCTACAGCATTAACCTACCGTACCTCGAAGTGTCACCATCCAGAGGGTGCCTGCC 3556

QY 41 LeuThrGlyThrThrAlaSerAsnAspLeuAlaSerLeuPheGluCysProValCys 60
|
|
|
Db 3557 CTGACTGGCACAACCTGCATCCAAACATGACTTGGCGAGTCTTTTTCAGTGTCCAGTCTGC 3616

QY 61 PheAspTyrValLeuProProIleLeuGlnCysGlnSerGlyHisLeuValCysSerAsn 80
|
|
|
Db 3617 TTTGACTATGTGTATCCGCCCATTTCTCAATGTTCAGAGTGGCCATCTTGTGTGTAGCAAC 3676

QY 81 CysArgProLysLeuThrCysCysProThrCysArgGlyProLeuGlySerIleArgAsn 100
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|
|
Db 3677 TGTGCCCCAAGCTCACAATGTTGTCCAACTTCCCGGGGCCCTTTTGGGATCCATTCGCAAC 3736

QY 101 LeuAlaMetGluLysValAlaAsnSerValLeuPheProCysLysTyrAlaSerSerGly 120
|
|
|
Db 3737 TTGGCTATGGAGAAAGTGGCTAATTCAGTACTTTTCCCTGTAAATATGCGTCTTCTGGA 3796

QY 121 CysGluIleThrLeuProHisThrGluLysAlaAspHisGluLeuCysGluPheArg 140
|
|
|
Db 3797 TGTGAAATAACTCTGCCACACACAGAAAAAGCAGACCATGAAAGAGCTCTGTGAGTTAGG 3856

QY 141 ProTyrSerCysProCysProGlyAlaSerCysLysTyrGlnGlySerLeuAspAlaVal 160
|
|
|
Db 3857 CCTTATTCTGTGCGCTGCTGCTTCTCTGTAATGCAAGGCTCTCTGTGATGCTGTA 3916
```



```
; PRIOR FILING DATE: 2001-06-21
; PRIOR APPLICATION NUMBER: US 60/301,572
; PRIOR FILING DATE: 2001-06-27
; PRIOR APPLICATION NUMBER: US 60/306,501
; PRIOR FILING DATE: 2001-07-18
; PRIOR APPLICATION NUMBER: US 60/325,002
; PRIOR FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: US 60/362,585
; PRIOR FILING DATE: 2002-03-05
; PRIOR APPLICATION NUMBER: US 60/xxx,xxx
; PRIOR FILING DATE: 2002-05-14
; NUMBER OF SEQ ID NOS: 506
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 426
; LENGTH: 2502
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-177-293-426

Alignment Scores:
Pred. No.:      8,66e-139      Length:      2502
Score:          1206.00        Matches:    228
Percent Similarity: 78.18%      Conservative: 30
Best Local Similarity: 69.09%    Mismatches: 30
Query Match:      74.86%      Indels:     42
DB:               15          Gaps:         5

US-10-679-246-2 (1-298) x US-10-177-293-426 (1-2502)

QY 10 ProTyrValPheIleSerGluMetSerArgGlnThrAlaThrAlaLeuProThrGlyThr 29
Db 506 CCATGGTTGTCGGAGCGCGATGAGCCGCCGCTCTCCACCGGC---CCAGCGGTAAT 562
QY 30 SerLysCys-----
Db 563 AAACCTGCGAGCAAGCAGCGCGCGCGAGCCAGCCACACATCCGTCGCCGGTGGCGCC 622
QY 33 -----ProSerGlnArgValProLa----- 40
Db 623 CGCGCGCGCGCCACCATCTCGGTGCGGGCGCGCGCTCGTCCGCGGTGCGCGCGCGG 682
QY 41 -----LeuThrGly-----ThrThrAlaSerAsn 49
Db 683 GCGGTGATCTCGGGCCCCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 742
QY 50 AspLeuAlaSerLeuPheGluCysProValCysPheAspTyrValLeuProLleLeu 69
Db 743 GAGCTGACCTCGCTCTTCGAGTGTCCGGTCTGCTTTGACTATGTCTGCTCTCTATTCTG 802
QY 70 GlnCysGlnSerGlyHisLeuValCysSerAsnCysArgProLysLeuThrCysCysPro 89
Db 803 CAGTGCAGCGCGCGCACCTGGTGTGTAAACCAATGCCGCCAGAGTTGAGCTGCTGCCG 862
QY 90 ThrCysArgGlyProLeu---GlySerIleArgAsnLeuAlaMetGluLysValAlaAsn 108
Db 863 ACCTGCGAGGGCGCCCTGAGCGCCACATCAGAACCTCGGCTATGAGAGGTGGCGCTCG 922
QY 109 SerValLeuPheProCysLysTyrAlaSerSerGlyCysGluIleThrLeuProHisThr 128
Db 923 CGAGTCTGTTCCTGTAGTATGTCACACCGGGCTGTTCCTGACCTTGACCATACG 982
QY 129 GluLysAlaAspHisGluGluLeuCysGluPheArgProTyrSerCysProCysProGly 148
Db 983 GAGAACCCAGAACATGAGACATATGTAATACCGTCCCTACTCTCGCCCATGCTCGTGT 1042
QY 149 AlaSerCysLysTyrGlnGlySerLeuAspAlaValMetProHisLeuMetHisGlnHis 168
Db 1043 GCTTCTCGAAGTGGCAGGGTCCCTGGAAGTGTGATGTCCATCTCATGACGCCAC 1102
QY 169 LysSerIleThrThrLeuGlnGlyGluAspIleValPheLeuAlaThrAspIleAsnLeu 188
Db 1103 AAGAGCATTACCACCCCTTCAGGGAGAAGACATCGTCTTCTAGCTACAGACATTACTTG 1162
```

```
QY 189 ProGlyAlaValAspTyrValMetMetGlnSerCysPheGlyPheHisPheMetLeuVal 208
Db 1163 CCAGGGGCTGTGCACTGGGTGATGATGAGTATGTTTGGCCATCCTCATGCTGGG 1222
QY 209 LeuGluLysGlnGluLysTyrAspGlyHisGlnGlnPhePheAlaIleValGlnLeuIle 228
Db 1223 CTGGAGAAACAAGAGAGTACGAGGCCACAGCAGTGTTCCTGCTCATTCCTGCTCAT 1282
QY 229 GlyThrArgLysGlnAlaGluAsnPheAlaTyrArgSerIleHisGluGlyLeuAlaThrAlaIleMet 248
Db 1283 GGCACCCCGCAGCAAGCCGAGAACTTTGCTCAGACTGGAGTGAATGGGAACCGCGCG 1342
QY 249 ArgLeuThrTrpGluAlaThrProArgSerIleHisGluGlyLeuAlaThrAlaIleMet 268
Db 1343 AGATTGACCTGGGAGGCCACGCCCTTCGATTCATGACGGTGTGCTCGGCCCATCATG 1402
QY 269 AsnSerAspCysLeuValPheAspThrSerIleAlaGlnLeuPheAlaGluAsnGlyAsn 288
Db 1403 AACAGGACTGCTGTGTTTCGACACAGCCATAGCACATCTTTTGCAGATAATGGGAAC 1462
QY 289 LeuGlyIleAsnValThrIleSerMetCys 298
Db 1463 CTTGGAATCAATGTTACTATTCTACATGT 1492

RESULT 9
US-10-172-118-1117
; Sequence 1117, Application US/10172118
; Publication No. US20030224374A1
; GENERAL INFORMATION:
; APPLICANT: Dai, Hongyue
; APPLICANT: He, Yudong
; APPLICANT: Linsley, Peter
; APPLICANT: Mao, Mao
; APPLICANT: Roberts, Chris
; APPLICANT: Van 't Veer, Laura
; APPLICANT: Van de Vijver, Marc
; APPLICANT: Bernards, Rene
; TITLE OF INVENTION: Diagnosis and Prognosis of Breast Cancer Patients
; FILE REFERENCE: 9301-175-999
; CURRENT APPLICATION NUMBER: US/10172,118
; CURRENT FILING DATE: 2002-06-14
; PRIOR APPLICATION NUMBER: 60/380,770
; PRIOR FILING DATE: 2002-05-14
; NUMBER OF SEQ ID NOS: 2699
; SEQ ID NO 1117
; LENGTH: 975
; TYPE: DNA
; ORGANISM: Homo sapiens
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: NM_005067
; DATABASE ENTRY DATE: 2001-06-18
US-10-172-118-1117

Alignment Scores:
Pred. No.:      1,58e-138      Length:      975
Score:          1199.00        Matches:    228
Percent Similarity: 84.90%      Conservative: 25
Best Local Similarity: 76.51%    Mismatches: 26
Query Match:      74.43%      Indels:     20
DB:               17          Gaps:         5

US-10-679-246-2 (1-298) x US-10-172-118-1117 (1-975)

QY 9 ProProTyrValPheIleSerGluMetSerArgGlnThrAlaThrAlaLeuProThrGly 28
Db 107 CCACCA-----TCTCGGCTCGGGCCCCCGCTCGTCCG----- 139
QY 29 ThrSerLysCysProProSerGln-----ArgValProAlaLeuThrGly----- 43
Db 140 -----CGGTGCCCCCGCGCGCGGTGATCTCGGGCCCCCGCGCGCGC-GGCGGGGC 192
QY 44 -----ThrThrAlaSerAsnAsnAspLeuAlaSerLeuPheGluCysProValCysPhe 61
Db 44 -----TCTCGGCTCGGGCCCCCGCTCGTCCG----- 139
```

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Db 193 GGCCCGGTGTCGCCGAGCACCAGACCTGACCTCGCTCTTCGAGTGTCCGGTCTGCTTT 252
Qy 62 AspTyrValLeuProProlLeuGlnCysGlnSerGlyHisLeuValCysSerAsnCys 81
Db 253 GACTATGTCCTGCTCTATTTGCAAGTCCAGCCGCGCAGCTGTGTGTAAACCAATGC 312
Qy 82 ArgProLysLeuThrCysCysProThrCysArgGlyProLeu---GlySerIleArgAsn 100
Db 313 CGCCAGAAAGTTGAGCTGCTGCCGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGT 372
Qy 101 LeuAlaMetGluLysValAlaAsnSerValLeuPheProCysLysTyrAlaSerSerGly 120
Db 373 CTGGCTATGAGAGAGTGGCTCGGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGT 432
Qy 121 CysGluIleThrLeuProHisThrGlnHisLysSerIleThrLeuGlnGlyGluAspIleVal 140
Db 433 TGTTCCTGACCTGACCATACGGAAGAACACAGAACATGATGTAATACCGT 492
Qy 141 ProTyrSerCysProCysProGlyAlaSerCysLysTyrGlnGlySerLeuAspAlaVal 160
Db 493 CCTACTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 552
Qy 161 MetProHisLeuMetHisGlnHisLysSerIleThrLeuGlnGlyGluAspIleVal 180
Db 553 ATGTCCCATCTCATGACGCCACACAGAGCATTTACCCCTTCAGGGAGAGACATCGTC 612
Qy 181 PheLeuAlaThrAspIleAsnLeuProGlyAlaValAspTyrValMetMetGlnSerCys 200
Db 613 TTTCCTAGCTACAGACATTAACCTTGCAGGGGCTGCTGCTGCTGCTGCTGCTGCTGCT 672
Qy 201 PheGlyPheHisPheMetLeuValLeuGluLysGlnGlyTyrAspGlyHisGlnGln 220
Db 673 TTTCGCTACCTCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 732
Qy 221 PhePheAlaIleValGlnLeuIleGlyThrArgLysGlnAlaGluAsnPheAlaTyrArg 240
Db 733 TTTTTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 792
Qy 241 LeuGluLeuAsnGlyHisArgArgLeuThrTyrGluAlaThrProArgSerIleHis 260
Db 793 CTGGAGTTGAATGGGAACCGCGGAGATTGACTGGAGGCCACCGCCCTTCGATTTCAT 852
Qy 261 GluGlyIleAlaThrAlaIleMetAsnSerAspCysLeuValPheAspThrSerIleAla 280
Db 853 GACGGTGTGCTGCGGCCCATCATGACAGCGACTGCTGCTGCTGCTGCTGCTGCTGCTGCT 912
Qy 281 GlnLeuPheAlaGluAsnGlyAsnLeuGlyIleAsnValThrIleSerMetCys 298
Db 913 CATCTTTTTCAGATAATGGGAACCTTGGAAATCAATGTTACTATTCTTACATGT 966
```

RESULT 10

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US-10-342-887-1117
; Sequence 1117, Application US/10342887
; Publication No. US20040058340A1
; GENERAL INFORMATION:
; APPLICANT: Dai, Hongyue
; APPLICANT: He, Yudong
; APPLICANT: Linsley, Peter S.
; APPLICANT: Mao, Mao
; APPLICANT: Roberts, Christopher J.
; APPLICANT: Van 't Veer, Laura Johanna
; APPLICANT: Van de Vijver, Marc J.
; APPLICANT: Bernards, Rene
; TITLE OF INVENTION: Diagnosis and Prognosis of Breast Cancer Patients
; FILE REFERENCE: 9301-188-999
; CURRENT APPLICATION NUMBER: US/10/342,887
; CURRENT FILING DATE: 2003-01-15
; PRIOR APPLICATION NUMBER: 60/298,918
; PRIOR FILING DATE: 2001-06-18
; PRIOR APPLICATION NUMBER: 60/380,710
; PRIOR FILING DATE: 2002-05-14
; PRIOR APPLICATION NUMBER: 10/172,118
; PRIOR FILING DATE: 2002-06-14
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; NUMBER OF SEQ ID NOS: 2699
; SEQ ID NO 1117
; LENGTH: 975
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-342-887-1117

Alignment Scores:
Pred. No.: 1,58e-138 Length: 975
Score: 1199.00 Matches: 228
Percent Similarity: 84.90% Conservative: 25
Best Local Similarity: 76.51% Mismatches: 26
Query Match: 74.43% Indels: 20
DB: 17 Gaps: 5

US-10-679-246-2 (1-298) x US-10-342-887-1117 (1-975)

Qy 9 ProProTyrValPheIleSerGluMetSerArgGlnThrAlaThrAlaLeuProThrGly 28
Db 107 CCACCA-----TCTGGCTGCGGGCCCGCGCTCGTCCG----- 139
Qy 29 ThrSerLysCysProProSerGln-----ArgValProAlaLeuThrGly----- 43
Db 140 -----CGGTGCGCCCGCGCGCGGTGATCTCGGGCCCGCGCGCGCGC--GGCGGGGCC 192
Qy 44 -----ThrAlaSerAsnAsnAspLeuAlaSerLeuPheGluCysProValCysPhe 61
Db 193 GGCCCGGTGTCGCCGAGCACCACGAGCTGACCTGCTCTTCGAGTGTCCGGTCTGCTTT 252
Qy 62 AspTyrValLeuProProlLeuGlnCysGlnSerGlyHisLeuValCysSerAsnCys 81
Db 253 GACTATGTCCTGCTCTATTTGCAAGTCCAGCCGCGCAGCTGTGTGTAAACCAATGC 312
Qy 82 ArgProLysLeuThrCysCysProThrCysArgGlyProLeu---GlySerIleArgAsn 100
Db 313 CGCCAGAAAGTTGAGCTGCTGCCGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGT 372
Qy 101 LeuAlaMetGluLysValAlaAsnSerValLeuPheProCysLysTyrAlaSerSerGly 120
Db 373 CTGGCTATGAGAGAGTGGCTCGGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGT 432
Qy 121 CysGluIleThrLeuProHisThrGlnHisLysSerIleThrLeuGlnGlyGluAspIleVal 140
Db 433 TGTTCCTGACCTGACCATACGGAAGAACACAGAACATGATGTAATACCGT 492
Qy 141 ProTyrSerCysProCysProGlyAlaSerCysLysTyrGlnGlySerLeuAspAlaVal 160
Db 493 CCTACTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 552
Qy 161 MetProHisLeuMetHisGlnHisLysSerIleThrThrLeuGlnGlyGluAspIleVal 180
Db 553 ATGTCCCATCTCATGACGCCACACAGAGCATTTACCCCTTCAGGGAGAGACATCGTC 612
Qy 181 PheLeuAlaThrAspIleAsnLeuProGlyAlaValAspTyrValMetMetGlnSerCys 200
Db 613 TTTCCTAGCTACAGACATTAACCTTGCAGGGGCTGCTGCTGCTGCTGCTGCTGCTGCT 672
Qy 201 PheGlyPheHisPheMetLeuValLeuGluLysGlnGlyTyrAspGlyHisGlnGln 220
Db 673 TTTCGCTACCTCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 732
Qy 221 PhePheAlaIleValGlnLeuIleGlyThrArgLysGlnAlaGluAsnPheAlaTyrArg 240
Db 733 TTTTTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 792
Qy 241 LeuGluLeuAsnGlyHisArgArgLeuThrTyrGluAlaThrProArgSerIleHis 260
Db 793 CTGGAGTTGAATGGGAACCGCGGAGATTGACTGGAGGCCACCGCCCTTCGATTTCAT 852
Qy 261 GluGlyIleAlaThrAlaIleMetAsnSerAspCysLeuValPheAspThrSerIleAla 280
Db 853 GACGGTGTGCTGCGGGCCCATCATGACAGCGACTGCTGCTGCTGCTGCTGCTGCTGCTGCT 912
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QY 281 GlnLeuPheAlaGluAenGlyLeuValThrIleSerMetCys 298
Db 913 CATCTTTTTCAGATTAATGGAACTTGAATCAATGTTACTATTCTACATGT 966

RESULT 11
US-10-177-293-424
; Sequence 424, Application US/10177293
; Publication No. US20030124128A1
; GENERAL INFORMATION:
; APPLICANT: Lillie, James
; APPLICANT: Glatt, Karen
; APPLICANT: Zhao, Xumei
; APPLICANT: Gannavarpu, Manjula
; APPLICANT: Kamatkar, Shubhangi
; APPLICANT: Mertens, Maureen
; APPLICANT: Myer, Vic
; APPLICANT: Wang, Youzhen
; APPLICANT: Xu, Yongyao
; APPLICANT: Hoersch, Sebastian
; APPLICANT: Monahan, John
; APPLICANT: Meyers, Rachel E.
; APPLICANT: East Jr., Robert C.
; APPLICANT: Hortobagyi, Gabriel N.
; APPLICANT: Pusztai, Lajos
; APPLICANT: Meric, Funda
; APPLICANT: Sahin, Aysegul
; APPLICANT: Mills, Gordon B.
; TITLE OF INVENTION: COMPOSITIONS, KITS, AND METHODS FOR IDENTIFICATION, ASSESSMENT,
; TITLE OF INVENTION: PREVENTION, AND THERAPY OF BREAST CANCER
; FILE REFERENCE: MRI-038
; CURRENT APPLICATION NUMBER: US/10/177,293
; CURRENT FILING DATE: 2002-06-21
; PRIOR APPLICATION NUMBER: US 60/299,887
; PRIOR FILING DATE: 2001-06-21
; PRIOR APPLICATION NUMBER: US 60/301,572
; PRIOR FILING DATE: 2001-06-27
; PRIOR APPLICATION NUMBER: US 60/306,501
; PRIOR FILING DATE: 2001-07-18
; PRIOR APPLICATION NUMBER: US 60/325,002
; PRIOR FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: US 60/362,585
; PRIOR FILING DATE: 2002-03-05
; PRIOR APPLICATION NUMBER: US 60/xxx,xxx
; PRIOR FILING DATE: 2002-05-14
; NUMBER OF SEQ ID NOS: 506
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 424
; LENGTH: 2240
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-177-293-424

Alignment Scores:
Pred. No.: 7,26e-138 Length: 2240
Score: 1198.00 Matches: 227
Percent Similarity: 77.88% Conservative: 30
Best Local Similarity: 68.79% Mismatches: 31
Query Match: 74.36% Indels: 42
DB: 15 Gaps: 5

US-10-679-246-2 (1-298) x US-10-177-293-424 (1-2240)

QY 10 ProTyrValPheIleSerGluMetSerArgGlnThrAlaThrAlaLeuProThrGlyThr 29
Db 506 CATGGTGGTTCGGAGCGGATGAGCCGCCGCTCTCCACCGGC---CCAGCGGTAA 562
QY 30 SerLysCys----- 32
Db 563 AAACCTCGCAGCAGCGCGCGCGCAGCCAGCACACCTCCGTCGCCGGTGGCGCC 622
QY 33 -----ProProSerGlnArgValProLa----- 40
Db 623 CGGCGCGCGCCACCATTCTCGGTGCGGCGCGCGCTCGTCCGCGGTGCGCGCGCG 682
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QY 41 -----LeuThrGly-----ThrThrAlaSerAsnAen 49
Db 683 GCGGTGATCTCGGGCCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCCAC 742
QY 50 AspLeuAlaSerLeuPheGluCysProValCysPheAspTyrValLeuProProIleLeu 69
Db 743 GAGTGAACCTCGCTCTTCGAGTGTGCGGTCTGCTTTGACTATGTCTGCTCTCTATCTG 802
QY 70 GlnCysGlnSerGlyHisLeuValCysSerAsnCysArgProLysLeuThrCysCysPro 89
Db 803 CAGTGCAGCGCGCGCACCTGGTGTAAACCAATGCCGCCAGAGTTGAGTGTCTGCCCG 862
QY 90 ThrCysArgGlyProLeu---GlySerIleArgAsnLeuAlaMetGluLysValAlaAen 108
Db 863 ACGTGCAGGGCGCCCTGACGCCAGCATCAGCACTGGCTATGGAGAGGTGGGCTCG 922
QY 109 SerValLeuPheProCysLysTyrAlaSerSerGlyCysGluIleThrLeuProHisThr 128
Db 923 GCAGTCTCTTTCCCTGTAAAGTATGCCACCGGGCTGTTCCCTGACCTGCACCATACG 982
QY 129 GluLysAlaAspHisGluGluLeuCysGluPheArgProTyrSerCysProCysProGly 148
Db 983 GAGAAACCAAGACATGAGACATATGTAATACCGCCCTACTCTCTGCCCATGTCTGCT 1042
QY 149 AlaSerCysLysTyrGlnGlySerLeuAspAlaValMetProHisLeuMetHisGlnHis 168
Db 1043 GCTTCTCTGCAAGTGGCAGGGTCTCCCTGGAAGCTGTGATGTCCCATCTCATGCACGCCAC 1102
QY 169 LysSerIleThrThrLeuGlnGlyGluAspIleValPheLeuAlaThrAspIleAenLeu 188
Db 1103 AAGAGCATTTACCACTTCCAGGAAGAGACATCGTCTTTCTAGCTACAGACATAACTTG 1162
QY 189 ProGlyAlaValAspTyrValMetMetGlnSerCysPheGlyPheHisPheMetLeuVal 208
Db 1163 CCAGGGGCTGTGACTGGGTGATGATGAGTATGTTTGGCCATCACTTCTGCTGGTG 1222
QY 209 LeuGluLysGlnGlyTyrAspGlyHisGlnGlnPhePheAlaIleValGlnLeuIle 228
Db 1223 CTGGAGAAACAAGAGAGTACGAAGGCCACAGCAGATTTTTTGCCATCGTCTCTCAAT 1282
QY 229 GlyThrArgLysGluAlaGluAsnPheAlaTyrArgLeuGluLeuAenGlyHisArgArg 248
Db 1283 GGCACCCGCAAGCAAGCCGAGAACTTTGCTCTACAGACTGGAGTTGAATGGGAACCGCGG 1342
QY 249 ArgLeuThrTyrGluAlaThrProArgSerIleHisGluGlyIleAlaThrAlaIleMet 268
Db 1343 AGATTGACCTGGAGGCCACGCCCTCGATTCATGCGGTGTGCTGCGGCCCATCATG 1402
QY 269 AsnSerAspCysLeuValPheAspThrSerIleAlaGlnLeuPheAlaGluAenGlyAen 288
Db 1403 AACAGCGACTGCTGTTTTCGACACAGCAGCATAGCACATCTTTTTCAGATAATGGGAAC 1462
QY 289 LeuGlyIleAsnValThrIleSerMetCys 298
Db 1463 CTTGGAATCAATGTTACTATTCTACATGT 1492

RESULT 12
US-10-717-597-137
; Sequence 137, Application US/10717597
; Publication No. US20040110221A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Burczynski, Michael E.
; APPLICANT: Twine, Natalie C.
; APPLICANT: Dornier, Andrew J.
; APPLICANT: Trepicchio, William L.
; APPLICANT: Slonim, Donna K.
; APPLICANT: Stover, Jennifer A.
; TITLE OF INVENTION: METHODS FOR DIAGNOSING RCC AND OTHER SOLID TUMORS
; FILE REFERENCE: AM101080L
; CURRENT APPLICATION NUMBER: US/10/717,597
; CURRENT FILING DATE: 2003-11-21
```

Qy	229	GlyThrArgLysGlnAlaGluAsn	PheAlaTyrArg	GluLeuLeuAsnGlyHis	ArgArg	248
Db	1283	GGCACCCGCGAAGCAAGCCGAGAACTTTG	CGCTACAGACTGGAGTTGAATGGGAAC	CGCGCG	1342	
Qy	249	ArgGluThrTrpGluAlaThrPro	ArgSerIleHis	GluGlyIleAlaThrAla	LeuMet	268
Db	1343	AGATTGACCTGGGAGGCGCACGCCCGCTG	ATTCAATGACGGTGTGGCTGGCGGCATCATG	1402		
Qy	269	AsnSerAspCysLeuValPheAsp	ThrSerIleAlaGlnLeuPheAlaGlu	AsnGlyAsn	288	
Db	1403	AACAGCGACTGCCTGTTTTCGACACAG	CCATAGCACATCTTTTTCGAGATATGGGAA	C	1462	
Qy	289	LeuGlyIleAsnValThrIleSer	MetCys	298		
Db	1463	CTTGGGAATCAATGTACTATTCTACATGT	1492			

RESULT 13
 US-10-755-889-123
 ; Sequence 123, Application US/10755889
 ; Publication No. US20040171823A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Bristol-Myers Squibb Company
 ; TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES ASSOCIATED WITH THE NF-
 ; TITLE OF INVENTION: PATHWAY
 ; FILE REFERENCE: D0284 NP
 ; CURRENT APPLICATION NUMBER: US/10/755,889
 ; PRIOR FILING DATE: 2004-01-13
 ; PRIOR APPLICATION NUMBER: U.S. 60/440,068
 ; PRIOR FILING DATE: 2003-01-14
 ; PRIOR APPLICATION NUMBER: U.S. 60/469,757
 ; PRIOR FILING DATE: 2003-05-12
 ; NUMBER OF SEQ ID NOS: 823
 ; SOFTWARE: PatentIn version 3.2
 ; SEQ ID NO 123
 ; LENGTH: 2240
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 US-10-755-889-123

Alignment Scores:			
Pred. No.:	7,26e-138	Length:	2240
Score:	1198.00	Matches:	227
Percent Similarity:	77.88%	Conservative:	30
Best Local Similarity:	68.79%	Mismatches:	31
Query Match:	74.36%	Indels:	42
DB:	18	Gaps:	5

US-10-679-246-2 (1-298) x US-10-755-889-123 (1-2240)

Qy	10	ProTyrValPheIleSerGluMetSer	ArgGlnThrAlaThrAlaLeuPro	ThrGlyThr	29	
Db	506	CCATGGTTGGTTCGGAGCGCGATGAG	CGCGCGCTCTCTCCACCGGC	---	562	
Qy	30	SerLysCys	-----	-----	32	
Db	563	AAACCTTCGACGAAAGCAGCGCGCG	CGCGAGCCCGCCAGCACACTCGTCCG	CGCGGTGCGCCC	622	
Qy	33	-----	-----	ProProSerGlnArgValPro	Ala	40
Db	623	CCGGCGCGCGCCACCATCTCGG	CTCGGCGCGCGCGCTGTCGCGCGGTG	CGCGCGCGCGCG	682	
Qy	41	-----	LeuThrGly	-----	ThrThrAlaSerAsn	49
Db	683	CGCGTGATCTCGGGCGCGCGCGCG	CGCGCGCGCGCGCGCGCGGTGTC	CGCGAGCACACC	742	
Qy	50	AspLeuAlaSerLeuPheGluCys	ProValCysPheAspTyrValLeu	ProProIleLeu	69	
Db	743	GAGCTGACCTCGCTCTCTCGAGT	CTCGGGTCTGTTGACTATGTCCTG	CTCTCTATTCG	802	
Qy	70	GlnCysGlnSerGlyHisIleuVal	CysSerAsnCysArgProLysLeu	ThrCysCys	Pro	89
Db	803	CAGTGCAGCGCGGACCTGGTGTGT	TAACCAATGCGCCAGAGTTGAGCTG	CTGCGCCG	862	

Qy	90	ThrCysArgGlyProLeu--GlySerIleArgAsnLeuAlaMetGluLysValAlaAsn	108
Db	863	ACGTGCAGGGCGCCCTGACCCCGAGCATCAGGAACCTGGCTATGGAGAAGGTGGCCCTCG	922
Qy	109	SerValLeuPheProCysLysTyTyrAlaSerSerGlyCysGluIleThrLeuProHisThr	128
		:::	
Db	923	GCAGTCTCTGTTTCCCTGTAAGTATGTCACCAACGGGCTGTTCCCTGCACCATACG	982
Qy	129	GluLysAlaAspHisGluGluLeuCysGluPheArgProTyrSerCysProCysProGly	148
Db	983	GAGAAACAGCAACATGAAGACATATGTAATACCGCCCTACTCTCTGCCCATGTCTGGT	1042
Qy	149	AlaSerCysLysTyrPheGlnGlySerLeuAspAlaValMetProHisLeuMetHisGlnHis	168
		:::	
Db	1043	GCTTCTCGAAGTGCAGGGGTCCCTGGGAAGCTGTGATGTCCCATCTCATGCAAGCCAC	1102
Qy	169	LysSerIleThrThrLeuGlnGlyGluAspIleValPheLeuAlaThrAspIleAsnLeu	188
Db	1103	AAGAGCATTTACACCCCTTCAGGAAGAAGACATCGCTCTTCTAGCTACAGACATTAACCTG	1162
Qy	189	ProGlyAlaValAspTvpValMetMetGlnSerCysPheGlyPheHisPheMetLeuVal	208
Db	1163	CCAGGGCTGTCTGACTGGGTGATGATGCAGTCATGTTTGGCCATCACTTCATGCTGGT	1222
Qy	209	LeuGluLysGlnGluLysTyrAspGlyHisGlnGlnPhePheAlaIleValGlnLeuIle	228
Db	1223	CTGAGAGAAACAAGAGAAGTACGAAGGGCCACAGCAGATTTTTTGGCATCGCTCTCATTT	1282
Qy	229	GlyThrArgLysGlnAlaGluAAsnPheAlaTyrArgLeuGluLeuAAsnGlyHisAspArg	248
Db	1283	GGCACCCGCAAGCAAGCCGAGACTTTGGCTTACAGACTGGAGTTGAATGGAAACCGCGG	1342
Qy	249	ArgLeuThrTrpGluAlaThrProArgSerIleHisGluGlyIleAlaThrAlaIleMet	268
Db	1343	AGATTGACTGGGAGGCCAGCCCGCTCGATTTCATGCGGTGGCTGGCGGCATCATG	1402
Qy	269	AsnSerAspCysLeuValPheAspThrSerIleAlaGlnLeuPheAlaGluAAsnGlyAsn	288
Db	1403	AACAGCACTGCCCTGTGTTTTCGACACACATAGCACATCTTTTTCAGATAATGGGAC	1462
Qy	289	LeuGlyIleAsnValThrIleSerMetCys	298
Db	1463	CTTGGAAATCAATGTTACTATTCTTACATGT	1492

RESULT 14

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US-09-925-297-84
; Sequence 84, Application US/09925297
; Patent No. US20020081659A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PA105
; CURRENT APPLICATION NUMBER: US/09/925,297
; CURRENT FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/05989
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 60/124,270
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 928
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 84
; LENGTH: 1535
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-297-84

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Alignment Scores:	
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Score:	474.00
Length:	1535
Percent Similarity:	98.95%
Best Local Similarity:	98.95%
Query Match:	29.42%
Matches:	94
Mismatches:	0
Indels:	1

DB:	9	Gaps:	0
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Db	2	TTCATGTTAGTCTTAGAGAAACAGAAAAAATACTGATGGTCACCGAGCTGTTCTTCGCAAT	61
Qy	224	eValGlnLeuIleGlyThrArgLysGlnAlaGluAsnPheAlaTyrArgLeuGluLueuAs	244
Db	62	CGTACAGCTGATAGGAACACGACGACGACGCTGAAAATTTTGGCTTACCGACTTGAGCTAAA	121
Qy	244	nGlyHisArgArgLeuThrTrpGluAlaThrProArgSerIleHisGluGlyIleAl	264
Db	122	TGGTCATAGGCGACGATTGACTTTGGGAGCGACTCTCTCGATCTATTTCATGAGGGAATTCG	181
Qy	264	arThrAlaIleMetAsnSerAspCysLeuValPheAspThrSerIleAlaGlnLeuPheAl	284
Db	182	AACAGCCATTATGAATACGCACTGTCTAGTCTTTTGACACCAACGACATTGACACGCTTTTTCG	241
Qy	284	aGluAsnGlyAsnLeuGlyIleAsnValThrIleSerMetCys	298
Db	242	AGAAAAATGGCAATTTAGGCATCAATGTAACATTATTTCCATGTGT	284

RESULT 15

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US-10-437-963-83416/c
; Sequence 83416, Application US/10437963
; Publication No. US20040123343A1
;
; GENERAL INFORMATION:
;
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
;
; TITLE OF INVENTION: Rice Nucleic Acid Molecules a
;
; TITLE OF INVENTION: Plants and Uses Thereof for
;
; FILE REFERENCE: 38-21(53221)B
;
; CURRENT APPLICATION NUMBER: US/10/437,963
;
; CURRENT FILING DATE: 2003-05-14
;
; NUMBER OF SEQ ID NOS: 204966
;
; SEQ ID NO 83416
;
; LENGTH: 1438
;
; TYPE: DNA
;
; ORGANISM: Oryza sativa
;
; FEATURE:
;
; OTHER INFORMATION: Clone ID: PAT_MRT4530_8274C.1
;
; US-10-437-963-83416

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Best Local Similarity:	39.36%
Query Match:	28.71%
DB:	18
Length:	1438
Matches:	111
Conservative:	44
Mismatches:	101
Indels:	27
Gaps:	10

US-10-679-246-2 (1-298) x US-10-437-963-83416 (1-1438)

QY	28	GlyThrSerLysCysPro-	-----SerGlnArgValProAlaLeu	41
Db	1154	GGAGATTCTACATGCAGCCCTGGTCTACATCACTACTGTGTCAAGTTGAGCTATCATCGCTG	1095	
QY	42	ThrGlyThrThrAlaSerAsnAsnAspLeuAlaSerLeuPheGluCysProValCysPhe	61	
Db	1094	ACGGGC-----TTGAATGATTTTGTCTCAGTGTCCAGTCTGCACA	1056	
QY	62	AspTyrValLeuProProlLeuGlnCysGlnSerGlyHisLeuValCysSerAsnCys	81	
Db	1055	AACTCAATGGCCCACTATCTACTGAGTGGCCCAATGGTCACAAATATGCTCTAACTGC	996	

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QY 82 ArgProLysLeu---ThrCysCysProThrCysArgGlyProLeuGlySerIleArgAsn 100
Db 995 AAGCATAGGTGGAGAAATCATTTGCTTCCCAAGAACTGGGTAATATCAGATGT 936
QY 101 LeuAlaMetGluLysValAlaAsnSerValLeuPheProCysLysTyrAlaSerSerGly 120
Db 935 TTGGCTCTTGAAGGTGGCTCAGTCACCTTCCATGCAAAATATCAAAAGCCTAGGC 876
QY 121 CysGluIleThrLeuProHisThrGluLysAlaAspHisGluGluLeuCysGluPheArg 140
Db 875 TGTGCTGAGATTTCCTTACCAAAACAACTTAAGCATGAGGAGCTTCGAGGTTCCAGG 816
QY 141 ProTyrSerCysProCysProGlyAlaSerCysLysTyrPngInGlySerLeuAspAlaVal 160
Db 815 CCATATAGTTGTCATATGACAGTTCCAGATGCTGATTTGCTGGCGATCTTCCGATGCTT 756
QY 161 MetProHisLeuMetHisGlnHisLysSerIleThrThrLeuGlnGlyGluAspIleVal 180
Db 755 GTCTCTCATCTCATAAACGACCATTAAG---GTGGACTTGCATGAAGGCTGCACCTTTAAC 699
QY 181 PheLeuAlaThrAspIleAsnLeuProGlyAlaValAsp-----TrpValMet--- 196
Db 698 CACCCTTATGTGAAGTCCAAAC---CCTATGAAGTGGAAACGCTACATGGATGCTGACG 642
QY 197 MetGlnSerCysPheGlyPheHisPheMetLeu-VallLeuGluLysGlnGluLysTyrAs 216
Db 641 GTTTTCAAGTGTTTGGACAGCACTTCTGCCTGCATTGTG---AGGCATTCTCTGTGGGG 585
QY 216 pGlyHisGlnGlnPhePheAlaIleValGlnLeuIleGlyThrArgLysGlnAlaGluAs 236
Db 584 ATGGCACCAGTG-TACATGGCGTCTCTGAGGTTTCATGGCGGAGGACAGCGAGGCCCGGAA 526
QY 236 nPheAlaTyrArgLeuGluLeuAsnGlyHisArgArgArgLeuThrTrpGluAlaThrPr 256
Db 525 CTTCGTACAGCCCTGAGGTGGCGGGAACGGCGGAGCTGACATGGCAGGGCATCCC 466
QY 256 oArgSerIleHisGluGlyIleAlaThrAlaIleMetAsnSerSerCysLeuValPheAs 276
Db 465 CCGGAGCATCAGGGACAGCCACAGAGAGTCCGGGACAGCTTCGACGGGCTCATCATCCA 406
QY 276 pThrSerIleAlaGlnLeuPheAlaGluAsnGlyAsn-----LeuGlyIleAsnVa 293
Db 405 CCGGAACATGGCC---CTCTTCTTCTCCGGCGGCAACAGGCAGGAGCTCAAGCTGGGGT 349
QY 293 lThr 294
Db 348 TACC 345
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Search completed: April 25, 2005, 10:57:04

Job time : 673 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: April 24, 2005, 22:57:31 ; Search time 5658 Seconds
(without alignments)
10910.559 Million cell updates/sec

Title: US-10-679-246-1

Perfect score: 1274

Sequence: 1 ttcttttagtggttatgtg.....ctctttcgtagtggaagc 1274

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 4708233 seqs, 24227607955 residues

Word size : 15

Total number of hits satisfying chosen parameters: 122303

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Database :

GenEmbl.*

1: gb.ba.*

2: gb.htg.*

3: gb.in.*

4: gb.om.*

5: gb.ov.*

6: gb.pat.*

7: gb.ph.*

8: gb.pl.*

9: gb.pr.*

10: gb.ro.*

11: gb.sta.*

12: gb.sy.*

13: gb.un.*

14: gb.vi.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	1274	100.0	1274	6	AR411820 Sequence
2	1274	100.0	1274	6	AX058082 Sequence
3	1274	100.0	2924	6	CQ491092 Sequence
4	1274	100.0	2924	6	CQ493590 Sequence
5	1274	100.0	2924	6	CQ496955 Sequence
6	1274	100.0	31705	9	HS2400626 Homo sapi
7	1274	100.0	173304	9	AC023818 Homo sapi
8	1223	96.0	2829	6	AX833145 Sequence
9	1223	96.0	2829	9	AK094663 Homo sapi
10	1172	92.0	2972	9	HSN807215 Homo sapi
11	1104	86.7	2128	9	AK056051 Homo sapi
12	1041	81.7	2440	6	AR380043 Sequence
13	958	75.2	1540	6	BC035562 Homo sapi
14	958	75.2	1874	6	CQ719559 Sequence
15	958	75.2	2048	9	HSU76247 Human hSIAB
16	957	75.1	2454	9	BC042550 Homo sapi
17	947	74.3	1886	9	HSU63295 Homo sapien
18	881	69.2	4030	6	AX780380 Sequence
19	838	65.8	2034	9	BC018193 Homo sapi

20	780	61.2	1884	6	A63558	A63558 Sequence 11
21	780	61.2	1884	6	AR271267	AR271267 Sequence
C 22	159	12.5	405	6	CQ506573	CQ506573 Sequence
C 23	154	12.1	277	6	CQ476643	CQ476643 Sequence
C 24	142	11.1	673	11	BV208831	BV208831 SIFA1 234
C 25	139	10.9	417	6	CQ511941	CQ511941 Sequence
C 26	128	10.0	473	6	CQ516613	CQ516613 Sequence
C 27	118	9.3	411	6	CQ481952	CQ481952 Sequence
C 28	118	9.3	441	6	CQ503091	CQ503091 Sequence
C 29	92	7.2	523	11	BV102520	BV102520 MARC 1442
C 30	88	6.9	194622	10	AC133654	AC133654 Mus muscu
C 31	85	6.7	438	6	CQ472783	CQ472783 Sequence
C 32	77	6.0	1845	10	BC046317	BC046317 Mus muscu
C 33	77	6.0	1968	6	AX305603	AX305603 Sequence
C 34	77	6.0	1968	10	MMSIAH1A	Z19579 M.musculus
C 35	77	6.0	175636	10	AC142211	AC142211 Mus muscu
C 36	62	4.9	732	11	BV104504	BV104504 MARC 1442
C 37	62	4.9	732	11	BV104504	BV104504 MARC 1442
C 38	53	4.2	1457	10	AB067814	AB067814 Rattus no
C 39	53	4.2	1465	10	AF389476	AF389476 Rattus no
C 40	53	4.2	220157	2	AC105462	AC105462 Rattus no
C 41	53	4.2	232382	2	AC098991	AC098991 Rattus no
C 42	52	4.1	426	6	CQ486802	CQ486802 Sequence
C 43	52	4.1	2123	10	MMSIAHPSA	Z19582 M.musculus
C 44	52	4.1	168091	10	AC139553	AC139553 Mus muscu
C 45	52	4.1	182733	10	AC123941	AC123941 Mus muscu
C 46	45	3.5	1713	10	MMSIAH1B	Z19580 M.musculus
C 47	45	3.5	1720	10	BC052887	BC052887 Mus muscu
C 48	45	3.5	112893	10	AL732294	AL732294 Mouse DNA
C 49	45	3.5	234105	10	AC091606	AC091606 Mus Muscu
C 50	37	2.9	523	11	BV102520	BV102520 MARC 1442
C 51	35	2.7	196	10	MMSIAHPBS	Z19583 M.musculus
C 52	35	2.7	600	5	AF411976	AF411976 Gallus ga
C 53	35	2.7	711	5	CR386772	CR386772 Gallus ga
C 54	32	2.5	89948	9	AL359734	AL359734 Human DNA
C 55	30	2.4	1212	10	AF389477	AF389477 Rattus no
C 56	30	2.4	2048	10	AB067815	AB067815 Rattus no
C 57	30	2.4	2198	6	AX305605	AX305605 Sequence
C 58	30	2.4	2198	10	MMSIAH2A	Z19581 M.musculus
C 59	30	2.4	2511	10	BC058400	BC058400 Mus muscu
C 60	30	2.4	164715	2	AC142228	AC142228 Mus muscu
C 61	30	2.4	181603	2	AC119873	AC119873 Mus muscu
C 62	30	2.4	221589	2	AC126910	AC126910 Rattus no
C 63	30	2.4	254091	2	AC112531	AC112531 Rattus no
C 64	28	2.2	1509	5	AF155509	AF155509 Xenopus l
C 65	26	2.0	1246	2	BC072747	BC072747 Xenopus l
C 66	25	2.0	280815	2	AC107562	AC107562 Rattus no
C 67	24	1.9	9462	3	AF466306	AF466306 Dictyoste
C 68	24	1.9	129435	9	AL391314	AL391314 Human DNA
C 69	24	1.9	140179	2	AC084688	AC084688 Homo sapi
C 70	24	1.9	211456	10	AL928926	AL928926 Mouse DNA
C 71	23	1.8	341	5	AF529483	AF529483 Acipenser
C 72	23	1.8	41352	3	AF190936	AF190936 Drosophil
C 73	22	1.7	143119	8	AP005068	AP005068 Oryza sat
C 74	22	1.7	149628	2	AC151175	AC151175 Bos tauru
C 75	22	1.7	160788	9	AC128653	AC128653 Homo sapi
C 76	22	1.7	181870	2	AC068474	AC068474 Homo sapi
C 77	22	1.7	184121	9	AC023119	AC023119 Homo sapi
C 78	22	1.7	186272	2	AC134495	AC134495 Rattus no
C 79	22	1.7	195419	2	CR550302	CR550302 Danio rer
C 80	22	1.7	204618	2	EX321889	EX321889 Danio rer
C 81	22	1.7	217636	10	AC127411	AC127411 Mus muscu
C 82	22	1.7	222312	2	AC122624	AC122624 Rattus no
C 83	22	1.7	227154	10	AC115121	AC115121 Mus muscu
C 84	22	1.7	235733	2	AC106933	AC106933 Rattus no
C 85	21	1.6	810	5	CR390245	CR390245 Gallus ga
C 86	21	1.6	1094	6	CQ771162	CQ771162 Sequence
C 87	21	1.6	1150	6	CQ771161	CQ771161 Sequence
C 88	21	1.6	1913	9	AK122746	AK122746 Homo sapi
C 89	21	1.6	5047	9	AF283519S7	AF283519S7 Homo sapi
C 90	21	1.6	35056	3	CER10H10	Z70586 Caenorhabdi
C 91	21	1.6	72735	8	AP004487	AP004487 Lotus cor
C 92	21	1.6	94430	8	AC149544	AC149544 Populus b

93	21	1.6	110000	2	AC109084_1	Continuation (2 of
94	21	1.6	116305	9	AC106876	Homo sapi
95	21	1.6	121764	8	AC149804	Medicago
96	21	1.6	139939	8	AC149804	Medicago
97	21	1.6	140031	2	AC121686	Homo sapi
98	21	1.6	149724	10	AC136637	Continuation (4 of
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137	20	1.6	609	11	AC133185	Continuation (4 of
138	20	1.6	640	11	AC133185	Continuation (4 of
139	20	1.6	720	9	AC133185	Continuation (4 of
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152	20	1.6	2866	8	AC133185	Continuation (4 of
153	20	1.6	2961	6	AC133185	Continuation (4 of
154	20	1.6	3157	6	AC133185	Continuation (4 of
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158	20	1.6	7274	9	AC133185	Continuation (4 of
159	20	1.6	8342	9	AC133185	Continuation (4 of
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164	20	1.6	46189	8	AC133185	Continuation (4 of
165	20	1.6	48600	9	AC133185	Continuation (4 of
166	20	1.6	52454	2	AC100936	Mus muscu
167	20	1.6	55339	9	AC093593	Homo sapi
168	20	1.6	56031	9	AL157377	Human DNA
169	20	1.6	77835	2	PFMAL13P2_3	Continuation (4 of
170	20	1.6	78794	9	AC003990	Homo sapi
171	20	1.6	84313	3	AC103565	Caenorhab
172	20	1.6	84367	3	AC005454	Drosophil
173	20	1.6	84550	3	PFMAL1P2_3	Continuation (4 of
174	20	1.6	84710	5	AL928945	Continuation (4 of
175	20	1.6	88412	2	AC141373	Continuation (4 of
176	20	1.6	89652	5	AC141373	Continuation (4 of
177	20	1.6	89755	9	AC141373	Continuation (4 of
178	20	1.6	91587	2	AC12924	Continuation (4 of
179	20	1.6	93853	2	CR381612	Continuation (4 of
180	20	1.6	100241	2	CR381612	Continuation (4 of
181	20	1.6	102306	5	AC141373	Continuation (4 of
182	20	1.6	110000	1	AC141373	Continuation (4 of
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185	20	1.6	110000	2	AC141373	Continuation (4 of
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189	20	1.6	119526	8	AC141373	Continuation (4 of
190	20	1.6	121506	4	AC141373	Continuation (4 of
191	20	1.6	124070	2	AC141373	Continuation (4 of
192	20	1.6	124595	2	AC141373	Continuation (4 of
193	20	1.6	125681	10	AC141373	Continuation (4 of
194	20	1.6	128803	9	AC141373	Continuation (4 of
195	20	1.6	128803	9	AC141373	Continuation (4 of
196	20	1.6	128422	9	AC141373	Continuation (4 of
197	20	1.6	128980	2	AC141373	Continuation (4 of
198	20	1.6	131535	9	AC141373	Continuation (4 of
199	20	1.6	132254	3	AC141373	Continuation (4 of
200	20	1.6	133954	9	AC141373	Continuation (4 of
201	20	1.6	134741	2	AC141373	Continuation (4 of
202	20	1.6	135011	2	AC141373	Continuation (4 of
203	20	1.6	135245	10	AC141373	Continuation (4 of
204	20	1.6	135653	2	AC141373	Continuation (4 of
205	20	1.6	136937	5	AC141373	Continuation (4 of
206	20	1.6	139583	2	AC141373	Continuation (4 of
207	20	1.6	140067	8	AC141373	Continuation (4 of
208	20	1.6	140915	9	AC141373	Continuation (4 of
209	20	1.6	141881	4	AC141373	Continuation (4 of
210	20	1.6	142340	10	AC141373	Continuation (4 of
211	20	1.6	143392	8	AC141373	Continuation (4 of
212	20	1.6	144248	2	AC141373	Continuation (4 of
213	20	1.6	145710	2	AC141373	Continuation (4 of
214	20	1.6	147097	9	AC141373	Continuation (4 of
215	20	1.6	147346	2	AC141373	Continuation (4 of
216	20	1.6	148394	2	AC141373	Continuation (4 of
217	20	1.6	149563	2	AC141373	Continuation (4 of
218	20	1.6	149807	10	AC141373	Continuation (4 of
219	20	1.6	152057	9	AC141373	Continuation (4 of
220	20	1.6	152121	2	AC141373	Continuation (4 of
221	20	1.6	152209	2	AC141373	Continuation (4 of
222	20	1.6	153505	3	AC141373	Continuation (4 of
223	20	1.6	154779	3	AC141373	Continuation (4 of
224	20	1.6	157134	2	AC141373	Continuation (4 of
225	20	1.6	158500	2	AC141373	Continuation (4 of
226	20	1.6	160303	2	AC141373	Continuation (4 of
227	20	1.6	162877	9	AC141373	Continuation (4 of
228	20	1.6	163053	2	AC141373	Continuation (4 of
229	20	1.6	163985	10	AC141373	Continuation (4 of
230	20	1.6	164823	9	AC141373	Continuation (4 of
231	20	1.6	165014	5	AC141373	Continuation (4 of
232	20	1.6	166685	2	AC141373	Continuation (4 of
233	20	1.6	167310	10	AC141373	Continuation (4 of
234	20	1.6	167702	2	AC141373	Continuation (4 of
235	20	1.6	167949	2	AC141373	Continuation (4 of
236	20	1.6	168499	9	AC141373	Continuation (4 of
237	20	1.6	169993	2	AC141373	Continuation (4 of
238	20	1.6	171752	2	AC141373	Continuation (4 of

C 239	20	1.6 172336	9	CNS06C7Z	AL391153 Human chr	C 312	20	1.6 244180	2	AC094031	Rattus no
240	20	1.6 173643	2	AC107793	AC107793 Mus muscu	C 313	20	1.6 244598	2	AC105871	Rattus no
241	20	1.6 173740	2	AC020964	AC020964 Mus muscu	C 314	20	1.6 245413	2	AC095423	Rattus no
C 242	20	1.6 173769	9	AC113933	AC113933 Homo sapi	315	20	1.6 246742	2	AC103033	Rattus no
243	20	1.6 174037	9	AC009995	AC009995 Homo sapi	316	20	1.6 247845	2	AC094039	Rattus no
244	20	1.6 174540	2	AC068801	AC068801 Homo sapi	317	20	1.6 248001	2	AC051614	Mus muscu
C 245	20	1.6 176349	8	AP002092	AP002092 Oryza sat	318	20	1.6 248178	2	AC097387	Rattus no
246	20	1.6 177488	8	AC146766	AC146766 Oryza sat	C 319	20	1.6 249107	2	AC094049	Rattus no
247	20	1.6 177613	10	AC101968	AC101968 Mus muscu	C 320	20	1.6 252420	3	AE014841	Plasmodiu
248	20	1.6 178142	2	AC133840	AC133840 Rattus no	C 321	20	1.6 252524	2	AC114081	Rattus no
249	20	1.6 178733	9	AC026003	AC026003 Homo sapi	322	20	1.6 252749	2	AC096611	Rattus no
250	20	1.6 179941	2	AC145934	AC145934 Gallus ga	323	20	1.6 253880	2	AC113716	Rattus no
251	20	1.6 180136	1	BAC180K	D26185 B. subtilis	324	20	1.6 265677	5	CNS09SBK	Clone A24
C 252	20	1.6 180714	8	AP005804	AP005804 Oryza sat	325	20	1.6 265677	5	CNS09SBP	AE0572609 Tetraodon
C 253	20	1.6 181096	10	AL592187	AL592187 Mouse DNA	326	20	1.6 269102	3	AE003628	AE003628 Drosophila
254	20	1.6 182371	10	AC147263	AC147263 Mus muscu	C 327	20	1.6 269797	2	AC120567	Rattus no
255	20	1.6 183156	2	AC023062	AC023062 Mus muscu	328	20	1.6 269854	2	AC107448	Rattus no
C 256	20	1.6 183958	2	BX530096	BX530096 Mus muscu	329	20	1.6 270153	2	AC096262	Rattus no
257	20	1.6 187984	2	AP001262	AP001262 Homo sapi	330	20	1.6 274417	2	AC128979	Rattus no
C 258	20	1.6 188008	10	AC078863	AC078863 Mus muscu	C 331	20	1.6 275351	2	AC117883	Rattus no
259	20	1.6 188218	10	AL136998	AL136998 Mouse DNA	C 332	20	1.6 280240	2	AC106683	Rattus no
C 260	20	1.6 188937	10	AC108433	AC108433 Mus muscu	C 333	20	1.6 281089	2	AC094473	Rattus no
261	20	1.6 189736	6	CO870483	CO870483 Sequence	C 334	20	1.6 284886	2	AC110112	Rattus no
262	20	1.6 190771	2	AC140346	AC140346 Mus muscu	335	20	1.6 289591	2	AC125748	Rattus no
263	20	1.6 191219	2	AC109499	AC109499 Mus muscu	C 336	20	1.6 297657	2	AC120626	Rattus no
C 264	20	1.6 191396	2	AC118776	AC118776 Rattus no	337	20	1.6 301278	1	AE0015939	Clostridi
265	20	1.6 191735	10	AC092711	AC092711 Mus muscu	C 338	20	1.6 302000	1	AB003187	AP003187 Clostridi
C 266	20	1.6 194310	9	AP001267	AP001267 Homo sapi	C 339	20	1.6 304923	1	AB017289	Leptospir
C 267	20	1.6 194449	2	AC103673	AC103673 Mus muscu	C 340	20	1.6 309014	2	AC129655	Rattus no
268	20	1.6 194602	2	AC124087	AC124087 Mus muscu	C 341	20	1.6 310003	1	AE014016	Buchnera
C 269	20	1.6 194849	2	AC147015	AC147015 Zea mays	C 342	20	1.6 312241	2	AC108636	Rattus no
C 270	20	1.6 195305	10	AL713967	AL713967 Mouse DNA	343	20	1.6 323222	2	AC112459	Rattus no
C 271	20	1.6 195814	2	AC129635	AC129635 Rattus no	344	20	1.6 328550	2	AC142772	Macaca mu
272	20	1.6 196803	10	AC132461	AC132461 Mus muscu	C 345	20	1.6 329753	2	AC096701	Rattus no
C 273	20	1.6 197943	2	AC129321	AC129321 Mus muscu	346	20	1.6 333321	3	AC116986	Dictyoste
274	20	1.6 198057	2	AC126072	AC126072 Rattus no	C 347	20	1.6 346597	2	AC134498	Rattus no
275	20	1.6 198573	10	AL529186	AL529186 Mouse DNA	C 348	20	1.6 346597	2	AC134498	Rattus no
C 276	20	1.6 201137	2	AC128312	AC128312 Rattus no	349	20	1.6 349980	6	CO870482	Sequence
C 277	20	1.6 203207	2	AC141523	AC141523 Rattus no	C 350	20	1.6 349980	6	AX344559	Sequence
C 278	20	1.6 206503	2	BX324197	BX324197 Danio rer	C 351	20	1.6 349980	6	AX344559	Sequence
C 279	20	1.6 207008	2	CR847513	CR847513 Danio rer	C 352	20	1.6 349980	6	AX344559	Sequence
280	20	1.6 207107	2	CR354437	CR354437 Danio rer	C 353	20	1.6 349980	6	AX344559	Sequence
281	20	1.6 208140	2	CR354437	CR354437 Danio rer	C 354	20	1.6 349980	6	AX344559	Sequence
282	20	1.6 208770	2	CR388155	CR388155 Danio rer	C 355	20	1.6 349980	6	AX344559	Sequence
C 283	20	1.6 209326	10	AC110247	AC110247 Mus muscu	C 356	20	1.6 349980	6	AX344559	Sequence
C 284	20	1.6 210427	10	AC124757	AC124757 Mus muscu	C 357	20	1.6 349980	6	AX344559	Sequence
C 285	20	1.6 211167	2	AC091249	AC091249 Mus muscu	C 358	20	1.6 349980	6	AX344559	Sequence
C 286	20	1.6 211381	10	AC116404	AC116404 Mus muscu	C 359	20	1.6 349980	6	AX344559	Sequence
C 287	20	1.6 212159	2	AC101877	AC101877 Mus muscu	C 360	20	1.6 349980	6	AX344559	Sequence
288	20	1.6 213080	1	BSUB0001	Z99104 Bacillus su	C 361	20	1.6 349980	6	AX344559	Sequence
289	20	1.6 213862	10	AC126552	AC126552 Mus muscu	C 362	20	1.6 349980	6	AX344559	Sequence
290	20	1.6 214250	9	AC108050	AC108050 Homo sapi	C 363	20	1.6 349980	6	AX344559	Sequence
291	20	1.6 214290	5	BX294379	BX294379 Zebrafish	C 364	20	1.6 349980	6	AX344559	Sequence
292	20	1.6 214308	10	AL590870	AL590870 Mouse DNA	C 365	20	1.6 349980	6	AX344559	Sequence
293	20	1.6 215638	10	AC124200	AC124200 Mus muscu	C 366	20	1.6 349980	6	AX344559	Sequence
294	20	1.6 217046	10	AC122389	AC122389 Mus muscu	C 367	20	1.6 349980	6	AX344559	Sequence
295	20	1.6 218573	10	AC111460	AC111460 Rattus no	C 368	20	1.6 349980	6	AX344559	Sequence
C 296	20	1.6 218573	10	AC111460	AC111460 Rattus no	C 369	20	1.6 349980	6	AX344559	Sequence
297	20	1.6 219812	10	AC118196	AC118196 Mus muscu	C 370	20	1.6 349980	6	AX344559	Sequence
C 298	20	1.6 220894	10	AL732410	AL732410 Mouse DNA	C 371	20	1.6 349980	6	AX344559	Sequence
C 299	20	1.6 221557	2	AC146538	AC146538 Gastrost	C 372	20	1.6 349980	6	AX344559	Sequence
300	20	1.6 223109	2	BX957336	BX957336 Danio rer	C 373	20	1.6 349980	6	AX344559	Sequence
301	20	1.6 224643	2	AC097155	AC097155 Rattus no	C 374	20	1.6 349980	6	AX344559	Sequence
302	20	1.6 225152	10	AC132454	AC132454 Mus muscu	C 375	20	1.6 349980	6	AX344559	Sequence
C 303	20	1.6 228961	2	AC103135	AC103135 Rattus no	C 376	20	1.6 349980	6	AX344559	Sequence
304	20	1.6 229791	2	CR391941	CR391941 Danio rer	C 377	20	1.6 349980	6	AX344559	Sequence
305	20	1.6 230701	10	AL713871	AL713871 Mouse DNA	C 378	20	1.6 349980	6	AX344559	Sequence
306	20	1.6 231276	2	AC128991	AC128991 Rattus no	C 379	20	1.6 349980	6	AX344559	Sequence
307	20	1.6 232617	2	AC135871	AC135871 Rattus no	C 380	20	1.6 349980	6	AX344559	Sequence
C 308	20	1.6 237164	2	AC114255	AC114255 Rattus no	C 381	20	1.6 349980	6	AX344559	Sequence
309	20	1.6 237165	10	AC112948	AC112948 Mus muscu	C 382	20	1.6 349980	6	AX344559	Sequence
310	20	1.6 237378	2	AC087038	AC087038 Mus muscu	C 383	20	1.6 349980	6	AX344559	Sequence
C 311	20	1.6 237754	10	AC125576	AC125576 Rattus no	384	20	1.6 349980	6	AX344559	Sequence
		1.6 241249	10	AL935147	AL935147 Mouse DNA						

C 385	19	1.5	2136	10	RNU37539	U37539 Rattus norv	458	19	1.5	40874	9	AF129108	Hom sapi i
C 386	19	1.5	2136	10	RNU37540	U37540 Rattus norv	C 459	19	1.5	41516	9	BX470067	Human DNA
C 387	19	1.5	2258	6	AR071580	AR071580 Sequence	C 460	19	1.5	41836	9	AC021052	Hom sapi
C 388	19	1.5	2258	6	AR380450	AR380450 Sequence	C 461	19	1.5	43379	9	CBC02C6	Z79596 Caenorhabdi
C 389	19	1.5	2258	6	AX409722	AX409722 Sequence	C 462	19	1.5	43944	9	AY642135	Hom sapi
C 390	19	1.5	2258	6	HUM2C18	M61853 Human cytoc	C 463	19	1.5	44521	3	AF045640	Caenorhab
C 391	19	1.5	2271	1	CDI300676	AX300676 Clostridi	C 464	19	1.5	46650	9	AC358783	Human DNA
C 392	19	1.5	2271	6	AX259458	AX259458 Sequence	C 465	19	1.5	47880	9	AC006651	Caenorhab
C 393	19	1.5	2271	6	AX512804	AX512804 Sequence	C 466	19	1.5	51340	2	AC025213	Hom sapi
C 394	19	1.5	2306	14	PNVICBPA	DI0331 Pneumonia v	C 467	19	1.5	55163	2	AC020517	Drosophil
C 395	19	1.5	2395	9	HUMSVF450A	I07093 Human cytoc	C 468	19	1.5	57969	2	AC100083	Mus muscu
C 396	19	1.5	2396	8	AY054495	AY054495 Arabidops	C 469	19	1.5	58149	2	AC102560	Mus muscu
C 397	19	1.5	2515	3	DMU34039	U34039 Drosophila	C 470	19	1.5	58822	6	AX695431	Sequence
C 398	19	1.5	2520	8	AX369264	AY69264 Cochliobo	C 471	19	1.5	59832	1	CR628339	Legionell
C 399	19	1.5	2859	3	DDGLPV	X62142 D. discoide	C 472	19	1.5	60945	9	AC079394	Hom sapi
C 400	19	1.5	2938	10	RNNAC	X78034 R.norvegicu	C 473	19	1.5	62190	9	AC116301	Hom sapi
C 401	19	1.5	2989	10	AF112187	AF112187 Mus muscu	C 474	19	1.5	63998	2	AC101027	Mus muscu
C 402	19	1.5	3001	6	BD265989	BD265989 Schizophr	C 475	19	1.5	65199	2	AC100669	Mus muscu
C 403	19	1.5	3012	6	AR244519	AR244519 Sequence	C 476	19	1.5	66066	8	AC149486	Populus b
C 404	19	1.5	3012	10	RNENACG	X77933 R.norvegicu	C 477	19	1.5	66262	9	AC132516	Continuation (4 of
C 405	19	1.5	3018	10	BC021338	BC021338 Mus muscu	C 478	19	1.5	66367	2	BX119990_3	Continuation (4 of
C 406	19	1.5	3127	6	C0583949	C0583949 Sequence	C 479	19	1.5	68256	8	AC149543	Mus muscu
C 407	19	1.5	3236	5	AY394964	AY394964 Danio rer	C 480	19	1.5	69830	2	AC100204	Mus muscu
C 408	19	1.5	3545	5	AF153446	AF153446 Danio rer	C 481	19	1.5	72334	2	AP000677	Hom sapi
C 409	19	1.5	3658	5	BC054623	BC054623 Danio rer	C 482	19	1.5	73740	10	AL954177	Mouse DNA
C 410	19	1.5	3662	6	C0872871	C0872871 Sequence	C 483	19	1.5	74573	9	AL954177	Mouse DNA
C 411	19	1.5	3888	10	D85517	D85517 Mesocricetu	C 484	19	1.5	75013	10	AL954177	Mouse DNA
C 412	19	1.5	3991	6	CQ581372	CQ581372 Sequence	C 485	19	1.5	75013	10	AL954177	Mouse DNA
C 413	19	1.5	4026	6	CQ580856	CQ580856 Sequence	C 486	19	1.5	75013	10	AL954177	Mouse DNA
C 414	19	1.5	4259	3	AB091123	AB091123 Halocynth	C 487	19	1.5	7519	2	AC124999	Human DNA
C 415	19	1.5	4340	8	AF213504	AF213504 Brassica	C 488	19	1.5	7519	2	AC124999	Human DNA
C 416	19	1.5	4372	6	C0581414	C0581414 Sequence	C 489	19	1.5	7538	2	CR4	

C 531	19	1.5	110000	1	AP006628_7	Continuation (8 of	C 604	19	1.5	139771	9	CR753846	CR753846 Human DNA
C 532	19	1.5	110000	1	AX908798_18	Continuation (19 of	C 605	19	1.5	139904	9	HS97D16	AL0091779 Human DNA
C 533	19	1.5	110000	2	AC096119_1	Continuation (2 of	C 606	19	1.5	139961	9	AL606477	AL606477 Human DNA
C 534	19	1.5	110000	2	AC096119_2	Continuation (3 of	C 607	19	1.5	140478	8	AC138988	AC138988 Homo sapi
C 535	19	1.5	110000	2	AC096343_0	AC096343 Rattus no	C 608	19	1.5	140643	8	AP003888	AP003888 Oryza sat
C 536	19	1.5	110000	2	AC118915_2	Continuation (3 of	C 609	19	1.5	140936	2	AC008630	AC008630 Homo sapi
C 537	19	1.5	110000	2	AY294423_0	AY294423 Mus muscu	C 610	19	1.5	141156	9	AL360093	AL360093 Human DNA
C 538	19	1.5	110000	2	BX842678_1	Continuation (2 of	C 611	19	1.5	141439	10	AC105403	AC105403 Mus muscu
C 539	19	1.5	110000	2	BX957276_1	Continuation (2 of	C 612	19	1.5	142159	10	AC092479	AC092479 Mus muscu
C 540	19	1.5	110000	2	BX957283_0	BX957283 Danio rer	C 613	19	1.5	142573	10	AC122045	AC122045 Mus muscu
C 541	19	1.5	110000	2	BX957283_1	Continuation (2 of	C 614	19	1.5	143280	10	AL845285	AL845285 Mouse DNA
C 542	19	1.5	110000	2	CEY10588_4	Continuation (5 of	C 615	19	1.5	144474	9	AF051934	AF051934 Homo sapi
C 543	19	1.5	110000	3	AC116984_1	Continuation (2 of	C 616	19	1.5	144848	2	AC140069	AC140069 Mus muscu
C 544	19	1.5	110000	3	AC116984_2	Continuation (3 of	C 617	19	1.5	145416	5	AC147826	AC147826 Xenopus t
C 545	19	1.5	110000	6	BD426631_13	Continuation (14 of	C 618	19	1.5	145496	8	AC144342	AC144342 Medicago
C 546	19	1.5	110000	6	BD426631_14	Continuation (15 of	C 619	19	1.5	145962	2	AC144373	AC144373 Felis cat
C 547	19	1.5	110000	6	AR274513_13	Continuation (14 of	C 620	19	1.5	146060	10	AC115849	AC115849 Mus muscu
C 548	19	1.5	110000	6	AR274513_14	Continuation (15 of	C 621	19	1.5	146259	10	AC102847	AC102847 Mus muscu
C 549	19	1.5	110000	6	AR541453_13	Continuation (14 of	C 622	19	1.5	146454	14	AF410153	AF410153 Swinepox
C 550	19	1.5	110000	6	AR541453_14	Continuation (15 of	C 623	19	1.5	146502	9	AC116456	AC116456 Homo sapi
C 551	19	1.5	110243	8	AC146945	AC146945 Oryza sat	C 624	19	1.5	147086	3	AC009182	AC009182 Drosophill
C 552	19	1.5	111130	8	AC144516	AC144516 Medicago	C 625	19	1.5	147118	3	AC007513	AC007513 Homo sapi
C 553	19	1.5	111271	9	AC011393	AC011393 Homo sapi	C 626	19	1.5	147318	2	AC138996	AC138996 Homo sapi
C 554	19	1.5	112027	9	AC007006	AC007006 Homo sapi	C 627	19	1.5	147369	2	AC147689	AC147689 Cercopith
C 555	19	1.5	113851	2	AP000571	AP000571 Homo sapi	C 628	19	1.5	147440	9	AP003971	AP003971 Homo sapi
C 556	19	1.5	114495	9	AC011743	AC011743 Homo sapi	C 629	19	1.5	147557	9	AL662789	AL662789 Human DNA
C 557	19	1.5	115177	9	AL583836	AL583836 Human DNA	C 630	19	1.5	148235	9	AC146372	AC146372 Pan trogl
C 558	19	1.5	115306	8	AC008615	AC008615 Homo sapi	C 631	19	1.5	148860	8	OSJN000093	AL607123 Mouse DNA
C 559	19	1.5	115808	8	AC104713	Oryza sat	C 632	19	1.5	149369	10	AL607123	Mouse DNA
C 560	19	1.5	116180	2	AC133296	Rattus no	C 633	19	1.5	149599	14	AY077835	AY077835 Goatpox v
C 561	19	1.5	116960	2	AC135632	AC135632 Human DNA	C 634	19	1.5	149662	14	AY077834	Sheepox
C 562	19	1.5	116989	8	AC137819	AC137819 Medicago	C 635	19	1.5	149723	14	AY077836	AY077836 Goatpox v
C 563	19	1.5	117303	9	AL773543	AL773543 Human DNA	C 636	19	1.5	149788	8	ATT6G321	AL589883 Arabidops
C 564	19	1.5	117645	8	AC144644	AC144644 Medicago	C 637	19	1.5	149955	14	AY077832	AY077832 Sheepox
C 565	19	1.5	118610	2	AC002344	AC002344 Homo sapi	C 638	19	1.5	150029	10	BX890639	BX890639 Mouse DNA
C 566	19	1.5	119077	2	AC147494	AC147494 Carollia	C 639	19	1.5	150057	14	AY077833	Sheepox
C 567	19	1.5	119660	2	AC149578	AC149578 Medicago	C 640	19	1.5	150434	9	AL138784	AL138784 Human DNA
C 568	19	1.5	119706	2	AC148352	AC148352 Sorex ara	C 641	19	1.5	150509	14	AF409138	AF409138 Lumby ski
C 569	19	1.5	119765	2	AC090705	AC090705 Homo sapi	C 642	19	1.5	150773	14	AF325528	Lumpy ski
C 570	19	1.5	120037	2	AC147766	AC147766 Dasypus n	C 643	19	1.5	150793	14	AF409137	AF409137 Lumby ski
C 571	19	1.5	121059	9	AL138918	AL138918 Human DNA	C 644	19	1.5	151254	5	BF649371	Zebrafish
C 572	19	1.5	121806	2	CR759819	CR759819 Danio rer	C 645	19	1.5	151329	9	BS000541	BS000541 Pan trogl
C 573	19	1.5	122489	2	AC027339	AC027339 Homo sapi	C 646	19	1.5	151349	2	AL353647	AL353647 Homo sapi
C 574	19	1.5	122880	9	AC016711	AC016711 Homo sapi	C 647	19	1.5	151517	9	AC105230	AC105230 Homo sapi
C 575	19	1.5	122948	9	AL355798	AL355798 Human DNA	C 648	19	1.5	151519	9	HS23114	AL022719 Human DNA
C 576	19	1.5	123323	9	AP001816	AP001816 Homo sapi	C 649	19	1.5	151551	2	AC021291	AC021291 Homo sapi
C 577	19	1.5	124372	10	AL731808	AL731808 Mouse DNA	C 650	19	1.5	151744	10	AL772406	AL772406 Mouse DNA
C 578	19	1.5	124787	9	BX248406	BX248406 Human DNA	C 651	19	1.5	152106	10	AC119857	AC119857 Mus muscu
C 579	19	1.5	125381	4	AY644517	AY644517 Bos tauru	C 652	19	1.5	152264	8	OSJN000090	AL606685 Oryza sat
C 580	19	1.5	125674	2	AP002018	AP002018 Homo sapi	C 653	19	1.5	152484	2	AC067992	AC067992 Homo sapi
C 581	19	1.5	126141	2	AC131240	AC131240 Medicago	C 654	19	1.5	152517	9	AC009468	AC009468 Homo sapi
C 582	19	1.5	127298	10	BX005130	BX005130 Mouse DNA	C 655	19	1.5	152649	2	CR356241	CR356241 Danio rer
C 583	19	1.5	128024	2	AC147955	AC147955 Dasypus n	C 656	19	1.5	152695	2	AP005152	AP005152 Oryza sat
C 584	19	1.5	128152	9	AC113347	AC113347 Homo sapi	C 657	19	1.5	152877	9	AC107399	AC107399 Homo sapi
C 585	19	1.5	129467	9	HS0601K24	AL109626 Human DNA	C 658	19	1.5	153031	2	AC105458	AC105458 Felis cat
C 586	19	1.5	131259	2	AP001805	AP001805 Homo sapi	C 659	19	1.5	153078	9	AP002782	AP002782 Homo sapi
C 587	19	1.5	131727	9	AC093850	AC093850 Homo sapi	C 660	19	1.5	153616	2	AC149696	AC149696 Bos tauru
C 588	19	1.5	131885	1	CR628338	CR628338 Legionell	C 661	19	1.5	154279	2	AC151077	AC151077 Bos tauru
C 589	19	1.5	132659	9	AC006917	AC006917 Genomic s	C 662	19	1.5	154373	2	AC146803	AC146803 Xenopus t
C 590	19	1.5	132742	2	AC145412	AC145412 Bos tauru	C 663	19	1.5	154713	9	AC013361	AC013361 Homo sapi
C 591	19	1.5	133330	10	AL928871	AL928871 Mouse DNA	C 664	19	1.5	154907	9	AC079631	AC079631 Homo sapi
C 592	19	1.5	134054	9	AC026730	AC026730 Homo sapi	C 665	19	1.5	155100	2	AC102514	AC102514 Mus muscu
C 593	19	1.5	135423	9	AC112195	AC112195 Homo sapi	C 666	19	1.5	155437	2	AC116872	AC116872 Mus muscu
C 594	19	1.5	135679	2	AC138993	AC138993 Homo sapi	C 667	19	1.5	155535	9	AC016909	AC016909 Homo sapi
C 595	19	1.5	135998	9	AC104021	AC104021 Homo sapi	C 668	19	1.5	155542	8	AP004662	AP004662 Oryza sat
C 596	19	1.5	136511	9	AC117424	AC117424 Homo sapi	C 669	19	1.5	156022	2	AC110560	AC110560 Mus muscu
C 597	19	1.5	136799	8	AP004564	AP004564 Oryza sat	C 670	19	1.5	156568	9	AC097474	AC097474 Homo sapi
C 598	19	1.5	137113	9	AC076966	AC076966 Homo sapi	C 671	19	1.5	157042	2	CR759826	CR759826 Danio rer
C 599	19	1.5	137325	8	AP005397	AP005397 Oryza sat	C 672	19	1.5	157330	9	AC146247	AC146247 Homo sapi
C 600	19	1.5	137525	8	AL357733	AL357733 Homo sapi	C 673	19	1.5	157530	9	AC025207	AC025207 Homo sapi
C 601	19	1.5	138391	2	AL357733	AL357733 Homo sapi	C 674	19	1.5	157556	2	CR354606	CR354606 Danio rer
C 602	19	1.5	139015	2	AC087581	AC087581 Homo sapi	C 675	19	1.5	157631	8	AP005445	AP005445 Oryza sat
C 603	19	1.5	139032	9	AC010656	AC010656 Homo sapi	C 676	19	1.5	157875	9	HS27216	AL002545 Human DNA

677	19	1.5	158180	9	AC100781	AC100781 Homo sapi	c	750	19	1.5	172750	2	AC119495	AC119495 Rattus no
678	19	1.5	158500	10	AC131983	AC131983 Mus muscu	751	19	1.5	173639	10	AL606921	AL606921 Mouse DNA	
c 679	19	1.5	158515	2	CR318625	Danio rer	752	19	1.5	174313	9	AC024060	AC024060 Homo sapi	
c 680	19	1.5	158563	2	AC150484	Bos tauru	c 753	19	1.5	174313	9	AC024060	AC024060 Homo sapi	
c 681	19	1.5	158830	10	AC131740	AC131740 Mus muscu	754	19	1.5	174896	2	AC022012	AC022012 Homo sapi	
c 682	19	1.5	159317	2	AC147520	AC147520 Otollemur	c 755	19	1.5	174927	9	AC010881	AC010881 Homo sapi	
c 683	19	1.5	159333	5	BX004980	Zebrafish	c 756	19	1.5	175003	10	AC115900	AC115900 Mus muscu	
c 684	19	1.5	159658	9	AC104062	AC104062 Homo sapi	c 757	19	1.5	175152	2	AC011965	AC011965 Mus muscu	
c 685	19	1.5	159705	2	AC021007	AC021007 Homo sapi	c 758	19	1.5	175179	2	AC072025	AC072025 Homo sapi	
c 686	19	1.5	159769	2	AC007337	AC007337 Homo sapi	c 759	19	1.5	175245	10	AC129188	AC129188 Mus muscu	
c 687	19	1.5	159792	10	AC139182	AC139182 Mus muscu	c 760	19	1.5	175467	2	AC079215	AC079215 Homo sapi	
c 688	19	1.5	160012	5	BX005254	Zebrafish	761	19	1.5	175809	10	AC099629	AC099629 Mus muscu	
c 689	19	1.5	160157	2	AC091294	AC091294 Mus muscu	762	19	1.5	175916	9	AC018842	AC018842 Homo sapi	
c 690	19	1.5	160462	2	CR318609	CR318609 Danio rer	c 763	19	1.5	175977	9	AC027691	AC027691 Homo sapi	
c 691	19	1.5	160511	2	AC022786	AC022786 Homo sapi	c 764	19	1.5	176051	9	AC022008	AC022008 Homo sapi	
c 692	19	1.5	160866	2	AC120170	AC120170 Mus muscu	765	19	1.5	176104	9	AC007163	AC007163 Homo sapi	
c 693	19	1.5	160713	2	AC007174	AC007174 Homo sapi	c 766	19	1.5	176594	2	AC119325	AC119325 Rattus no	
c 694	19	1.5	161099	10	AC132624	AC132624 Mus muscu	c 767	19	1.5	176983	2	AC120820	AC120820 Rattus no	
c 695	19	1.5	161300	2	AC026169	AC026169 Homo sapi	c 768	19	1.5	177087	2	AC093687	AC093687 Homo sapi	
c 696	19	1.5	161377	2	AC141827	AC141827 Apis mell	769	19	1.5	177097	2	AP001569	AP001569 Homo sapi	
c 697	19	1.5	161739	9	AC013302	AC013302 Homo sapi	c 770	19	1.5	177245	9	AC121341	AC121341 Homo sapi	
c 698	19	1.5	162030	2	AC018601	AC018601 Homo sapi	c 771	19	1.5	177363	9	AC073856	AC073856 Homo sapi	
c 699	19	1.5	162270	2	AC140170	AC140170 Homo sapi	c 772	19	1.5	177623	2	AC067825	AC067825 Homo sapi	
c 700	19	1.5	162598	2	AC079091	AC079091 Homo sapi	c 773	19	1.5	177789	2	BX927353	BX927353 Danio rer	
701	19	1.5	162709	10	AL807237	AL807237 Mouse DNA	c 774	19	1.5	177929	9	AC125624	AC125624 Homo sapi	
c 702	19	1.5	163025	2	AC024063	AC024063 Homo sapi	775	19	1.5	178046	2	AC137949	AC137949 Mus muscu	
c 703	19	1.5	163126	9	AC110012	AC110012 Homo sapi	c 776	19	1.5	178207	9	AC140172	AC140172 Homo sapi	
c 704	19	1.5	163228	9	AC009039	AC009039 Homo sapi	c 777	19	1.5	178317	9	AC012081	AC012081 Homo sapi	
c 705	19	1.5	163331	9	AL162575	AL162575 Human DNA	c 778	19	1.5	178420	9	AP003548	AP003548 Homo sapi	
c 706	19	1.5	163385	10	AC121593	AC121593 Mus muscu	c 779	19	1.5	178534	2	AC024956	AC024956 Homo sapi	
707	19	1.5	163814	5	AL953863	AL953863 Zebrafish	c 780	19	1.5	178800	2	AC149166	AC149166 Otollemur	
708	19	1.5	163926	9	AC096634	AC096634 Homo sapi	781	19	1.5	178824	5	BX323024	BX323024 Zebrafish	
709	19	1.5	164190	9	AC025448	AC025448 Homo sapi	c 782	19	1.5	179042	10	AC119905	AC119905 Mus muscu	
710	19	1.5	164575	2	AC024736	AC024736 Homo sapi	c 783	19	1.5	179547	2	CR762491	CR762491 Danio rer	
711	19	1.5	164781	9	AC104419	AC104419 Homo sapi	c 784	19	1.5	179583	2	CR788312	CR788312 Danio rer	
712	19	1.5	164808	2	AC023969	AC023969 Homo sapi	c 785	19	1.5	179590	10	AC113293	AC113293 Mus muscu	
713	19	1.5	165349	10	AC134870	AC134870 Rattus no	c 786	19	1.5	179681	2	AC013785	AC013785 Homo sapi	
714	19	1.5	165789	2	AC119054	AC119054 Homo sapi	c 787	19	1.5	179726	9	AC007052	AC007052 Homo sapi	
715	19	1.5	165992	2	AC149707	AC149707 Bos tauru	c 788	19	1.5	179814	9	AC068314	AC068314 Homo sapi	
716	19	1.5	166351	10	AC118747	AC118747 Mus muscu	789	19	1.5	179934	2	AC128793	AC128793 Rattus no	
717	19	1.5	166398	9	AC090568	AC090568 Homo sapi	c 790	19	1.5	180000	2	AC006428	AC006428 Homo sapi	
c 718	19	1.5	166522	2	AL357072	AL357072 Homo sapi	c 791	19	1.5	180311	2	AC140086	AC140086 Cercopith	
c 719	19	1.5	166644	9	AC001352	AC001352 Homo sapi	c 792	19	1.5	180401	9	AC007489	AC007489 Homo sapi	
c 720	19	1.5	166743	9	AC005598	AC005598 Homo sapi	c 793	19	1.5	180425	2	CR381605	CR381605 Danio rer	
c 721	19	1.5	166847	9	CNS06C7S	AL390801 Human chr	c 794	19	1.5	180861	2	CR391970	CR391970 Danio rer	
c 722	19	1.5	167207	2	BX571889	BX571889 Mus muscu	c 795	19	1.5	180973	9	AC097462	AC097462 Homo sapi	
c 723	19	1.5	167292	2	AC068365	AC068365 Homo sapi	c 796	19	1.5	181258	2	AC147355	AC147355 Xenopus t	
c 724	19	1.5	167386	2	AC013704	AC013704 Homo sapi	c 797	19	1.5	181963	2	AC102659	AC102659 Mus muscu	
c 725	19	1.5	167596	2	AC013177	AC013177 Drosophil	c 798	19	1.5	182028	2	AC102442	AC102442 Mus muscu	
c 726	19	1.5	169048	9	AL158011	AL158011 Human DNA	c 799	19	1.5	182411	2	AC090408	AC090408 Homo sapi	
c 727	19	1.5	169063	9	AC098677	AC098677 Homo sapi	c 800	19	1.5	182520	10	AL627392	AL627392 Mouse DNA	
c 728	19	1.5	169199	9	AC018812	AC018812 Homo sapi	c 801	19	1.5	182555	9	AC068531	AC068531 Homo sapi	
c 729	19	1.5	169455	10	AL606976	AL606976 Mouse DNA	c 802	19	1.5	182555	9	AC007282	AC007282 Homo sapi	
c 730	19	1.5	169686	2	BX465864	BX465864 Danio rer	c 803	19	1.5	182632	9	AC007282	AC007282 Homo sapi	
c 731	19	1.5	169891	2	AC114479	AC114479 Homo sapi	c 804	19	1.5	182696	10	AC126424	AC126424 Mus muscu	
c 732	19	1.5	170022	2	AC021559	AC021559 Homo sapi	c 805	19	1.5	182743	2	AC046132	AC046132 Homo sapi	
c 733	19	1.5	170254	10	AC137678	AC137678 Mus muscu	c 806	19	1.5	183007	3	AC007257	AC007257 Drosophil	
734	19	1.5	170452	8	AF152364	AF152364 Homo sapi	c 807	19	1.5	183330	9	AC011372	AC011372 Homo sapi	
735	19	1.5	170523	8	AP004764	AP004764 Oryza sat	c 808	19	1.5	183344	9	AC147112	AC147112 Pan trogl	
c 736	19	1.5	170624	9	AC006031	AC006031 Homo sapi	c 809	19	1.5	183477	2	BX957239	BX957239 Danio rer	
737	19	1.5	170635	2	AC144620	AC144620 Mus muscu	c 810	19	1.5	183638	10	AC132345	AC132345 Mus muscu	
738	19	1.5	170631	9	AC020751	AC020751 Homo sapi	c 811	19	1.5	184010	2	AC150025	AC150025 Papio anu	
739	19	1.5	170750	2	AC103898	AC103898 Bos tauru	c 812	19	1.5	184562	2	AC102371	AC102371 Mus muscu	
740	19	1.5	170755	9	AL38994	AL38994 Homo sapi	c 813	19	1.5	184591	9	AL365443	AL365443 Human DNA	
741	19	1.5	170765	9	AL589745	AL589745 Human DNA	c 814	19	1.5	184989	2	AC113392	AC113392 Homo sapi	
742	19	1.5	170807	9	AC023812	AC023812 Homo sapi	c 815	19	1.5	185138	10	AL845172	AL845172 Mouse DNA	
743	19	1.5	171019	3	AC099031	AC099031 Drosophil	c 816	19	1.5	185209	9	AC145856	AC145856 Pan trogl	
744	19	1.5	171185	2	AP002424	AP002424 Homo sapi	c 817	19	1.5	185242	10	AC124597	AC124597 Mus muscu	
745	19	1.5	171747	2	AC087678	AC087678 Homo sapi	c 818	19	1.5	185806	2	AC147049	AC147049 Pan trogl	
746	19	1.5	172155	9	AC018653	AC018653 Homo sapi	c 819	19	1.5	186058	2	AC112245	AC112245 Homo sapi	
747	19	1.5	172285	2	CR381538	CR381538 Danio rer	c 820	19	1.5	186064	2	AC020752	AC020752 Homo sapi	
c 748	19	1.5	172346	2	AC016349	AC016349 Homo sapi	c 821	19	1.5	186561	2	AC102764	AC102764 Mus muscu	
749	19	1.5	172748	9	AC025871	AC025871 Homo sapi	c 822	19	1.5	186608	9	AC093274	AC093274 Homo sapi	

C 823	19	1.5	186670	9	AC080188	Homo sapi	AC080188	Homo sapi	C 896	19	1.5	200290	2	BX000350
824	19	1.5	186742	5	AL928736	Zebrafish	AL928736	Zebrafish	897	19	1.5	200774	2	AP001592
825	19	1.5	186773	10	AC135356	Mus muscu	AC135356	Mus muscu	898	19	1.5	201162	10	AC069561
826	19	1.5	186839	10	AC147152	Mus muscu	AC147152	Mus muscu	899	19	1.5	201359	2	AC128640
827	19	1.5	187059	2	CR318671	Danio rer	CR318671	Danio rer	900	19	1.5	201611	2	AC021185
828	19	1.5	187127	2	AC119942	Mus muscu	AC119942	Mus muscu	901	19	1.5	201657	9	AC006840
829	19	1.5	187241	5	AL772146	Zebrafish	AL772146	Zebrafish	902	19	1.5	202396	2	AC140011
C 830	19	1.5	187417	2	AC105154	Mus muscu	AC105154	Mus muscu	C 903	19	1.5	202412	10	AL670673
831	19	1.5	187595	2	AC138878	Homo sapi	AC138878	Homo sapi	904	19	1.5	202469	2	AC099607
832	19	1.5	187727	2	AC064806	Homo sapi	AC064806	Homo sapi	905	19	1.5	202676	2	AC129140
C 833	19	1.5	187898	2	AC016715	Homo sapi	AC016715	Homo sapi	906	19	1.5	203061	9	AC105054
C 834	19	1.5	188084	2	BX324153	Danio rer	BX324153	Danio rer	C 907	19	1.5	203120	2	AC148499
C 835	19	1.5	188275	2	AC150869	Bos tauru	AC150869	Bos tauru	C 908	19	1.5	203204	9	AC092052
836	19	1.5	188476	10	AL773549	Mouse DNA	AL773549	Mouse DNA	C 909	19	1.5	203399	2	AC121559
C 837	19	1.5	188484	10	AC122749	Mus muscu	AC122749	Mus muscu	C 910	19	1.5	204632	2	AC097583
C 838	19	1.5	188700	10	AC121525	Mus muscu	AC121525	Mus muscu	911	19	1.5	204988	2	CR293501
C 839	19	1.5	188958	10	AL844605	Mouse DNA	AL844605	Mouse DNA	912	19	1.5	205033	2	AC111383
C 840	19	1.5	188963	2	CR762411	Danio rer	CR762411	Danio rer	C 913	19	1.5	205152	9	AP002985
C 841	19	1.5	189412	2	AC023532	Homo sapi	AC023532	Homo sapi	914	19	1.5	206332	2	AC116270
C 842	19	1.5	189466	9	AC018887	Homo sapi	AC018887	Homo sapi	C 915	19	1.5	206474	2	AC129671
C 843	19	1.5	189563	5	BX000364	Zebrafish	BX000364	Zebrafish	C 916	19	1.5	207365	2	AC093653
844	19	1.5	189718	2	AC128388	Rattus no	AC128388	Rattus no	917	19	1.5	207802	10	AC127326
845	19	1.5	189988	2	CR376768	Danio rer	CR376768	Danio rer	C 918	19	1.5	208059	5	AL935193
846	19	1.5	190015	2	AC140056	Rattus no	AC140056	Rattus no	C 919	19	1.5	208499	2	CR376859
C 847	19	1.5	190220	9	AC142323	Pan trogl	AC142323	Pan trogl	920	19	1.5	208726	9	AP006287
C 848	19	1.5	190379	2	AC022386	Homo sapi	AC022386	Homo sapi	C 921	19	1.5	209176	2	AC110516
849	19	1.5	190577	2	AC073721	Mus muscu	AC073721	Mus muscu	922	19	1.5	209848	2	CR388132
850	19	1.5	190702	5	BX119962	Zebrafish	BX119962	Zebrafish	923	19	1.5	210161	2	BX470245
C 851	19	1.5	190816	2	AC116446	Mus muscu	AC116446	Mus muscu	C 924	19	1.5	210640	5	BX293994
C 852	19	1.5	191355	2	AC151028	Callithri	AC151028	Callithri	925	19	1.5	210772	2	AC121080

c 969 1.5 228044 5 BX682552
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ALIGNMENTS

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AR411820 1274 bp DNA linear PAT 18-DEC-2003
LOCUS
DEFINITION Sequence 1 from patent US 6638734.
ACCESSION AR411820
VERSION AR411820.1 GI:40164258
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE
1 (bases 1 to 1274)
Reed, J.C. and Matuzawa, S.-i.
Nucleic acid encoding proteins involved in protein degradation,
products and methods related thereto
Patent US 6638734-A 1 28-OCT-2003;
JOURNAL Location/Qualifiers
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 DEFINITION Sequence 1 from Patent WO0077207.
 ACCESSION AX058082
 VERSION AX058082.1 GI:12310662
 KEYWORDS Homo sapiens (human)
 SOURCE
 ORGANISM Homo sapiens

REFERENCE
 AUTHORS Reed, J.C. and Matsuzawa, S. I.
 TITLE Nucleic acid encoding proteins involved in protein degradation,
 products and methods related thereto
 JOURNAL Patent: WO 0077207-A 1 21-DEC-2000;
 The Burnham Institute (US)

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ORIGIN
 Query Match 100.0%; Score 1274; DB 6; Length 1274;
 Best Local Similarity 100.0%; Pred. No. 0;
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RESULT 3
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 DEFINITION Sequence 22959 from Patent WO0160860.
 ACCESSION CO491092
 VERSION CO491092.1 GI:41456711
 KEYWORDS Homo sapiens (human)
 SOURCE
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1
 AUTHORS Schlegel, R., Endege, W.O. and Mohahan, J.E.

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RESULT 5
Q496955
LOCUS
DEFINITION
Sequence 28822 from Patent WO0160860.
Q496955
ACCESSION
Q496955.1
VERSION
GI:41462591
KEYWORDS
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SOURCE
ORGANISM
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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REFERENCE
AUTHORS
Schlegel, R., Endege, W.O. and Monahan, J.E.
TITLE
Genes differentially expressed in human prostate cancer and their
use
JOURNAL
Patent: WO 0160860-A 28822 23-AUG-2001;
Millennium Predictive Medicine, Inc. (US)
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Best Local Similarity 100.0%; Pred. No. 0;
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DEFINITION AC023818
ACCESSION AC023818
VERSION AC023818.5 GI:40556309
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Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
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REFERENCE 1 (bases 1 to 173304)
AUTHORS DOE Joint Genome Institute, Stanford Human Genome Center and Los
Alamos National Laboratory.
TITLE Direct Submission
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 173304)
AUTHORS DOE Joint Genome Institute.
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TITLE Direct Submission
JOURNAL Submitted (18-FEB-2000) Production Sequencing Facility, DOE Joint
REFERENCE Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
AUTHORS 3 (bases 1 to 173304)
DOE Joint Genome Institute.
TITLE Direct Submission
JOURNAL Submitted (03-MAY-2002) Production Sequencing Facility, DOE Joint
REFERENCE Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
AUTHORS 4 (bases 1 to 173304)
DOE Joint Genome Institute, Stanford Human Genome Center and Los
Alamos National Laboratory.
TITLE Direct Submission
JOURNAL Submitted (03-JAN-2004) DOE Joint Genome Institute, 2800 Mitchell
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On Jan 3, 2004 this sequence version replaced gi:20429291.
Draft Sequence Produced by DOE Joint Genome Institute
www.jgi.doe.gov
Finishing Completed at Stanford Human Genome Center and Los Alamos
National Laboratory
www-shgc.stanford.edu
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RESULT 8
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LOCUS
DEFINITION Sequence 269 from Patent EPI347046.
ACCESSION AX833145
VERSION AX833145.1 GI:39919280
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1
REFERENCE
AUTHORS Isogai,T., Sugiyama,T., Otsuki,T., Wakamatsu,A., Sato,H., Ishii,S.,
Yamamoto,J.I., Isono,Y., Hio,Y., Otsuka,K., Nagai,K., Irie,R.,
Tamechika,I., Seki,N., Yoshikawa,T., Otsuka,M., Nagahari,K. and
Masuho,Y.
Full-length cDNA sequences
TITLE Patent: EP 1347046-A 269 24-SEP-2003;
JOURNAL Research Association for Biotechnology (JP)
FEATURES
Location/Qualifiers
source 1..2829
/organism="Homo sapiens"

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/mol_type="unassigned DNA"
/db_xref="taxon:9606"

ORIGIN

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Best Local Similarity 99.9%; Pred. No. 0;
Matches 1273; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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AK094663
LOCUS
DEFINITION Homo sapiens CDNA FLJ37344 fis, clone BRAMY2021139, highly similar to Seven in absentia.
ACCESSION AK094663
VERSION AK094663.1 GI:21753769
KEYWORDS oligo capping; fis (full insert sequence).
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

1
Ota, T., Suzuki, Y., Nishikawa, T., Otsuki, T., Sugiyama, T., Irie, R., Wakamatsu, A., Hayashi, K., Sato, H., Nagai, K., Kimura, K., Makita, H., Sekine, M., Ohyashi, M., Nishi, T., Shibahara, T., Tanaka, T., Ishii, S., Yamamoto, J., Saito, K., Kawai, Y., Isono, Y., Nakamura, Y., Nagahara, K., Murakami, K., Yasuda, T., Iwayanagi, T., Wagatsuma, M., Shiratori, A., Sudo, H., Hosoiri, T., Kaku, Y., Kodaira, H., Kondo, H., Sugawara, M., Takahashi, M., Kanda, K., Yokoi, T., Furuya, T., Kikkawa, E., Omura, Y., Abe, K., Kamihara, K., Katsuta, N., Sato, K., Tanikawa, M., Yamazaki, M., Ninomiya, K., Ishibashi, T., Yamashita, H., Murakawa, K., Fujimori, K., Tanai, H., Kimata, M., Watanabe, M., Hirooka, S., Chiba, Y., Ishida, S., Ono, Y., Takiguchi, S., Watanabe, S., Yosida, M., Hotuta, T., Kusano, J., Kanehori, K., Takahashi-Fujii, A., Hara, H., Tanase, T., Nomura, Y., Togiya, S., Komai, F., Hara, R., Takeuchi, K., Arita, M., Imose, N., Musashino, K., Yuuki, H., Oshima, A., Sasaki, N., Aotsuka, S., Yoshikawa, Y., Matsunawa, H., Ichihara, T., Shichata, N., Sano, S., Moriya, S., Momiyama, H., Satoh, N., Takami, S., Terashima, Y., Suzuki, O., Nakagawa, S., Senoh, A., Mizoguchi, H., Goto, Y., Shimizu, F., Wakebe, H., Hishigaki, H., Watanabe, T., Sugiyama, A., Takemoto, M., Kawakami, B., Yamazaki, M., Watanabe, K., Kumagai, A., Itakura, S., Fukuzumi, Y., Fujimori, Y., Komiyama, M., Tashiro, H., Tanigami, A., Fujiwara, T., Ono, T., Yamada, K., Fujii, Y., Ozaki, K., Hiro, M., Ohmori, Y., Kawabata, A., Hiki, J., Kobatake, N., Inagaki, H., Ikema, Y., Okamoto, S., Okitani, R., Kawakami, T., Noguchi, S., Itoh, T., Shigetani, K., Senba, T., Matsumura, K., Nakajima, Y., Mizuno, T., Morinaga, M., Sasaki, M., Togashi, T., Oyama, M., Hata, H., Watanabe, M., Komatsu, T., Mizushima-Sugano, J., Satoh, T., Shirai, Y., Takahashi, Y., Nakagawa, K., Okumura, K., Nagase, T., Nomura, N., Kikuchi, H., Masuho, Y., Yamashita, R., Nakai, K., Yada, T., Nakamura, Y., Ohara, O., Isogai, T. and Sugano, S. Complete sequencing and characterization of 21,243 full-length human cDNAs
Nat. Genet. 36 (1), 40-45 (2004)

TITLE

JOURNAL
PUBMED
REFERENCE
AUTHORS
Ninomiya, K., Wagatsuma, M., Kanda, K., Kondo, H., Yokoi, T., Kodaira, H., Furuya, T., Takahashi, M., Kikkawa, E., Omura, Y., Abe, K.,

Kamihara, K., Katsuta, N., Sato, K., Tanikawa, M., Yamazaki, M., Sugiyama, T., Irie, R., Otsuki, T., Sato, H., Wakamatsu, A., Ishii, S., Yamamoto, J., Isono, Y., Kawai-Hio, Y., Saito, K., Nishikawa, T., Kimura, K., Yamashita, H., Matsuo, K., Nakamura, Y., Sekine, M., Kikuchi, H., Murakawa, K., Kanehori, K., Takahashi-Fujii, A., Oshima, A., Sugiyama, A., Kawakami, B., Suzuki, Y., Sugano, S., Nagahara, K., Masuho, Y., Nagai, K. and Isogai, T.
NEDO human cDNA sequencing project
Unpublished
3 (bases 1 to 2829)
Isogai, T. and Yamamoto, J.
Direct Submission
Submitted (04-JUL-2002) Takao Isogai, FLJ Project (HRI Team); 2-6-7 Kazusa-Genomatrix, Kisarazu, Chiba 292-0812, Japan
(E-mail: genomics@hri.co.jp, Tel: 81-438-52-3975, Fax: 81-438-52-3986)
NEDO human cDNA sequencing project supported by Ministry of Economy, Trade and Industry of Japan; cDNA full insert sequencing: Research Association for Biotechnology (RAB); cDNA library construction: Helix Research Institute (HRI) (supported by Japan Key Technology Center etc.); 5'- & 3'-end one pass sequencing: RAB, HRI, and Biotechnology Center, National Institute of Technology and Evaluation; clone selection for full insert sequencing: HRI and RAB; annotation: HRI and RAB.
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Best Local Similarity 99.9%; Pred. No. 0;
Matches 1273; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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Qy 61 CCAAGACGATTAAGGGAGTCCACATGTTTTCGGAAACATTTTGAAGAGAGCTTATC 120
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COMMENT

Clone from S. Wiemann, Molecular Genome Analysis, German Cancer Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de; sequenced by BMFZ (Biomedical Research Center at the Heinrich-Heine-University, Duesseldorf/Germany) within the cDNA sequencing consortium of the German Genome Project. This clone (DKFZp686L1897) is available at the RZPD in Berlin. Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059 Berlin-Charlottenburg, GERMANY; Email: clone@rzd.de Further information about the clone and the sequencing project is available at <http://mips.gsf.de/proj/cDNA/>.

FEATURES

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Best Local Similarity 99.8%; Pred. No. 0;

Matches 1272; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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DB 801 CCAAGACGATTAAAGGAGTTCACATGTTTCCGGAACATTTTCAAAGAGAGGCTTATC 860

QY 121 CAGTGTACAGATCCCTAATAAGTGACATTCAGTGTAAATTTTATTTTATATCTTTT 180

DB 861 CAGTGTACAGATCCCTAATAAGTGACATTCAGTGTAAATTTTATTTTATATCTTTT 920

QY 181 TTAATCTTATTTTCT 240

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DB 1101 TCGAAGTGTCCACCATCCAGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1160

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DB 2394 CGGTAGTGGGAAGC 2407

RESULT 10

LOCUS HSM807215

DEFINITION Homo sapiens mRNA; cDNA DKFZp686L1897 (from clone DKFZp686L1897); complete cds.

ACCESSION BX647064

VERSION BX647064.1

KEYWORDS GI:34366097

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 2972)

AUTHORS Koehler,K., Beyer,A., Mewes,H.W., Weil,B., Amid,C., Oesanger,A., Fobo,G., Han,M. and Wiemann,S.

CONSTRM The German Human cDNA Consortium

TITLE Direct Submission

JOURNAL Submitted (26-AUG-2003) MIPS, Ingolstaedter Landstr.1, D-85764 Neuburg, GERMANY

QY	421	GACTTGGCGAGCTTTTTCAGTGTCCAGTCTGCTTTGACTATGTGTGTACGCCCACTCTT	480
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ACCESSION	AK056051		
VERSION	AK056051.1	GI:16551141	
KEYWORDS	oligo capping; fis (full insert sequence).		
SOURCE	Homo sapiens		
ORGANISM	Homo sapiens		
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	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
REFERENCE	1		

AUTHORS

Ota.T., Suzuki, Y., Nishikawa, T., Otsuki, T., Sugiyama, T., Irie, R., Wakamatsu, A., Hayashi, K., Sato, H., Nagai, K., Kimura, K., Makita, H., Sekine, M., Obayashi, M., Nishi, T., Shibahara, T., Tanaka, T., Ishii, S., Yamamoto, J., Saito, K., Kawai, Y., Isono, Y., Nakamura, Y., Nagahara, K., Murakami, K., Yasuda, T., Iwayanagi, T., Wagatsuma, M., Shiratori, A., Sudo, H., Hosoiri, T., Kaku, Y., Kodaira, H., Kondo, H., Sugawara, M., Takahashi, M., Kanda, K., Yokoi, T., Furuya, T., Kikkawa, E., Omura, Y., Kikkawa, M., Kamihara, K., Tanikawa, M., Yamazaki, M., Sugiyama, T., Irie, R., Otsuki, T., Sato, H., Wakamatsu, A., Ishii, S., Yamamoto, J., Isono, Y., Kawai-Hio, Y., Saito, K., Nishikawa, T., Kimura, K., Yamashita, H., Matsuo, K., Nakamura, Y., Sekine, M., Kikuchi, H., Murakawa, K., Kanehori, K., Takahashi-Fujii, A., Oshima, A., Sugiyama, A., Kawakami, B., Suzuki, Y., Sugano, S., Nagahara, K., Masuho, Y., Nagai, K. and Isogai, T.

NEDO human cDNA sequencing project

Unpublished

3 (bases 1 to 2128)

Isogai, T., Otsuki, T. and Sugiyama, T.

Direct Submission

Submitted (24-OCT-2001) Takao Isogai, Helix Research Institute, Genomics Laboratory; 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan (E-mail: genomics@hri.co.jp, Tel: 81-438-52-3975, Fax: 81-438-52-3986)

NEDO human cDNA sequencing project supported by Ministry of Economy, Trade and Industry of Japan; cDNA full insert sequencing: Research Association for Biotechnology (RAB); cDNA library construction: Helix Research Institute (HRI) (supported by Japan Key Technology Center etc.); 5'- & 3'-end one pass sequencing: RAB, HRI, and Biotechnology Center, National Institute of Technology and Evaluation; clone selection for full insert sequencing: RAB and HRI.

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ACCESSION
BC035562
VERSION
BC035562.1 GI:23274141
KEYWORDS
MGC
SOURCE
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ORGANISM
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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REFERENCE
1 (bases 1 to 1540)
Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
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Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L.,
Schetz T.E., Brownstein M.J., Udén T.B., Toshiyuki S.,
Carninci P., Prange C., Raja S.S., Loquellano N.A., Peters G.J.,
Abramson R.D., Mullaly S.J., Bosak S.A., McEwan P.J.,
McKernan K.J., Malek J.A., Gunaratne P.H., Richards S.,
Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S.,
Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y.,
Boutard G.G., Blakesley R.W., Touchman J.W., Green E.D.,
Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
Butterfield Y.S., Krzywinski M.I., Skalska U., Smailus D.E.,
Scherch A., Schein J.E., Jones S.J. and Marra M.A.
Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
12477932
REFERENCE
2 (bases 1 to 1540)
Strausberg R.
Direct Submission
TITLE
Submitted (31-JUL-2002) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer

Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
USA
NIH-MGC Project URL: <http://mgc.nci.nih.gov>
Contact: MGC help desk
Email: cgabbs@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
DNA Sequencing by: The I.M.A.G.E. Consortium (LLNL)
Sequencing Center (NISC),
Gaithersburg, Maryland;
Web site: <http://www.nisc.nih.gov/>
Contact: nisc_mgc@nih.gov
Akhter N., Ayele K., Beckstrom-Sternberg S.M., Benjamin B.,
Blakesley R.W., Bouffard G.G., Breen K., Brinkley C., Brooks S.,
Dietrich N.L., Granite S., Guan X., Gupta J., Haghighi P.,
Hansen N., Ho S.-L., Karlins E., Kwong P., Laric P., Legaspi R.,
Maduro O.L., Masiello C., Maskeri B., Mastrian S.D., McCloskey J.C.,
McDowell J., Pearson R., Stantripop S., Thomas P.J., Touchman J.W.,
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Young A., Zhang L.-H. and Green E.D.
Clone distribution: MGC clone distribution information can be found
through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
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This clone was selected for full length sequencing because it
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FEATURES

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seven in absentia (sina) gene was first identified in
Drosophila. The Drosophila Sina protein is essential for
the determination of the R7 pathway in photoreceptor cell
development; the loss of functional Sina results in the
transformation of the R7 precursor cell to a non-neuronal
cell type. The Sina protein contains an N-terminal RING
finger domain pfam00097. Through this domain, Sina binds
E2 ubiquitin-conjugating enzymes (UbcD1). Sina also
interacts with Tramtrack (TTK88) via PHYL. Tramtrack is a
transcriptional repressor that blocks photoreceptor
determination, while PHYL down-regulates the activity of
TTK88. In turn, the activity of PHYL requires the
activation of the Sevenless receptor tyrosine kinase, a
process essential for R7 determination. It is thought that
thus Sina targets TTK88 for degradation, therefore

promoting the R7 pathway. Murine and human homologues of Sina have also been identified. The human homologue Siah-1 also binds E2 enzymes (UbcH5) and through a series of physical interactions, targets beta-catenin for ubiquitin degradation. Siah-1 expression is enhanced by p53, itself promoted by DNA damage. Thus this pathway links DNA damage to beta-catenin degradation. Sina proteins, therefore, physically interact with a variety of proteins. The N-terminal RING finger domain that binds ubiquitin conjugating enzymes is described in pfam00097, and does not form part of the alignment for this family. The remainder C-terminal part is involved in interactions with other proteins, and is included in this alignment. In addition to the Drosophila protein and mammalian homologues, whose similarity was noted previously, this family also includes putative homologues from *Caenorhabditis elegans*, *Arabidopsis thaliana* "/db_xref="CDD:pfam03145"

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Matches 958; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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SOURCE      Homo sapiens
ORGANISM    Homo sapiens
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AUTHORS     Venter,C.J., Adams,M.C., Li,P.W. and Myers,E.W.
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JOURNAL      Patent: WO 02068579-A 5493 06-SEP-2002;
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VERSION U76247.1 GI:2673965
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Hu, G., Chung, Y.-L., Glover, T., Valentine, V., Look, A.T. and
Fearon, E.R.
Characterization of human homologs of the Drosophila seven in
absentia (sina) gene
Genomics 46 (1), 103-111 (1997)
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2 (bases 1 to 2048)
Hu, G., Chung, Y.-L., Look, A.T. and Fearon, E.R..
Direct Submission
Submitted (24-OCT-1996) Internal Medicine, University of Michigan,
4301 MSRB III, BOX 0638, 1150 W. Medical Center Dr., Ann Arbor, MI
48109-0638, USA
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QY 317 CAGAAATGAGCCGTACAGCTGTCTACAGCAATTAACCTACCGGTACCTCGAAGTGTCCACCAT 376
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QY 737 GCTCTCTGAGTGTGAATGCGCCCATCTGATGATCAGCATAGTTCATTTACAACCCCTAC 796
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QY 797 AGGAGAGATATAGTGTCTTCTGCTACAGACATTAATCTTCTGCTGCTGTGACTGGG 856
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VTISM"
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Db 481 GAGGATATAGTTTTCTTCTGCTACAGACATTAATCTCTCTGGTGTCTGTTGACTGGGTGATG 540
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RESULT 10
AX780380/c
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1
AUTHORS
Haerlach,T., Schoch,C., Kern,W., Kohlmann,A., Schnittger,S.,
Dugas,M., Eils,R., Broré,B. and Mergenthaler,S.
TITLE
Novel genetic markers for leukemias
JOURNAL
Patent: WO 03039443-A 2537 15-MAY-2003;
Deutsches Krebsforschungszentrum (DE) ;
Ludwig-Maximilians-Universitaet Muenchen (DE) ;
PD Dr. Dr. (DE) ; Schoch, Claudia (DE) ; Kern, Wolfgang (DE)
FEATURES
Location/Qualifiers
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/mol_type="unassigned DNA"
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source

ORIGIN
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Best Local Similarity 99.6%; Pred. No. 0;
Matches 1271; Conservative 0; Mismatches 3; Indels 2; Gaps 2;

QY 1 TTTCTTTAGTTGTTATGTCATCTTTCTATTTTAGCATTTATTTCTATGATGCTAT 60
Db 3611 TTTCTTTAGTTGTTATGTCATCTTTCTATTTTAGCATTTATTTCTATGATGCTAT 3552
QY 61 CCAAGACGATTAAGGAGTTCACATGTTTTCGGAACATTTTGAAGAGAGGCTTATC 120
Db 3551 CCAAGACGATTAAGGAGTTCACATGTTTTCGGAACATTTTGAAGAGAGGCTTATC 3492
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QY 121 CAGTGTACAGATCTTAATAAAGTCACATTCAGTGTAAATTTTATTTTAAATATCTTTT 180
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QY 181 TTAATCCTATTTTCTCTCTTTTGGCTCAGTAAATTTTGTATGAAACTTTTAAAGGACT 240
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QY 241 TATGCATGTAAACATTAATTTATAAAGTAAGTCATGGTTATAATTTATTTTCTCTGCT 300
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QY 361 TCGAAGTGTCCACATCCAGAGGGTGTCTGCCCTGACTGGCACAACCTGCATCCACAT 420
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QY 481 CAATCTCAGAGTGGCCATCTTTTGTAGCAACTGTCTGCCCAAAAGCTCACATGTTGTCCA 540
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QY 541 ACTTGGCGGGGCCCTTTTGGATCCATTCGCACTTGGCTATGGAGAAAGTGGCTAATTC 600
Db 3071 ACTTGGCGGGGCCCTTTTGGATCCATTCGCACTTGGCTATGGAGAAAGTGGCTAATTC 3012
QY 601 GTACTTTTCCCTGTAAATATGCGTCTTCTGGATGTGAAATAACTCTGCAACACAGAA 660
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QY 959 GAAACAGCAAGCAAGCTGAAAATTTTGGTTTACCGACTTACGCTAAATGCTATAGSCGAC 1018
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QY 1079 ATAGGAGCTGTCTAGTCTTTGACACAGCATTCAGCTTTTTCAGAAAAATGGCAAT 1138
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QY 1139 TAGGCATCAATGTAATTAATTTCCATGTTGAAATGGCAATCAAACTTTTCTGGCCAGT 1198
Db 2471 TAGGCATCAATGTAATTAATTTCCATGTTGAAATGGCAATCAAACTTTTCTGGCCAGT 2412
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Qy	1259	TTTCGGTAGTGAAGC	1274
Db	2351	TTTCGGTAGTGAAGC	2336
RESULT 19			
LOCUS	BC018193	2034 bp	mRNA linear PRI 24-SEP-2004
DEFINITION	Homo sapiens seven in absentia homolog 1 (Drosophila), mRNA (cDNA clone IMAGE:3857590), partial cds.		
ACCESSION	BC018193		
VERSION	BC018193.1	GI:17390431	
KEYWORDS			
SOURCE	Homo sapiens (human)		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
AUTHORS	1 (bases 1 to 2034) Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G., Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D., Altschul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K., Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Hsieh,F., Diatchenko,L., Marusina,K., Farmer,A.A., Rubin,G.M., Hong,L., Stapleton,M., Soares,M.B., Bonaldo,M.F., Casavant,T.L., Scheetz,T.E., Brownstein,M.J., Usdin,T.B., Toshiyuki,S., Carninci,P., Prange,C., Raha,S.S., Loquellano,N.A., Peters,G.J., Abramson,R.D., Mullahy,S.J., Bosak,S.A., McEwan,P.J., McKernan,K.J., Malek,J.A., Gunaratne,P.H., Richards,S., Worley,K.C., Hale,S., Garcia,A.M., Gay,L.J., Hulyk,S.W., Villalon,D.K., Muzny,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A., Fahney,J., Helton,E., Kettaman,M., Madan,A., Rodriguez,S., Sanchez,A., Whiting,M., Madan,A., Young,A.C., Shevchenko,Y., Bouffard,G.G., Blakesley,R.W., Touchman,J.W., Green,E.D., Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M., Butterfield,Y.S., Krzywinski,M.I., Skalska,U., Smalish,D.E., Schnerch,A., Schein,J.E., Jones,S.J. and Marra,M.A.		
TITLE	Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences		
JOURNAL	Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)		
PUBMED	12477932		
REFERENCE	2 (bases 1 to 2034)		
AUTHORS	Director MGC Project.		
TITLE	Direct Submission		
JOURNAL	Submitted (03-DEC-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA		
REMARK	NIH-MGC Project URL: http://mgc.nci.nih.gov		
COMMENT	Contact: MGC help desk Email: cgapbs-r@mail.nih.gov Tissue Procurement: DCTD/DTF cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: The I.M.A.G.E.B. Consortium (LINL) DNA Sequencing by: Baylor College of Medicine Human Genome Sequencing Center Center code: BCM-HGSC Web site: http://www.hgsc.bcm.tmc.edu/cdna/ Contact: amg@bcm.tmc.edu Günaratne, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Loulseged, H., Kowis, C.R., Sneed, A.J., Martin, R.G., Muzny, D.M., Nanavati, A.N., Gibbs, R.A.		
Clone distribution:	MGC clone distribution information can be found through the I.M.A.G.E.B. Consortium/LINL at: http://image.llnl.gov		
Series:	IRAK Plate: 21 Row: b Column: 9		
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 40254443.			
Location/Qualifiers	1. .2034 /organism="Homo sapiens"		

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CDS	Query Match 65.8%; Score 838; DB 9; Length 2034; Best Local Similarity 99.9%; Pred. No. 0; Matches 958; Conservative 0; Mismatches 0; Indels 1; Gaps 1; QY 317 CAGAATGAGCGCTCAGACTGCTACAGCAATACCTACCGGTACCTCGAAAGTGTCCACCAT 376 DB 100 CAGAATGAGCGCTCAGACTGCTCAGCAATACCTACCGGTACCTCGAAAGTGTCCACCAT 159 QY 377 CCCAGAGGTGCTCCCTGACTGCGCAACTGCATCCAAATGACATTTGGCGAGTCTTT 436 DB 160 CCCAGAGGTGCTCCCTGACTGCGCAACTGCATCCAAATGACATTTGGCGAGTCTTT 219 QY 437 TTGAGTGTCCAGTCTGCTTTGACTATGTTTACCGCCCATCTTCAATGTCAGAGTGGCC 496 DB 220 TTGAGTGTCCAGTCTGCTTTGACTATGTTTACCGCCCATCTTCAATGTCAGAGTGGCC 279 QY 497 ATCTTTGTTGTAGCAACTGTGCGCCAAAGCTCACAATGTTGTCCAACTTCCCGGGGCCCTT 556 DB 280 ATCTTTGTTGTAGCAACTGTGCGCCAAAGCTCACAATGTTGTCCAACTTCCCGGGGCCCTT 339 QY 557 TGGGATCCATTCGCAACTTGGCTATGGAGAAAGTGGCTAAATTCAGTACTTTTTCCCTGTGA 616 DB 340 TGGGATCCATTCGCAACTTGGCTATGGAGAAAGTGGCTAAATTCAGTACTTTTTCCCTGTGA 399 QY 617 AATATGCGTCTTCGTGATGTGAATAAATCTTCCACACACACAGAAAAGCAGACCATGAAG 676 DB 400 AATATGCGTCTTCGTGATGTGAATAAATCTTCCACACACACAGAAAAGCAGACCATGAAG 459 QY 677 AGCTCTGTGAGTTTAGGCGCTTATCTGTCGTCGCTGCTTCTCTCTGTAATGCGCAAG 736 DB 460 AGCTCTGTGAGTTTAGGCGCTTATCTGTCGTCGCTGCTTCTCTCTGTAATGCGCAAG 519 QY 737 GCTCTCTGGATGCTGTAATGCGCCCATCTGATGCATCAGCATTAAGTCCATTAACAACCTTAC 796 DB 520 GCTCTCTGGATGCTGTAATGCGCCCATCTGATGCATCAGCATTAAGTCCATTAACAACCTTAC 579 QY 797 AGGAGAGGATATAGTTTTTCTTGCTACAGACATTAATCTTCTGCTGCTGTTGACTGGG 856 DB 580 AGGAGAGGATATAGTTTTTCTTGCTACAGACATTAATCTTCTGCTGCTGTTGACTGGG 639 QY 857 TGATCATGCAAGTCTGTTTGGCTTTTCACTTTCATGTTAGTCTTTAGAGAAACAGGAAAAAT 916 DB 640 TGATCATGCAAGTCTGTTTGGCTTTTCACTTTCATGTTAGTCTTTAGAGAAACAGGAAAAAT 699		

Query Match	12.5%; Score 159; DB 6; Length 405;
Best Local Similarity	100.0%; Pred. No. 4e-72;
Matches 159; Conservative	0; Mismatches 0; Indels 0; Gaps 0;
Qy	177 TTTTAAATCCTATTTTCTCTTTGCTCAGTAAATTTTGTATGAAACTTTTAAAG 236
Db	
Qy	212 TTTTAAATCCTATTTTCTCTTTGCTCAGTAAATTTTGTATGAAACTTTTAAAG 153
Db	
Qy	237 GACTTATGGCATGTAAACATATTATTAAAGTAAAGTCATCGTTATATATTTTCTCCT 296
Db	152 GACTTATGGCATGTAAACATATTATTAAAGTAAAGTCATCGTTATATATTTTCTCCT 93
Qy	297 GCCTCCCTATGTATTTATTTTCAGAAATGAGCCGTCAGAC 335
Db	92 GCCTCCCTATGTATTTATTTTCAGAAATGAGCCGTCAGAC 54
RESULT 23	
CO476643/c	
LOCUS	CO476643 277 bp DNA linear PAT 30-JAN-2004
DEFINITION	Sequence 8510 from Patent WO0160860.
ACCESSION	CO476643
VERSION	CO476643.1 GI:41442262
KEYWORDS	
SOURCE	Homo sapiens (human)
ORGANISM	Homo sapiens
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
TITLE	Schlegel, R., Endege, W.O. and Monahan, J.E.
JOURNAL	Genes differentially expressed in human prostate cancer and their use
FEATURES	Patent: WO 0160860-A 8510 23-AUG-2001;
source	Millennium Predictive Medicine, Inc. (US)
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Best Local Similarity	100.0%; Pred. No. 1.8e-69;
Matches 154; Conservative	0; Mismatches 0; Indels 0; Gaps 0;
Qy	182 TAATCCTATTTTCTCCTCTTTGCTCAGTAAATTTTGTATGAAACTTTAAAGGACTT 241
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Qy	242 ATGCATGTAAACATATTATTATAAGTAACTCATGGTTATATATTTTCTCTCGCTC 301
Db	152 ATGCATGTAAACATATTATTATAAGTAACTCATGGTTATATATTTTCTCTCGCTC 93
Qy	302 CTTATGTATTTATTTTCAGAAATGAGCCGTCAGAC 335
Db	92 CTTATGTATTTATTTTCAGAAATGAGCCGTCAGAC 59
RESULT 24	
BV208831	
LOCUS	BV208831 673 bp DNA linear STS 01-JUL-2004
DEFINITION	STAH1 2345 Rhesus macaque genomic DNA Macaca mulatta STS genomic clone WMA2345, sequence tagged site.
ACCESSION	BV208831
VERSION	BV208831.1 GI:49533514
KEYWORDS	STS.
SOURCE	Macaca mulatta (rhesus monkey)
ORGANISM	Macaca mulatta
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
	Mammalia; Eutheria; Primates; Catarrhini; Cercopitheidae;
	Cercopitheinae; Macaca.
	1 (bases 1 to 673)

AUTHORS Spindel,E.R., Pauley,M., Jia,Y., Boyle,N., Jiang,S., Gravett,C.,
 Lupo,S.L., Ali,H., Ojeda,S.R. and Norgren,R.B.
TITLE Targeted amplification of the 3' end of rhesus macaque orthologs of
 human genes
JOURNAL Unpublished (2004)

COMMENT
 Contact: Spindel ER
 Division of Neuroscience
 Oregon National Primate Research Center
 505 NW 185th Avenue, Beaverton, OR 97006, USA
 Tel: 403-690-5388
 Fax: 503-690-5384
 Email: spindel@ohsu.edu

Primer A: gaatagcgactgttagctt
 Primer B: ttattaccataaaccaatgac
 STS size: 673

PCR Profile:
 Hot Start: 95 degrees C for 2.00 min
 Denaturation: 95 degrees C for 0.50 min
 Annealing: 48 degrees C for 0.50 min
 Polymerization: 72 degrees C for 1.00 min
 PCR Cycles: 35
 Extension: 72 degrees C for 7.0 min
 Thermal Cycler: MJ Instruments PTC100

Protocol:
 Template: 200 ng
 Primer: each 1uM
 dNTP's: each 200 uM
 Tag Polymerase: 0.05 units/ul (Fast Start High
 Fidelity, Roche)
 Total Vol: 50 ul

Buffer: MgCl2: 1.8 mM
 Fast Start polymerase reaction buffer (Roche)

Bases 1-392 are 98% homologous (Blast) to bases 1838-2229 of
 NM_003031.2. Bases 405-673 are 95% homologous (Blast) to bases
 2231-2489 of NM_003031.2. Primers were chosen to amplify genomic
 DNA in the 3' region of SIAH1. As human sequence was used to
 design the primers, the primer sequences are not included in the
 rhesus sequence provided below. To obtain additional information
 regarding primers or clones contact: Dr. Robert Norgren, Dept of
 Genetics, Cell Biology & Anatomy; University of Nebraska Medical
 Center; 986395 Nebraska Medical Center; Omaha, NE 68198. Email:
 rnorgren@unmc.edu

A database containing sequences associated with this project can be
 found at: <http://rhesusgenomechip.unomaha.edu/index.html>.

FEATURES
 source

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/note="Organ: Liver; Vector: pGEM-T Easy; V-type: Plasmid;
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forward and reverse primers listed above and subcloned
into pGEM-T Easy."
gene
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ORIGIN

Query Match 11.1%; Score 142; DB 11; Length 673;
 Best Local Similarity 100.0%; Pred. No. 3.7e-63;
 Matches 142; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1098 TGACACGACATGACACGCTTTTGCAGAAAATGCAATTTAGGCATCAATGTAACAT 1157

Db 1 TGACACGACATGACACGCTTTTGCAGAAAATGCAATTTAGGCATCAATGTAACAT 60
 QY 1158 TTCCATGTGTTGAAATGCAATCAAAACATTTTCTGCCAGTGTGTTAAACATTCAGTTTCA 1217
 Db 61 TTCCATGTGTTGAAATGCAATCAAAACATTTTCTGCCAGTGTGTTAAACATTCAGTTTCA 120

QY 1218 CAGAAAATAAGGCCACCCATCTG 1239

Db 121 CAGAAAATAAGGCCACCCATCTG 142

RESULT 25

LOCUS CQ511941/c

DEFINITION Sequence 43808 from Patent WO0160860.

ACCESSION CQ511941

VERSION CQ511941.1

KEYWORDS GI:41478205

ORGANISM Homo sapiens (human)

SOURCE Homo sapiens

REFERENCE 1

AUTHORS Schlegel,R., Endege,W.O. and Monahan,J.E.

TITLE Genes differentially expressed in human prostate cancer and their

JOURNAL use

Patent: WO 0160860-A 43808 23-AUG-2001;

Millennium Predictive Medicine, Inc. (US)

FEATURES Location/Qualifiers

source

1..417

/organism="Homo sapiens"

/mol_type="unassigned DNA"

/db_xref="taxon:9606"

ORIGIN

Query Match 10.9%; Score 139; DB 6; Length 417;

Best Local Similarity 100.0%; Pred. No. 1.5e-61;

Matches 139; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1136 ATTATAGGCATCAATGTAACATTTTCCATGTGTGAAATGGCAATCAAAACATTTCTGGCC 1195

Db 413 ATTATAGGCATCAATGTAACATTTTCCATGTGTGAAATGGCAATCAAAACATTTCTGGCC 354

QY 1136 AGTGTGTTAAACTTCAGTTTCACGAAAATAAGGCCACCCATCTGTCGCCAACCTTAAAC 1255

Db 353 AGTGTGTTAAACTTCAGTTTCACGAAAATAAGGCCACCCATCTGTCGCCAACCTTAAAC 294

QY 1256 TCTTTCGGTAGTGAAGC 1274

Db 293 TCTTTCGGTAGTGAAGC 275

RESULT 26

LOCUS CQ516613/c

DEFINITION Sequence 48480 from Patent WO0160860.

ACCESSION CQ516613

VERSION CQ516613.1

KEYWORDS GI:41482877

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE 1

AUTHORS Schlegel,R., Endege,W.O. and Monahan,J.E.

TITLE Genes differentially expressed in human prostate cancer and their

JOURNAL use

Patent: WO 0160860-A 48480 23-AUG-2001;

Millennium Predictive Medicine, Inc. (US)

FEATURES Location/Qualifiers

source

1..473

/organism="Homo sapiens"

ORIGIN

ORIGIN

/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 10.0%; Score 128; DB 6; Length 473;
Best Local Similarity 100.0%; Pred. No. 9.8e-56;
Matches 128; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 969 GCAAGCTGAAATTTTGGCTTACCGACTTGAGCTTAATAGTTCATAGCGAGATGACTTG 1028
|||||
Db 473 GCAAGCTGAAATTTTGGCTTACCGACTTGAGCTTAATAGTTCATAGCGAGATGACTTG 414
|||||

QY 1029 GGAAGCGACTCTCCGATCTATTTCATGAGCAATGCAACAGCCATTATGATGAGCACTG 1088
|||||
Db 413 GGAAGCGACTCTCCGATCTATTTCATGAGCAATGCAACAGCCATTATGATGAGCACTG 354
|||||

QY 1089 TCTAGTCT 1096
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Db 353 TCTAGTCT 346
|||||

RESULT 27
CQ481952/c
LOCUS CQ481952 411 bp DNA linear PAT 30-JAN-2004
DEFINITION Sequence 13819 from Patent WO0160860.
ACCESSION CQ481952
VERSION CQ481952.1 GI:41447571
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens

REFERENCE 1
AUTHORS Schlegel, R., Endege, W.O. and Monahan, J.E.
TITLE Genes differentially expressed in human prostate cancer and their use
JOURNAL Patent: WO 0160860-A 13819 23-AUG-2001;
Millennium Predictive Medicine, Inc. (US)
FEATURES
source
1. .411
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

ORIGIN

Query Match 9.3%; Score 118; DB 6; Length 411;
Best Local Similarity 100.0%; Pred. No. 1.9e-50;
Matches 118; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1157 TTTCATGTGTTGAATGCAATCAAACTTTCTGCGCAGTGTAAAACTTCAGTTTC 1216
|||||
Db 364 TTTCATGTGTTGAATGCAATCAAACTTTCTGCGCAGTGTAAAACTTCAGTTTC 305
|||||

QY 1217 ACAGAAATAAGCACCACCTCTCTGCCAACCTAAACTTTTCGGTAGTGGGAAGC 1274
|||||
Db 304 ACAGAAATAAGCACCACCTCTCTGCCAACCTAAACTTTTCGGTAGTGGGAAGC 247
|||||

RESULT 28
CQ503091/c
LOCUS CQ503091 441 bp DNA linear PAT 30-JAN-2004
DEFINITION Sequence 34958 from Patent WO0160860.
ACCESSION CQ503091
VERSION CQ503091.1 GI:41468727
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens

REFERENCE 1
AUTHORS Schlegel, R., Endege, W.O. and Monahan, J.E.
TITLE Genes differentially expressed in human prostate cancer and their use

JOURNAL Patent: WO 0160860-A 34958 23-AUG-2001;
Millennium Predictive Medicine, Inc. (US)
FEATURES
source
1. .441
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

ORIGIN

Query Match 9.3%; Score 118; DB 6; Length 441;
Best Local Similarity 100.0%; Pred. No. 1.9e-50;
Matches 118; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1157 TTTCATGTGTTGAATGCAATCAAACTTTCTGCGCAGTGTAAAACTTCAGTTTC 1216
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Db 399 TTTCATGTGTTGAATGCAATCAAACTTTCTGCGCAGTGTAAAACTTCAGTTTC 340
|||||

QY 1217 ACAGAAATAAGCACCACCTCTCTGCCAACCTAAACTTTTCGGTAGTGGGAAGC 1274
|||||
Db 339 ACAGAAATAAGCACCACCTCTCTGCCAACCTAAACTTTTCGGTAGTGGGAAGC 282
|||||

RESULT 29
BV102520
LOCUS BV102520 523 bp DNA linear STS 28-FEB-2004
DEFINITION MARC 14423-14424:1027951438:1 SCF - porcine spleen Sus scrofa STS genomic, sequence tagged site.
ACCESSION BV102520
VERSION BV102520.1 GI:44680182
KEYWORDS STS.
SOURCE Sus scrofa (pig)
ORGANISM Sus scrofa

REFERENCE 1
AUTHORS Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
TITLE 1 (bases 1 to 523)
Freking, B.A., Nonneman, D.P., Rohrer, G.A., Fahrenkrug, S.C., Smith, T.P.L. and Keele, J.W.
JOURNAL Development of a comprehensive SNP-based comparative linkage map for pigs
COMMENT Unpublished (2004)

Contact: Freking BA
USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4278
Fax: 402 762 4173
Email: freking@email.marc.usda.gov
Primer A: ATGCCCTCTCTGGATGTGAGA
Primer B: CGCGCCTATGACCATTTAG
STS size: 400
PCR Profile:
Hotstart: 95 degrees for 15 minutes
Denature: 95 degrees for 30 seconds
Anneal: 56 degrees
Extension: 68 degrees for 2 minutes
Cycles: 32 to 45
Protocol:
Template: 50-200 ng genomic DNA
Primer: each 20 pmoles
dNTPs: each 88 uM
Tag Polymerase: 0.25 units (Qiagen HotStar)
Buffer: Commercially supplied Qiagen HotStar buffer

The STS is derived from PCR amplicons generated from genomic DNA, sequenced from each end using the amplification primers. The sequence does not necessarily represent the entire amplicon. Sequence derived from PolyPhred was trimmed from each end of each unique contig until five consecutive bases exceeded a quality score threshold of 20, and the next ten bases averaged a quality score of 20 or greater. Amplicon size was estimated by agarose gel electrophoresis.

	Direct Submission	TITLE	Submitted (02-OCT-2003) Genome Sequencing Center, 4444 Forest Park Parkway, St. Louis, MO 63108, USA
	6 (bases 1 to 194622)	REFERENCE	Wilson,R.
	Direct Submission	AUTHORS	Wilson,R.
	Submitted (27-NOV-2003) Department of Genetics, Washington University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA	JOURNAL	On Oct 2, 2003 this sequence version replaced gi:33636837.
	Center: Washington University Genome Sequencing Center	COMMENT	----- Center code: WUGSC Web site: http://genome.wustl.edu Contact: submissions@wustl.edu ----- Summary Statistics ----- Center project name: M_BB0332N10
	NOTICE:		This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.
	This sequence was finished as follows unless otherwise noted: all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by restriction digest.		MAPPING INFORMATION: Mapping information for this clone was provided by Dr. Wes Warren, Department of Genetics, Washington University, St. Louis MO. For additional information about the map position of this sequence, see http://genome.wustl.edu
	SOURCE INFORMATION: The RPCI-24 BAC Library has been constructed by Pieter de Jong and coworkers (http://www.chori.org) from male C57BL/6J mouse spleen and/or brain genomic DNA. The clone and detailed information can be obtained from Pieter de Jong and coworkers at http://www.chori.org		NEIGHBORING SEQUENCE INFORMATION: This sequence is the entire insert of the clone. FEATURES source 1..194622 Location/Qualifiers /organism="Mus musculus" /mol_type="genomic DNA" /db_xref="taxon:10090" /chromosome="15" /map="15" /clone="RP24-332N10" /clone_lib="RPCI-24" 143..1005 repeat_region /rpt_family="MaLR" 1020..1158 repeat_region /rpt_family="B4" 2576..2612 repeat_region /rpt_family="ERVK" 2613..2778 repeat_region /rpt_family="RMR19B" 2779..3057 repeat_region /rpt_family="ERVK" 3055..3297 repeat_region /rpt_family="MaLR" 4466..4807 repeat_region /rpt_family="MaLR" 5016..5225 repeat_region /rpt_family="B4" 5382..5451 repeat_region /rpt_family="B4" 5603..5872 repeat_region

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/rpt_family="L1"
6054_6149
/rpt_family="Alu"
6240_6368
/rpt_family="B2"
6377_6503
/rpt_family="ERV1"
10251_10300
/rpt_family="ERV1"
10350_10463
/rpt_family="Alu"
10908_11077
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12158_12280
/rpt_family="ID"
12281_12467
/rpt_family="B2"
12468_12498
/rpt_family="ID"
13303_13391
/rpt_family="ID"
Complement(13318..13388)
/product="tRNA-Val"
/note="likely pseudogene (HMM Sc=27.16 / Sec struct
Sc=-6.26)"

repeat_region 13780_13967
/rpt_family="B2"
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/rpt_family="Alu"
repeat_region 14526_14927
/rpt_family="MaLR"
15873_16228
/rpt_family="MaLR"
16241_16459
/rpt_family="B2"
repeat_region 17324_17611
/rpt_family="MaLR"
18038_18186
/rpt_family="Alu"
18484_18588
/rpt_family="Alu"
19067_19249
/rpt_family="B2"
repeat_region 19263_19473
/rpt_family="L1"
repeat_region 19531_19718
/rpt_family="B2"
repeat_region 20889_21104
/rpt_family="MaLR"
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22024_22178
/rpt_family="B2"
repeat_region 22205_22386
/rpt_family="B2"
repeat_region 22470_22612
/rpt_family="Alu"
22975_23153
/rpt_family="B2"
repeat_region 23561_23635
/rpt_family="ID"
23927_24076
/rpt_family="Alu"
24624_24748
/rpt_family="Alu"
27545_27621
/rpt_family="B4"
repeat_region 27622_27716
/rpt_family="Alu"

Query Match 6.9%; Score 88; DB 10; Length 194622;
Best Local Similarity 100.0%; Pred. No. 7.5e-35;
Matches 88; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1096 TTTCACACGAGTCACAGCTTTTGCAGAAATGGCAATTTAGGCATCAATGTAAC 1155
Db 142060 TTTCACACGAGTCACAGCTTTTGCAGAAATGGCAATTTAGGCATCAATGTAAC 142119

QY 1156 ATTTCATGTGTGAATGGCAATCAAA 1183
Db 142120 ATTTCATGTGTGAATGGCAATCAAA 142147

RESULT 31
CO472783/c 438 bp DNA linear PAT 30-JAN-2004
LOCUS
DEFINITION Sequence 4650 from Patent WO0160860.
ACCESSION CO472783
VERSION CO472783.1 GI:41438402
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Schlegel,R., Endege,W.O. and Monahan,J.E.
TITLE Genes differentially expressed in human prostate cancer and their
use
JOURNAL Patent: WO 0160860-A 4650 23-AUG-2001;
Millennium Predictive Medicine, Inc. (US)
FEATURES
source
Location/Qualifiers
1..438
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

ORIGIN

Query Match 6.7%; Score 85; DB 6; Length 438;
Best Local Similarity 100.0%; Pred. No. 5.4e-33;
Matches 85; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1190 CTGGCCAGTGTAAACCTTCAGTTTCAGAAATAAGGCACCCATCTGTCTGCCAAC 1249
Db 366 CTGGCCAGTGTAAACCTTCAGTTTCAGAAATAAGGCACCCATCTGTCTGCCAAC 307

QY 1250 TAAACTCTTCGGTAGGTGGAGC 1274
Db 306 TAAACTCTTCGGTAGGTGGAGC 282
```

```
RESULT 32
BC046317
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

BC046317 1645 bp mRNA linear ROD 30-JUN-2004
IMAGE:6314641, complete cds.
BC046317
BC046317.1 GI:28277393
MGC.
Mus musculus (house mouse)
Mus musculus
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 1645)
Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G.,
Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D.,
Altshuler,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K.,
Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Hsieh,P.,
Diatchenko,L., Marusina,K., Farmer,A.A., Rubin,G.M., Hong,L.,
Stapleton,M., Soares,M.B., Bonaldo,M.P., Casavant,T.L.,
Schaeetz,T.E., Brownstein,M.J., Usdin,T.B., Toshiyuki,S.,
Carrinci,P., Prange,C., Rana,S.S., Loquellano,N.A., Peters,G.J.,
Abramson,R.D., Mullaly,S.J., Bosak,S.A., McEwan,P.J.,
McKernan,K.J., Malek,J.A., Gunaratne,P.H., Richards,S.,
Worley,K.C., Hale,S., Garcia,A.M., Gay,L.J., Hulyk,S.W.,
Villalón,D.K., Muzny,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A.,
Fahey,J., Helton,E., Kettner,M., Madan,A., Rodriguez,S.,
Sanchez,A., Whitting,M., Madan,A., Young,A.C., Shevchenko,Y.,
Bouffard,G.G., Blakeley,R.W., Touchman,J.W., Green,E.D.,
Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M.,
Butterfield,Y.S., Krzywicki,M.I., Skalska,U., Smalls,D.E.,
Schnerch,A., Schein,J.E., Jones,S.J. and Marra,M.A.
Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
12477932
2 (bases 1 to 1645)
Strausberg,R.
Direct Submission
Submitted (31-JAN-2003) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
USA
NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Susan L. Sullivan, PhD.
CDNA Library Preparation: ResGen, Invitrogen Corp
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: National Institutes of Health Intramural
Sequencing Center (NISC),
Gaithersburg, Maryland;
Web site: http://www.nisc.nih.gov/
Contact: nisc\_mgc@hgri.nih.gov
Akhter,N., Avele,K., Beckstrom-Sternberg,S.M., Benjamin,B.,
Blakesley,R.W., Bouffard,G.G., Breen,K., Brinkley,C., Brooks,S.,
Dierich,N.L., Grante,S., Guan,X., Gupta,J., Haghghi,P.,
Hansen,N., Ho,S.-L., Karlins,E., Kwong,P., Laric,P., Legaspi,R.,
Maduro,Q.L., Masiello,C., Maskeri,B., Mastrian,S.D., McCloskey,J.C.,
McDowell,J., Pearson,R., Stantripop,S., Thomas,P.J., Touchman,J.W.,
Tsurgon,C., Vogt,J.L., Walker,M.A., Wetherby,K.D., Wiggins,L.,
Young,A., Zhang,L.-H. and Green,E.D.
Clone distribution: MGC clone distribution information can be found
through the I.M.A.G.E. Consortium/LNL at: http://image.llnl.gov
Series: IRAC Plate: 100 Row: e Column: 20.
Location/Qualifiers
1. 1645
/organism="Mus musculus"
/mol_type="mRNA"
/db_xref="taxon:10090"
/clone="MGC:54763 IMAGE:6314641"

FEATURES
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1. 1645
/organism="Mus musculus"
/mol_type="mRNA"
/db_xref="taxon:10090"
/clone="MGC:54763 IMAGE:6314641"

/tissue_type="Olfactory epithelium, neonatal mouse,
C57Bl/6"
/clone_lib="NIH MGC_129"
/lab_host="DH10B"
/note="Vector: pCMV-SPORT6"
1. 1645
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/db_xref="LocusID:20437"
/db_xref="MGI:108064"
193..1041
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/product="seven in absentia 1A"
/db_xref="AAH46317.1"
/db_xref="GI:28277394"
/db_xref="LocusID:20437"
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1096 TTTGACACGAGTTCGACAGCTTTTGCAGAAATGGCAATTTAGGCATCAATGTAAC 1155
967 TTTGACACGAGTTCGACAGCTTTTGCAGAAATGGCAATTTAGGCATCAATGTAAC 1026
1156 ATTTCCATGTGTGAAA 1172
1027 ATTTCCATGTGTGAAA 1043

ORIGIN
Query Match 6.0%; Score 77; DB 10; Length 1645;
Best Local Similarity 100.0%; Pred. No. 8.1e-29;
Matches 77; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1096 TTTGACACGAGTTCGACAGCTTTTGCAGAAATGGCAATTTAGGCATCAATGTAAC 1155
Db 967 TTTGACACGAGTTCGACAGCTTTTGCAGAAATGGCAATTTAGGCATCAATGTAAC 1026
QY 1156 ATTTCCATGTGTGAAA 1172
Db 1027 ATTTCCATGTGTGAAA 1043

RESULT 33
AX305603
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

AX305603 1968 bp DNA linear PAT 11-DEC-2001
Sequence 354 from Patent WO0188188.
AX305603
AX305603.1 GI:17645071
Mus musculus (house mouse)
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1
Ishikawa,K., Asai,S., Takahashi,Y., Nagata,T. and Ishii,Y.
Method for examining ischemic conditions
Patent: WO 0188188-A 354 22-NOV-2001;
School Juridical Person Nihon University (JP)
Location/Qualifiers
1. 1968
/organism="Mus musculus"
/mol_type="unassigned DNA"
/db_xref="taxon:10090"

REFERENCE
AUTHORS
TITLE
JOURNAL
FEATURES
source
1. 1968
/organism="Mus musculus"
/mol_type="unassigned DNA"
/db_xref="taxon:10090"

ORIGIN
Query Match 6.0%; Score 77; DB 6; Length 1968;
Best Local Similarity 100.0%; Pred. No. 7.9e-29;
Matches 77; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1096 TTTGACACGAGTTCGACAGCTTTTGCAGAAATGGCAATTTAGGCATCAATGTAAC 1155
Db 895 TTTGACACGAGTTCGACAGCTTTTGCAGAAATGGCAATTTAGGCATCAATGTAAC 954
QY 1156 ATTTCCATGTGTGAAA 1172
Db 955 ATTTCCATGTGTGAAA 971
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SOURCE ORGANISM	Mus musculus (house mouse)
REFERENCE	Mus musculus
AUTHORS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
TITLE	1 (bases 1 to 175636)
JOURNAL	Cotton, M., Haakenson, W. and Shahid, S.
AUTHORS	The sequence of Mus musculus BAC clone RP24-501B23
TITLE	Unpublished (2001)
JOURNAL	2 (bases 1 to 175636)
AUTHORS	McPherson, J.D. and Waterston, R.H.
TITLE	Direct Submission
JOURNAL	Submitted (25-MAR-2003) Genome Sequencing Center, 4444 Forest Park Parkway, St. Louis, MO 63108, USA
AUTHORS	3 (bases 1 to 175636)
TITLE	McPherson, J.D. and Waterston, R.H.
JOURNAL	Direct Submission
AUTHORS	Submitted (26-MAR-2003) Genome Sequencing Center, 4444 Forest Park Parkway, St. Louis, MO 63108, USA
TITLE	4 (bases 1 to 175636)
JOURNAL	Wilson, R.K.
AUTHORS	Direct Submission
TITLE	Submitted (12-JUN-2004) Genome Sequencing Center, 4444 Forest Park Parkway, St. Louis, MO 63108, USA
JOURNAL	5 (bases 1 to 175636)
AUTHORS	Wilson, R.K.
TITLE	Direct Submission
JOURNAL	Submitted (10-JUL-2004) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St. Louis, MO 63108, USA
COMMENT	On Jun 12, 2004 this sequence version replaced gi:29244764. ----- Genome Center Center: Washington University Genome Sequencing Center Center code: WUGSC Web site: http://genome.wustl.edu Contact: submissions@watson.wustl.edu ----- Summary Statistics ----- Center project name: M_BB0501B23
NOTICE:	This sequence was finished as follows unless otherwise noted: all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by restriction digest.
MAPPING INFORMATION:	Mapping information for this clone was provided by Dr. Wes Warren, Department of Genetics, Washington University, St. Louis MO. For additional information about the map position of this sequence, see http://genome.wustl.edu
SOURCE INFORMATION:	The RPCI-24 BAC library has been constructed by Pieter de Jong and coworkers (http://www.chori.org) from male C57BL/6J mouse spleen and/or brain genomic DNA. The clone and detailed information can be obtained from Pieter de Jong and coworkers at http://www.chori.org
NEIGHBORING SEQUENCE INFORMATION:	This sequence is the entire insert of the clone.
FEATURES	Location/Qualifiers
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repeat region	5. .754

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898. 1045
/rpt_family="B4"
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/notes="Likely pseudogene (HMM Sc=34.44 / Sec struct
Sc=-9.72)"
2848. 3027
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repeat_region      3043. 3183
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3901. 4186
/rpt_family="MaLR"
4637. 4953
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4958. 5210
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5211. 5580
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5563. 5684
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5685. 5776
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5708. 5780
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6154. 6358
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6489. 6669
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6671. 6864
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6865. 6878
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6879. 7027
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7028. 7088
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7680. 7883
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8256. 8757
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9203. 9293
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10285. 10327
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10331. 10827
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11819. 12024
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12030. 12203
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12320. 12669
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12730. 12839
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12897. 13082
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13526. 13593
/rpt_family="MaLR"
13750. 13925
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13941. 14158
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14436. 14584
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15670. 15743
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16031. 16083
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16332. 16525
/rpt_family="B4"

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16829. 17245
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17253. 17350
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17578. 17727
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18489. 18769
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18987. 19304
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19694. 19900
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20599. 20725
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23168. 23278
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23456. 23520
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25698. 25886
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26091. 26240
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26241. 26382
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26383. 26516
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Query Match      6.0%; Score 77; DB 10; Length 175636;
Best Local Similarity 100.0%; Pred. No. 5e-29;
Matches 77; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1096 TTGCACACGAGTCACAGCTTTTCAGAAAATGCAATTTAGGCATCAATGTAAC 1155
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Db 97733 TTGCACACGAGTCACAGCTTTTCAGAAAATGCAATTTAGGCATCAATGTAAC 97792
|||||

QY 1156 ATTTCCATGTGTGAAA 1172
|||||
Db 97793 ATTTCCATGTGTGAAA 97809
|||||

RESULT 36
BV104504
LOCUS BV104504
DEFINITION MARC 14423-14424:1010076472:1 RTS-1 Bos indicus x Bos taurus STS
ACCESSION BV104504
VERSION BV104504.1 GI:45182422
KEYWORDS STS.
SOURCE Bos indicus x Bos taurus (hybrid cattle)
ORGANISM Bos indicus x Bos taurus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
```

ORGANISM Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Bovinae; Bos.
REFERENCE 1 (bases 1 to 732)
AUTHORS Snelling,W.M., Casas,E., Stone,R.T., Smith,T.P.L., Keele,J.W. and Bennett,G.L.
TITLE Linkage mapping bovine ESTs
JOURNAL Unpublished (2004)
COMMENT

Contact: Stone RT
USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4166
Fax: 402 762 4173
Email: stone@mail.marc.usda.gov
Primer A: ATGCCCTCTCTGGATGTGAGA
Primer B: CGCCGCTATGACCATTTAG
STS size: 400
PCR Profile:

Hotstart: 95 degrees for 15 minutes
Denature: 95 degrees for 30 seconds
Anneal: 58 degrees for 30 seconds
Extension: 68 degrees for 1 minute
Cycles: 32 to 45

Protocol:
Template: 25-50 ng genomic DNA
Primer: each 0.4 uM
dNTPs: each 100 uM
Taq Polymerase: 0.25 units (Qiagen HotStar)

Buffer: Commercially supplied Qiagen HotStar buffer

The STS is derived from PCR amplicons generated from genomic DNA, sequenced from each end using the amplification primers. The sequence does not necessarily represent the entire amplicon. Sequence derived from PolyPhred was trimmed from each end of each unique contig until five consecutive bases exceeded a quality score threshold of 20, and the next ten bases averaged a quality score of 20 or greater. Amplicon size was estimated by agarose gel electrophoresis.

FEATURES

Location/Qualifiers
1..732
/organism="Bos indicus x Bos taurus"
/mol_type="genomic DNA"
/db_xref="taxon:30522"
/clone_lib="RTS-1"
/dev_stage="adult"
/note="taurus and indicus crossbreds"
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STS

ORIGIN

Query Match 4.9%; Score 62; DB 11; Length 732;
Best Local Similarity 100.0%; Pred. No. 7.5e-21;
Matches 62; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 808 ATAGTTTTCTTGCTACAGACATTAACTCTCGTGCTGTGACGGTGATGTCAG 867
Db 521 ATAGTTTTCTTGCTACAGACATTAACTCTCGTGCTGTGACGGTGATGTCAG 580
QY 868 TC 869
Db 581 TC 582

RESULT 37
BV104504/c

LOCUS BV104504 732 bp DNA linear STS 05-MAR-2004
DEFINITION MARC 14423-14424:1010076472:1 RTS-1 Bos indicus x Bos taurus STS
genomic, sequence tagged site.
ACCESSION BV104504
VERSION BV104504.1 GI:45182422
KEYWORDS STS.
SOURCE Bos indicus x Bos taurus (hybrid cattle)

ORGANISM

Bos indicus x Bos taurus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Bovinae; Bos.

REFERENCE

1 (bases 1 to 732)

AUTHORS

Snelling,W.M., Casas,E., Stone,R.T., Smith,T.P.L., Keele,J.W. and Bennett,G.L.

TITLE

Linkage mapping bovine ESTs

JOURNAL

Unpublished (2004)

COMMENT

Contact: Stone RT
USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4166
Fax: 402 762 4173

Email: stone@mail.marc.usda.gov

Primer A: ATGCCCTCTCTGGATGTGAGA

Primer B: CGCCGCTATGACCATTTAG

STS size: 400

PCR Profile:

Hotstart: 95 degrees for 15 minutes
Denature: 95 degrees for 30 seconds
Anneal: 58 degrees for 30 seconds
Extension: 68 degrees for 1 minute
Cycles: 32 to 45

Protocol:
Template: 25-50 ng genomic DNA
Primer: each 0.4 uM
dNTPs: each 100 uM
Taq Polymerase: 0.25 units (Qiagen HotStar)

Buffer:

Commercially supplied Qiagen HotStar buffer

The STS is derived from PCR amplicons generated from genomic DNA, sequenced from each end using the amplification primers. The sequence does not necessarily represent the entire amplicon. Sequence derived from PolyPhred was trimmed from each end of each unique contig until five consecutive bases exceeded a quality score threshold of 20, and the next ten bases averaged a quality score of 20 or greater. Amplicon size was estimated by agarose gel electrophoresis.

FEATURES

Location/Qualifiers
1..732
/organism="Bos indicus x Bos taurus"
/mol_type="genomic DNA"
/db_xref="taxon:30522"
/clone_lib="RTS-1"
/dev_stage="adult"
/note="taurus and indicus crossbreds"
<1..>732

STS

ORIGIN

Query Match 4.9%; Score 62; DB 11; Length 732;
Best Local Similarity 100.0%; Pred. No. 7.5e-21;
Matches 62; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 808 ATAGTTTTCTTGCTACAGACATTAACTCTCGTGCTGTGACGGTGATGTCAG 867
Db 192 ATAGTTTTCTTGCTACAGACATTAACTCTCGTGCTGTGACGGTGATGTCAG 133
QY 868 TC 869
Db 132 TC 131

RESULT 38
AB067814

LOCUS AB067814 1457 bp mRNA linear ROD 31-OCT-2001
DEFINITION Rattus norvegicus Shiahia mRNA for shiahia protein, complete cds.
ACCESSION AB067814
VERSION AB067814.1 GI:16549114
KEYWORDS

SOURCE Rattus norvegicus (Norway rat)
ORGANISM Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.

REFERENCE
AUTHORS Yamaguchi, A., Hori, O. and Tohyama, M.
TITLE rat Slahla
JOURNAL Unpublished
2 (bases 1 to 1457)
AUTHORS Yamaguchi, A., Hori, O. and Tohyama, M.
TITLE Direct Submission
JOURNAL Submitted (05-AUG-2001) Ateushi Yamaguchi, Graduate School of
Medicine, Osaka University, Anatomy and Neuroscience; 2-2,
Yamada-oka, Suita, Osaka 565-0871, Japan
(E-mail: yama@anat2.med.osaka-u.ac.jp, Tel: 81-6-6879-3221 (ex. 3221),
Fax: 81-6-6879-3229)

FEATURES
source Location/Qualifiers
1. .1457
/organism="Rattus norvegicus"
/mol_type="mRNA"
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1. .1457
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19. .888
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/codon_start=1
/product="slahla protein"
/protein_id="BAB70753.1"
/db_xref="GI:16549115"
/translation="MCRLEMSRQTALPTGTSKPPSRQVPALTGTASNNDLAS
LPCKVYSSGCEITLPHTEKABHEELCEFRPYSCPGASCKWQSGSLDAMVHMQHVK
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NGLNGINVTISM"

ORIGIN
Query Match 4.2%; Score 53; DB 10; Length 1457;
Best Local Similarity 100.0%; Pred. No. 4e-16;
Matches 53; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1120 TTTGCAGAAATGGCAATTAGGCATCAATGTAACATTTCCATGTGTTGAAA 1172
|||||
Db 838 TTTGCAGAAATGGCAATTAGGCATCAATGTAACATTTCCATGTGTTGAAA 890
|||||

RESULT 39
AF389476
LOCUS Rattus norvegicus SIAH-1A mRNA linear ROD 20-MAR-2002
DEFINITION Rattus norvegicus SIAH-1A mRNA, complete cds.
ACCESSION AF389476
VERSION AF389476.1 GI:19550382
KEYWORDS Rattus norvegicus (Norway rat)
SOURCE Rattus norvegicus
ORGANISM Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.

REFERENCE
AUTHORS Wheeler, T.C., Chin, L.S., Li, Y., Roudabush, F.L. and Li, L.
TITLE Regulation of synaptophysin degradation by mammalian homologues of
seven in absentia
J. Biol. Chem. 277 (12), 10273-10282 (2002)

JOURNAL
MEDLINE 21895831
PUBMED 11786535
REFERENCE Wheeler, T.C., Roudabush, F.L., Chin, L.-S. and Li, L.
AUTHORS 2 (bases 1 to 1465)
TITLE Direct Submission
JOURNAL Submitted (08-JUN-2001) Department of Pharmacology, University of
North Carolina at Chapel Hill, CB 7365, Chapel Hill, NC 27599, USA
Location/Qualifiers
1. .1465

/organism="Rattus norvegicus"
/mol_type="mRNA"
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1. .849
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/protein_id="AAL91362.1"
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/translation="MSRQTALPTGTSKPPSRQVPALTGTASNNDLASLFECPVC
FDYVLPPILOQSGHLVCSNCRPKLTCCPTCRGLGSIIRNLAMKAVNSVLFPCKYAS
SGCEITLPHTEKABHEELCEFRPYSCPGASCKWQSGSLDAMVHMQHKSITTLQKQ
EDIVFLATDINLPGADVWQSCFGFHMVLVLEKQYDGHQGFALVOLIGTRKQA
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VTISM"

ORIGIN
Query Match 4.2%; Score 53; DB 10; Length 1465;
Best Local Similarity 100.0%; Pred. No. 4e-16;
Matches 53; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1120 TTTGCAGAAATGGCAATTAGGCATCAATGTAACATTTCCATGTGTTGAAA 1172
|||||
Db 799 TTTGCAGAAATGGCAATTAGGCATCAATGTAACATTTCCATGTGTTGAAA 851
|||||

RESULT 40
AC105462
LOCUS Rattus norvegicus clone CH230-145D2, WORKING DRAFT SEQUENCE.
DEFINITION Rattus norvegicus clone CH230-145D2, WORKING DRAFT SEQUENCE.
ACCESSION AC105462
VERSION AC105462.7 GI:30521365
KEYWORDS HTG; HTGS PHASE2; HTGS DRAFT; HTGS FULLTOP.
SOURCE Rattus norvegicus (Norway rat)
ORGANISM Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.

REFERENCE
AUTHORS 1 (bases 1 to 220157)
Muzny, D., Marie, Metzker, M., Lee, Abramson, S., Adams, C., Alder, J.,
Allen, C., Allen, H., Alsbrooks, S., Amin, A., Anguiano, D.,
Anyalebechi, V., Aoyagi, A., Ayodeji, M., Baca, E., Baden, H.,
Baldwin, D., Bandaranaike, D., Barber, M., Barnstead, M., Benahmed, F.,
Biswal, K., Blair, J., Blankenburg, K., Blyth, P., Brown, M.,
Bryant, N., Buhay, C., Burch, P., Burrell, K., Calderon, E.,
Cardenas, V., Carter, K., Cavazos, I., Ceasar, H., Center, A.,
Chacko, J., Chavez, D., Chen, G., Chen, R., Chen, Y., Chen, Z., Chu, J.,
Cleveland, C., Cockrell, R., Cox, C., Coyle, M., Cree, A., D'Souza, L.,
Davila, M., Davis, C., Davy-Carroll, L., De Anda, C., Dederich, D.,
Delgado, O., Denson, S., Deramo, C., Ding, Y., Dinh, H., Divya, K.,
Draper, H., Dugan-Rocha, S., Dunn, A., Durbin, K., Duval, B., Eaves, K.,
Egan, A., Escotto, M., Eugene, C., Evans, C.A., Falls, T., Fan, G.,
Fernandez, S., Finley, M., Flagg, N., Forbes, L., Foster, M., Foster, P.,
Fraser, C.M., Gabisi, A., Ganta, R., Garcia, A., Garner, T., Garza, M.,
Gebregorgis, E., Geer, K., Gill, R., Grady, M., Guerra, W., Guevara, W.,
Gunaratne, P., Haaland, W., Hamil, C., Hamilton, C., Hamilton, K.,
Harvey, Y., Havlak, P., Hawes, A., Henderson, N., Hernandez, J.,
Hernandez, R., Hines, S., Hladun, S.L., Hodgson, A., Hogues, J.,
Hollins, B., Howells, S., Hulyk, S., Hume, J., Idlebird, D., Jackson, A.,
Jackson, L., Jacob, L., Jiang, H., Johnson, B., Johnson, R., Jolivet, A.,
Karpachy, S., Kelly, S., Kelly, S., Khan, Z., King, L., Kovar, C.,
Kowis, C., Kraft, C.L., Lebow, H., Levan, J., Lewis, L., Li, Z., Liu, J.,
Liu, J., Liu, W., Liu, Y., London, P., Longacre, S., Lopez, J.,
Lorensuhewa, L., Loulseghe, H., Lozada, R.J., Lu, X., Ma, J.,
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Mawhinney, S., McLeod, M.P., McNeill, T.Z., Meenen, E.,
Milosavljevic, A., Miner, G., Minja, E., Montemayor, J., Moore, S.,
Morgan, M., Morris, K., Morris, S., Munidasa, M., Murphy, M., Nair, L.,
Nankervis, C., Neal, D., Newton, N., Nguyen, N., Norris, S.,
Nwaokemele, O., Okwuonu, G., Olarnpunsagoon, A., Pal, S., Parks, K.,
Pasternak, S., Paul, H., Perez, A., Perez, L., Pfankoch, C.,
Plopper, F., Poindexter, A., Popovic, D., Primus, E., Pu, L.-L.,

Puazo, M., Quiroz, J., Rachlin, E., Reeves, K., Regier, M.A., Reigh, R., Reilly, B., Reilly, M., Ren, Y., Reuter, M., Richards, S., Riggs, F., Rives, C., Rodkey, T., Rojas, A., Rose, M., Rose, R., Ruiz, S.J., Sanders, W., Savary, G., Scherer, S., Scott, G., Shatsman, S., Shen, H., Shetty, J., Shvartsbeyn, A., Sisson, I., Sitter, C.D., Smajs, D., Sneed, A., Sodergren, E., Song, X.-Z., Sorelle, R., Sosa, J., Steinkle, M., Strong, R., Sutton, A., Svatek, A., Tabor, P., Taylor, C., Taylor, T., Thomas, N., Thomas, S., Tingey, A., Trejos, Z., Usmani, K., Valas, R., Vera, V., Villalana, D., Waldron, L., Walker, B., Wang, J., Wang, Q., Wang, S., Warren, J., Warren, R., Wei, X., White, F., Williams, G., Willson, R., Wleczyk, R., Wooden, H., Worley, K., Wright, D., Wright, R., Wu, J., Yakub, S., Yen, J., Yoon, L., Yoon, V., Yu, F., Zhang, J., Zhou, J., Zhou, X., Zhao, S., Dunn, D., von Niederhauser, A., Weiss, R., Smith, D.R., Holt, R.A., Smith, H.O., Weinstein, G., and Gibbs, R.A.

Direct Submission
Unpublished
2 (bases 1 to 220157)
Worley, K.C.

REFERENCE JOURNAL
TITLE
AUTHORS
JOURNAL

Submitted (09-JAN-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
3 (bases 1 to 220157)
Rat Genome Sequencing Consortium.

REFERENCE JOURNAL
TITLE
AUTHORS
JOURNAL

Submitted (10-MAY-2003) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
On May 10, 2003 this sequence version replaced gi:25008590.
The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas (<http://www.hgsc.bcm.tmc.edu/projects/rat/>). Each contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence may extend beyond the ends of the clone and there may be sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence only contigs will be indicated in the feature table.

----- Genome Center
Center: Baylor College of Medicine
Center code: BCM
Web site: <http://www.hgsc.bcm.tmc.edu/>
Contact: hgsc-help@bcm.tmc.edu
----- Project Information
Center project name: GHPW
Center clone name: CH230-145D2
----- Summary Statistics
Assembly program: Atlas 3.0:
Consensus quality: 215295 bases at least Q40
Consensus quality: 216317 bases at least Q30
Consensus quality: 217167 bases at least Q20
Estimated insert size: 223095; sum-of-contigs estimation
Quality coverage: 9x in Q20 bases; sum-of-contigs estimation

* NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/genbank_draft_data.html).
* NOTE: This is a 'working draft' sequence. It currently consists of 1 contigs. Gaps between the contigs are represented as runs of N. The order of the pieces is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have been provided by the submitter.
* This sequence will be replaced
* By the finished sequence as soon as it is available and
* the accession number will be preserved.
* the accession number will be 220157 bp in length.
1 220157: contig of 220157 bp in length.
Location/Qualifiers
1. .220157
/organism="Rattus norvegicus"

* NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/genbank_draft_data.html).
* NOTE: This is a 'working draft' sequence. It currently consists of 1 contigs. Gaps between the contigs are represented as runs of N. The order of the pieces is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have been provided by the submitter.
* This sequence will be replaced
* By the finished sequence as soon as it is available and
* the accession number will be preserved.
* the accession number will be 220157 bp in length.
1 220157: contig of 220157 bp in length.
Location/Qualifiers
1. .220157
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1295..2037
misc_feature
clone end: T7
/note="clone boundary"
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site: EcoRI
end_sequence: BH297589"

ORIGIN
Query Match 4.2%; Score 53; DB 2; Length 220157;
Best Local Similarity 100.0%; Pred. No. 2.4e-16;
Matches 53; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1120 TTTCAGAAATGGCAATTTAGGCATCAATGTAACTATTTCATGTTGAAA 1172
|||||
Db 118973 TTTCAGAAATGGCAATTTAGGCATCAATGTAACTATTTCATGTTGAAA 119025
|||||

RESULT 41
AC098991/c
LOCUS
DEFINITION
Rattus norvegicus clone CH230-84N8, WORKING DRAFT SEQUENCE, 2
unordered pieces.
AC098991
AC098991.7 GI:30520816
HTG; HTGS PHASE1; HTGS DRAFT; HTGS_FULLTOP.
KEYWORDS
Rattus norvegicus
Rattus norvegicus (Norway rat)
SOURCE
ORGANISM
Rattus
REFERENCE
1 (bases 1 to 232382)
Muzny, D., Marie, Metzker, M. Lee., Abramson, S., Adams, C., Alder, J., Allen, C., Allen, H., Alsbrooks, S., Amin, A., Anguiano, D., Anyalebechi, V., Aoyagi, A., Ayodeji, M., Baca, E., Baden, H., Baldwin, D., Bandaranaike, D., Barber, M., Barnstead, M., Benahmed, F., Biswal, K., Blair, J., Blankenburg, K., Blyth, P., Brown, M., Bryant, N., Buhay, C., Burch, P., Burrell, K., Calderon, E., Cardenas, V., Carter, K., Cavazos, I., Ceasar, H., Center, A., Chacko, J., Chavez, D., Chen, G., Chen, R., Chen, Y., Chen, Z., Chu, J., Cleveland, C., Cockrell, R., Cox, C., Coyle, M., Cree, A., D'Souza, L., Davila, M.L., Davis, C., Davy-Carroll, L., De Anda, C., Dederich, D., Delgado, O., Denson, S., Deramo, C., Ding, Y., Dinh, H., Divya, K., Draper, H., Dugan-Rocha, S., Dunn, A., Durbin, K., Duval, B., Eaves, K., Egan, A., Escotto, M., Eugene, C., Evans, C.A., Falls, T., Fan, G., Fernandez, S., Finley, M., Flagg, N., Forbes, L., Foster, M., Foster, P., Fraser, C.M., Gabisi, A., Ganta, R., Garcia, A., Garner, T., Garza, M., Gebregeorgis, E., Geer, K., Gill, R., Grady, M., Guerra, W., Guevara, W., Gunaratne, P., Haaland, W., Hamill, C., Hamilton, C., Hamilton, K., Harvey, Y., Havlak, P., Hawes, A., Henderson, N., Hernandez, J., Hernandez, R., Hines, S., Hladun, S.L., Hodgson, A., Hogues, M., Hollins, B., Howells, S., Hulyk, S., Hume, J., Idlebird, D., Jackson, A., Jackson, L., Jacob, L., Jiang, H., Johnson, B., Johnson, R., Jolivet, A., Karpathy, S., Kelly, S., Khan, Z., King, L., Kovar, C., Kowis, C., Kraft, C.L., Lebow, H., Levan, J., Lewis, L., Li, Z., Liu, J., Liu, J., Liu, W., Liu, Y., London, P., Longacre, S., Lopez, J., Lorenshew, L., Lousegh, H., Lozado, R.J., Lu, X., Ma, J., Maheshwari, M., Mahindartne, M., Mahmoud, M., Malloy, K., Mangum, A., Mangum, B., Mapua, P., Martin, K., Martin, R., Martinez, E., Mawhney, S., McLeod, M.P., McNeill, T.Z., Meenen, E., Milosavljevic, A., Miner, G., Minja, E., Montemayor, J., Moore, S., Morgan, M., Morris, K., Morris, S., Munidasa, M., Murphy, M., Nair, L., Nankervis, C., Neal, D., Newton, N., Nguyen, N., Norris, S., Nwokedeme, O., Okwuon, G., Olarnpusagoon, A., Pal, S., Parks, K., Pasternak, S., Paul, H., Perez, A., Perez, L., Pfannkuch, C., Plopper, F., Poindexter, A., Popovic, D., Primus, E., Pu, L.-L., Puazo, M., Quiroz, J., Rachlin, E., Reeves, K., Regier, M.A., Reigh, R., Reilly, B., Reilly, M., Ren, Y., Reuter, M., Richards, S., Riggs, F., Rives, C., Rodkey, T., Rojas, A., Rose, M., Rose, R., Ruiz, S.J.,

Sanders, W., Savary, G., Scherer, S., Scott, G., Shatsman, S., Shen, H., Shetty, J., Shvartsbeyn, A., Sisson, I., Sitter, C.D., Smajls, D., Sneed, A., Sodergren, E., Song, X.-Z., Sorelle, R., Sosa, J., Steimle, M., Strong, R., Sutton, A., Svatek, A., Tabor, P., Taylor, C., Taylor, T., Thomas, N., Thomas, S., Tingey, A., Trejos, Z., Umanil, K., Valas, R., Vera, V., Villasana, D., Waldron, L., Walker, B., Wang, J., Wang, Q., Wang, S., Warren, J., Warren, R., Wei, X., White, F., Williams, G., Willison, R., Wleczky, R., Wooden, H., Worley, K., Wright, D., Wright, R., Wu, J., Yakub, S., Yen, J., Yoon, L., Yoon, V., Yu, F., Zhang, J., Zhou, X., Zhao, S., Zhao, S., Dunn, D., von Niederhausern, A., Weiss, R., Smith, D.R., Holt, R.A., Smith, H.O., Weinstein, G., and Gibbs, R.A.

TITLE JOURNAL

REFERENCE AUTHORS

TITLE JOURNAL

REFERENCE AUTHORS

TITLE JOURNAL

REFERENCE AUTHORS

TITLE JOURNAL

COMMENT

Submitted (08-NOV-2001) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
3 (bases 1 to 232382)
Rat Genome Sequencing Consortium.

Submitted (10-MAY-2003) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
On May 10, 2003 this sequence version replaced gi:25090763.

The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas (<http://www.hgsc.bcm.tmc.edu/projects/rat/>). Each contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence may extend beyond the ends of the clone and there may be sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence only contigs will be indicated in the feature table.

----- Genome Center

Center: Baylor College of Medicine

Center code: BCM

Web site: <http://www.hgsc.bcm.tmc.edu/>

Contact: hgsc-help@bcm.tmc.edu

----- Project Information

Center project name: GHZA

Center clone name: CH230-84N8

----- Summary Statistics

Assembly program: Atlas 3.0;

Consensus quality: 222927 bases at least Q40

Consensus quality: 225089 bases at least Q30

Consensus quality: 226508 bases at least Q20

Estimated insert size: 232565; sum-of-contigs estimation

Quality coverage: 7x in Q20 bases; sum-of-contigs estimation

* NOTE: Estimated insert size may differ from sequence length
* (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).

* NOTE: This is a 'working draft' sequence. It currently

* consists of 2 contigs. The true order of the pieces

* is not known and their order in this sequence record is

* arbitrary. Gaps between the contigs are represented as

* runs of N, but the exact sizes of the gaps are unknown.

* This record will be updated with the finished sequence

* as soon as it is available and the accession number will

* be preserved.

* 1 230782: contig of 230782 bp in length

* 230783 230882: gap of unknown length

* 230883 232382: contig of 1500 bp in length.

Location/Qualifiers

1..232382

/organism="Rattus norvegicus"

/mol_type="genomic DNA"

/db_xref="taxon:10116"

FEATURES

source

misc_feature

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/clone="CH230-84N8"

/note="wgs_contig"

34268..35647

/note="wgs_contig"

ORIGIN

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Best Local Similarity 100.0%; Pred. No. 2.4e-16;
Matches 53; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1120 TTTCGAGAAATGGCAATTTAGGCATCAATGTAACATATTTCATGTTGAAA 1172

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Db 5705 TTTCGAGAAATGGCAATTTAGGCATCAATGTAACATATTTCATGTTGAAA 5653

RESULT 42

CQ486802/c

LOCUS

DEFINITION

Sequence 18669 from Patent WO0160860.

ACCESSION

CQ486802

VERSION

CQ486802.1

GI:41452421

KEYWORDS

SOURCE

Homo sapiens (human)

ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

1

AUTHORS

Schlegel, R., Endege, W.O. and Monahan, J.E.

TITLE

Genes differentially expressed in human prostate cancer and their use

JOURNAL

Patent: WO 0160860-A 18669 23-AUG-2001;

Millennium Predictive Medicine, Inc. (US)

FEATURES

source

Location/Qualifiers

1..426

/organism="Homo sapiens"

/mol_type="unassigned DNA"

/db_xref="taxon:9606"

ORIGIN

Query Match 4.1%; Score 52; DB 6; Length 426;
Best Local Similarity 100.0%; Pred. No. 1.5e-15;
Matches 52; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 965 GCAAGCAAGCTGAAATTTGCTTACCAGCTTGAGCTAAATGGTCATAGGCG 1016

|||||

Db 426 GCAAGCAAGCTGAAATTTGCTTACCAGCTTGAGCTAAATGGTCATAGGCG 375

RESULT 43

MM5IAHPSA

LOCUS

DEFINITION

M.musculus pseudogene.

ACCESSION

Z19582

VERSION

Z19582.1

GI:297038

KEYWORDS

pseudogene.

SOURCE

Mus musculus (house mouse)

ORGANISM

Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE

1 (bases 1 to 2123)

AUTHORS

Della.N.G., Senior, P.V. and Bowtell, D.D.

TITLE

Isolation and characterisation of murine homologues of the

Drosophila seven in absentia gene (sina)

JOURNAL

Development (1993) In press

REFERENCE

2 (bases 1 to 2123)

AUTHORS

Bowtell, D.D.

TITLE

Direct Submission

JOURNAL

Submitted (15-JAN-1993) David D.L. Bowtell, Developmental Biology

Group, Howard Florey, Institute of Exp. Physiology and Medicine,

University of Melbourne, Parkville, Victoria, 3052, Australia

Location/Qualifiers

1..2123

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/organism="Mus musculus"
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Query Match      4.1%  Score 52;  DB 10;  Length 2123;
Best Local Similarity 100.0%;  Pred. No. 1.3e-15;
Matches 52;  Conservative 0;  Mismatches 0;  Indels 0;  Gaps 0;

OY 395 TGACTGGCACTGATCCACAAATGACTTGGCGAGTCTTTTGAGTGCTCC 446
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Db 397 TGACTGGCACTGATCCACAAATGACTTGGCGAGTCTTTTGAGTGCTCC 448

RESULT 44
AC139553/C
LOCUS       AC139553
DEFINITION Mus musculus chromosome 19, clone RP24-386E18, complete sequence.
ACCESSION   AC139553
VERSION     AC139553.5 GI:45917411
KEYWORDS    HTG.
SOURCE      Mus musculus (house mouse)
ORGANISM    Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 168091)
Birren,B., Nusbaum,C. and Lander,E.
Mus musculus chromosome 19, clone RP24-386E18
Unpublished
2 (bases 1 to 168091)
Birren,B., Nusbaum,C., Lander,E., Abouelleil,A., Allen,N.,
Anderson,S., Arachchi,H.M., Barna,N., Bastien,V., Bloom,T.,
Boguslavskiy,L., Boukhgalter,B., Camarata,J., Chang,J., Choepel,Y.,
Collimore,A., Cook,A., Cooke,P., Corum,B., DeArellano,K.,
Diaz,J.S., Dodge,S., Dooley,K., Dorris,L., Erickson,J., Faro,S.,
Ferreira,P., FitzGerald,M., Gage,D., Galagan,J., Gardyna,S.,
Graham,L., Grand-Pierre,N., Hafez,N., Hagopian,D., Hagos,B.,
Hall,J., Horton,L., Hulme,W., Iliev,I., Johnson,R., Jones,C.,
Kamat,A., Karatas,A., Kells,C., Landers,T., Levine,R.,
Lindblad-Toh,K., Liu,G., Lui,A., Mabbitt,R., Maclean,C.,
Macdonald,P., Major,J., Manning,J., Matthews,C., McCarthy,M.,
McDonald,J., Meneus,L., Mihova,T., Mlenga,V., Murphy,T., Naylor,J.,
Nguyen,C., Nicol,R., Norbu,C., O'Connor,T., O'Donnell,P.,
O'Neill,D., Oliver,J., Peterson,K., Phunkhang,P., Pierre,N.,
Rachupka,A., Ramasamy,U., Raymond,C., Retta,R., Rise,C., Rogov,P.,
Roman,J., Schauer,S., Schuback,R., Seaman,S., Severy,P., Smith,C.,
Spencer,B., Stange-Thomann,N., Stojanovic,N., Stubbbs,M.,
Talamas,J., Teefaye,S., Theodor,J., Topham,K., Travers,M.,
Vassiliev,H., Venkataraman,V.S., Viel,R., Vo,A., Wilson,B., Wu,X.,
Wyman,D., Young,G., Zainoun,J., Zembek,L., Zimmer,A. and Zody,M.
Direct Submission
Submitted (05-FEB-2003) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
3 (bases 1 to 168091)
Birren,B., Nusbaum,C., Lander,E., Abouelleil,A., Allen,N.,
Anderson,M., Arachchi,H.M., Barna,N., Bastien,V., Bloom,T.,
Boguslavskiy,L., Boukhgalter,B., Camarata,J., Chang,J., Choepel,Y.,
Collimore,A., Cook,A., Cooke,P., Corum,B., DeArellano,K.,
Diaz,J.S., Dodge,S., Dooley,K., Dorris,L., Erickson,J., Faro,S.,
Ferreira,P., FitzGerald,M., Gage,D., Galagan,J., Gardyna,S.,
Graham,L., Grand-Pierre,N., Hafez,N., Hagopian,D., Hagos,B.,
Hall,J., Horton,L., Hulme,W., Iliev,I., Johnson,R., Jones,C.,
Kamat,A., Karatas,A., Kells,C., Landers,T., Levine,R.,
Lindblad-Toh,K., Liu,G., Lui,A., Mabbitt,R., Maclean,C.,
Macdonald,P., Major,J., Manning,J., Matthews,C., McCarthy,M.,
McDonald,J., Meneus,L., Mihova,T., Mlenga,V., Murphy,T., Naylor,J.,
Nguyen,C., Nicol,R., Norbu,C., O'Connor,T., O'Donnell,P.,
O'Neill,D., Oliver,J., Peterson,K., Phunkhang,P., Pierre,N.,
Rachupka,A., Ramasamy,U., Raymond,C., Retta,R., Rise,C., Rogov,P.,

```

```

TITLE
JOURNAL
REFERENCE
AUTHORS
Roman,J., Schauer,S., Schuback,R., Seaman,S., Severy,P., Smith,C.,
Spencer,B., Stange-Thomann,N., Stojanovic,N., Stubbbs,M.,
Talamas,J., Teefaye,S., Theodor,J., Topham,K., Travers,M.,
Vassiliev,H., Venkataraman,V.S., Viel,R., Vo,A., Wilson,B., Wu,X.,
Wyman,D., Young,G., Zainoun,J., Zembek,L., Zimmer,A. and Zody,M.
Direct Submission
Submitted (14-JAN-2004) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
4 (bases 1 to 168091)
Birren,B., Nusbaum,C., Lander,E., Abouelleil,A., Allen,N.,
Anderson,M., Anderson,S., Arachchi,H.M., Barna,N., Bastien,V.,
Bloom,T., Boguslavskiy,L., Boukhgalter,B., Camarata,J., Chang,J.,
Choepel,Y., Collimore,A., Cook,A., Cooke,P., Corum,B.,
DeArellano,K., Diaz,J.S., Dodge,S., Dooley,K., Dorris,L.,
Erickson,J., Faro,S., Ferreira,P., FitzGerald,M., Gage,D.,
Galagan,J., Gardyna,S., Graham,L., Grand-Pierre,N., Hafez,N.,
Hagopian,D., Hagos,B., Hall,J., Horton,L., Hulme,W., Iliev,I.,
Johnson,R., Jones,C., Kamat,A., Karatas,A., Kells,C., Landers,T.,
Levine,R., Lindblad-Toh,K., Liu,G., Lui,X., Lui,A., Mabbitt,R.,
Maclean,C., Macdonald,P., Major,J., Manning,J., Matthews,C.,
McCarthy,M., Meldrim,J., Meneus,L., Mihova,T., Mlenga,V.,
Murphy,T., Naylor,J., Nguyen,C., Nguyen,T., Nicol,R., Norbu,C.,
O'Connor,T., O'Donnell,P., O'Neill,D., Oliver,J., Peterson,K.,
Phunkhang,P., Pierre,N., Rachupka,A., Ramasamy,U., Raymond,C.,
Retta,R., Rise,C., Rogov,P., Roman,J., Schauer,S., Schuback,R.,
Seaman,S., Severy,P., Smith,C., Spencer,B., Stange-Thomann,N.,
Stojanovic,N., Stubbbs,M., Talamas,J., Teefaye,S., Theodor,J.,
Topham,K., Travers,M., Vassiliev,H., Venkataraman,V.S., Viel,R.,
Vo,A., Wilson,B., Wu,X., Wyman,D., Young,G., Zainoun,J., Zembek,L.,
Zimmer,A. and Zody,M.
Direct Submission
Submitted (01-APR-2004) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
On Apr 1, 2004 this sequence version replaced gi:40841749.
All repeats were identified using RepeatMasker:
http://ftp.genome.washington.edu/RM/RepeatMasker.html
Smit,A.F.A. & Green,P. (1996-1997)
----- Genome Center
Center: Whitehead Institute/MIT Center for Genome Research
Center code: WIBR
Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@broad.mit.edu
----- Project Information
Center project name: L21117
Center clone name: 386_E_18
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Some of the sequence contained within base pairs 1 - 85216 was
stolen from accession AC123941.
Location/Qualifiers
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/mol_type="genomic DNA"
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/chromosome="19"
/map="19"
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/clone_lib="RP24-386E18"
1..5217
/note="wgs end extension
clone_end:SP6"
complement(785..909)
/rpt_family="B1P"
986..1164
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/rpt_family="MER59A"
1554..2073
/rpt_family="RMRIB"
2074..2127
/rpt_family="RMRIB"
2128..2243
/rpt_family="RMRIB"
complement(3146..3420)
/rpt_family="B4A"

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5218..5221
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site:Nboi"
repeat_region 5666..5941
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repeat_region 6238..6970
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repeat_region 6971..7159
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repeat_region complement(7575..7698)
/rpt_family="MLTIF2"
repeat_region 8181..8213
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/rpt_family="B3"
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repeat_region 9453..9483
/rpt_family="(CAAAA)n"
repeat_region complement(10015..10576)
/rpt_family="MER31-int"
repeat_region 11076..11248
/rpt_family="MER5C"
repeat_region 12991..13013
/rpt_family="(TTTG)n"
repeat_region 13169..13304
/rpt_family="GA-rich"
repeat_region 13371..13393
/rpt_family="(TTA)n"
repeat_region 13948..13977
/rpt_family="(TA)n"
repeat_region 13985..14012
/rpt_family="AT-rich"
repeat_region 14647..14683
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repeat_region complement(15104..15421)
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repeat_region 15434..15599
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repeat_region 17365..17437
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repeat_region 17532..17815
/rpt_family="Lx"
repeat_region 18009..18120
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repeat_region complement(18524..19070)
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repeat_region 19069..19459
/rpt_family="Lx9"
repeat_region 19760..19808
/rpt_family="(CA)n"
repeat_region complement(20381..20565)
/rpt_family="B3"
repeat_region 22263..22489
/rpt_family="L2"
repeat_region complement(23375..23649)
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repeat_region 24147..24195
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repeat_region 25258..25431
/rpt_family="MIR"
repeat_region 25881..25903

/rpt_family="(A)n"
Query Match 4.1%; Score 52; DB 10; Length 168091;
Best Local Similarity 100.0%; Pred.No. 8.3e-16;
Matches 52; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 395 TGACTGGCACAACTGCATCCCAACATGACTGGCGAGTCTTTTTCAGTGTCC 446
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Db 48075 TGACTGGCACAACTGCATCCCAACATGACTGGCGAGTCTTTTTCAGTGTCC 48024
RESULT 45
AC123941 182733 bp DNA linear ROD 01-JAN-2004
LOCUS Mus musculus BAC clone RP23-458G24 from chromosome 19, complete
DEFINITION sequence.
ACCESSION AC123941
VERSION AC123941.3 GI:38229437
KEYWORDS HTG.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 182733)
AUTHORS Goyea,E., Cotton,M., Spalding,L., Haakenson,W. and Schatzkamer,K.
TITLE The sequence of Mus musculus BAC clone RP23-458G24
JOURNAL Unpublished (2001)
REFERENCE 2 (bases 1 to 182733)
AUTHORS Wilson,R.
TITLE Sequencing of Mus musculus
JOURNAL Unpublished (2001)
REFERENCE 3 (bases 1 to 182733)
AUTHORS McPherson,J.D. and Waterston,R.H.
TITLE Direct Submission
JOURNAL Submitted (05-JUN-2002) Genome Sequencing Center, 4444 Forest Park
Parkway, St. Louis, MO 63108, USA
REFERENCE 4 (bases 1 to 182733)
AUTHORS McPherson,J.D. and Waterston,R.H.
TITLE Direct Submission
JOURNAL Submitted (20-SEP-2002) Genome Sequencing Center, 4444 Forest Park
Parkway, St. Louis, MO 63108, USA
REFERENCE 5 (bases 1 to 182733)
AUTHORS Wilson,R.K.
TITLE Direct Submission
JOURNAL Submitted (08-NOV-2003) Genome Sequencing Center, 4444 Forest Park
Parkway, St. Louis, MO 63108, USA
REFERENCE 6 (bases 1 to 182733)
AUTHORS Wilson,R.
TITLE Direct Submission
JOURNAL Submitted (01-JAN-2004) Department of Genetics, Washington
University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
COMMENT On Nov 8, 2003 this sequence version replaced gi:23238069.
----- Genome Center
Center: Washington University Genome Sequencing Center
Web site: http://genome.wustl.edu
Contact: submissions@watson.wustl.edu
----- Summary Statistics

Center project name: M_BA0458G24

NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.
This sequence was finished as follows unless otherwise noted:
all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by restriction digest.

MAPPING INFORMATION:

Mapping information for this clone was provided by Dr. Wes Warren, Department of Genetics, Washington University, St. Louis MO. For additional information about the map position of this sequence, see <http://genome.wustl.edu>

SOURCE INFORMATION:

The RPCI-23 BAC Library has been constructed by Kazutoyo Osegawa and Minako Tateno in the laboratory of Pieter de Jong (<http://www.chori.org>) from female C57BL/6J mouse kidney and/or brain genomic DNA. The clone and detailed information can be obtained from Research Genetics, Inc. (<http://www.resgen.com>) or Pieter de Jong and coworkers at <http://www.chori.org>

NEIGHBORING SEQUENCE INFORMATION:

This sequence is the entire insert of the clone. This clone is overlapped by AC108421

FEATURES

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source
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    /location/Qualifiers
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        repeat_region
      1668. .1720
        /rpt_family="B2"
        repeat_region
      4179. .4767
        /rpt_family="RMR19B"
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/rpt_family="L1"
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/rpt_family="B2"
repeat_region 26627. .27426
/rpt_family="L1"
repeat_region 28298. .28500
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repeat_region 28688. .28941
/rpt_family="L1"
repeat_region 29068. .29286
/rpt_family="L1"
repeat_region 30687. .31216
/rpt_family="L1"
repeat_region 31425. .32157
/rpt_family="L1"
repeat_region 33002. .33311
/rpt_family="L2"
repeat_region 34081. .34405
/rpt_family="ERVK"
repeat_region 36448. .36645
/rpt_family="L1"
repeat_region 36822. .36969
/rpt_family="Alu"
repeat_region 39590. .39805
/rpt_family="ERVK"
repeat_region 40632. .40774
/rpt_family="MIR"
repeat_region 40941. .41286
/rpt_family="MaLR"
repeat_region 42085. .42298
/rpt_family="B4"
repeat_region 44879. .45003
/rpt_family="L1"
repeat_region 45994. .46181
/rpt_family="B2"
repeat_region 46506. .46845
/rpt_family="MaLR"
repeat_region 46846. .47124
/rpt_family="MaLR"
repeat_region 48070. .48221
/rpt_family="L1"
repeat_region 48285. .48416
/rpt_family="B4"
repeat_region 52362. .53090
/rpt_family="L1"
repeat_region 53089. .53492
/rpt_family="L1"
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Best Local Similarity 100.0%; Pred. No. 8.2e-16;
Matches 52; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 395 TGACTGGCACAACTGCTGCATCCACAATGACTTGGCGAGTCTTTTGTGATGTC 446

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/db_xref="taxon:10090"
/clone="MGC:60693 IMAGE:33433"
/tissue_type="Egg, unfertilized"
/clone_lib="NIA Mouse Unfertilized Oocytes (Long)"
/lab_host="DH10B"
/notes="vector: pSPORT1"
1. 1720
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/db_xref="LocusID:20438"

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gene

CDS

/db_xref="MGI:108063"
329..1177
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VTISM"

ORIGIN

Query Match 3.5%; Score 45; DB 10; Length 1720;
Best Local Similarity 100.0%; Pred. No. 6.7e-12;
Matches 45; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 402 CACAACGTGCATCAACAATGACTTGGCGAGTCTTTTGGAGTGTC 446
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Db 409 CACAACGTGCATCAACAATGACTTGGCGAGTCTTTTGGAGTGTC 453
|||||

RESULT 48
AL732294/c
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

AL732294 112893 bp DNA linear ROD 30-NOV-2003
Mouse DNA sequence from clone RP23-59N7 on chromosome X, complete
sequence.
AL732294
AL732294.18 GI:38568122
HTG.
Mus musculus (house mouse)
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 112893)
Clark, S.
Direct Submission
Submitted (27-NOV-2003) Wellcome Trust Sanger Institute, Hinxton,
Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
humquery@sanger.ac.uk
On Nov 30, 2003 this sequence version replaced gi:38304169.
Sequence from the Mouse Genome Sequencing Consortium whole genome
shotgun may have been used to confirm this sequence. Sequence data
from the whole genome shotgun alone has only been used where it has
a phred quality of at least 30.
----- Genome Center
Center: Wellcome Trust Sanger Institute
Center code: SC
Web site: <http://www.sanger.ac.uk>
Contact: humquery@sanger.ac.uk

During sequence assembly data is compared from overlapping clones.
where differences are found these are annotated as variations
together with a note of the overlapping clone name. Note that the
variation annotation may not be found in the sequence submission
corresponding to the overlapping clone, as we submit sequences with
only a small overlap as described above.
This sequence was finished as follows unless otherwise noted: all
regions were either double-stranded or sequenced with an alternate
chemistry or covered by high quality data (i.e., phred quality >=
30); an attempt was made to resolve all sequencing problems, such
as compressions and repeats; all regions were covered by at least
one plasmid subclone or more than one M13 subclone; and the
assembly was confirmed by restriction digest, except on the rare
occasion of the clone being a YAC.
The following abbreviations are used to associate primary accession
numbers given in the feature table with their source databases:
Em:, EMBL; Sw:, SWISSPROT; Tr:, TrEMBL; Wp:, WORMPEP; Information
on the WORMPEP database can be found at

http://www.sanger.ac.uk/Projects/C_elegans/wormpep RP23-59N7 is
from the RPCI-23 Mouse BAC library
constructed by the group of Pieter de Jong.
For further details see <http://www.chori.org/bacpac/home.htm>
VECTOR: pBACE3.6.
Location/Qualifiers
1..112893
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ORIGIN

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Best Local Similarity 100.0%; Pred. No. 4.3e-12;
Matches 45; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 402 CACAACGTGCATCAACAATGACTTGGCGAGTCTTTTGGAGTGTC 446
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Db 63845 CACAACGTGCATCAACAATGACTTGGCGAGTCTTTTGGAGTGTC 63801
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RESULT 49
AC091606/c
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
REFERENCE
AUTHORS
TITLE
JOURNAL
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

AC091606 234105 bp DNA linear ROD 21-MAY-2003
Mus Musculus Strain C57BL6/J chromosome X BAC, RP23-75P20, complete
sequence.
AC091606
AC091606.8 GI:30962723
HTG.
Mus musculus (house mouse)
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 234105)
Grills, G., Li, L., Montgomery, K.T., Chiu, D., Decker, J., Fusina, M.,
Goltz, J., Haider, A., Hall, L., Han, J., Ioshikhes, I.P., Lee, E.,
Perera, A., Shim, C., Thomas, E. and Kucherlapati, R.
High Throughput Mouse Sequencing
Unpublished
2 (bases 1 to 234105)
Grills, G., Li, L., Montgomery, K.T., Chiu, D., Decker, J., Fusina, M.,
Goltz, J., Haider, A., Hall, L., Han, J., Ioshikhes, I.P., Lee, E.,
Perera, A., Shim, C., Thomas, E. and Kucherlapati, R.
Direct Submission
Submitted (09-MAY-2001) Department of Molecular Genetics, Albert
Einstein College of Medicine Genome Center, 1300 Morris Park Ave.,
Bronx, NY 10461, USA
3 (bases 1 to 234105)
Grills, G., Li, L., Montgomery, K.T., Chiu, D., Decker, J., Fusina, M.,
Goltz, J., Haider, A., Hall, L., Han, J., Ioshikhes, I.P., Lee, E.,
Perera, A., Shim, C., Thomas, E., Gendal, L.J. and Kucherlapati, R.
Direct Submission
Submitted (21-MAY-2003) Harvard Partners Center for Genetics and
Genomics, Harvard Medical School, 65 Landsdowne St, Cambridge, MA
02139, USA
On May 21, 2003 this sequence version replaced gi:18057068.
----- Genome Center
Center: Harvard Partners Genome Center
Center Code: HPGC
Web site: <http://www.hpcgg.org/sequence/mouse.html>
Contact: hpgc@mcldel.mgh.harvard.edu

CLONE LENGTH: This sequence represents the entire insert of this
clone unless otherwise noted. If there are overlapping clones, the
overlaps are noted in the beginning and end of the Features
listing.
ANNOTATION OF FEATURES:
STSs are identified using ePCR (Genome Res. 7:541-550).
Repeats are identified using RepeatMasker (A. Smit and P. Green,


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repeat_region 19619..19682
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repeat_region 20665..20792

Query Match 3.5%; Score 45; DB 10; Length 234105;
Best Local Similarity 100.0%; Pred. NO. 4e-12;
Matches 45; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 402 CACACTGTCATCCACAATGACTTGGCGAGTCTTTTGGAGTGCC 446
      |||||||
Db 57942 CACAATGTCATCCACAATGACTTGGCGAGTCTTTTGGAGTGCC 57898

RESULT 50
LOCUS BV102520/c 523 bp DNA linear STS 28-FEB-2004
DEFINITION MARC 14423-14424:1027951438:1 SCF - porcine spleen Sus scrofa STS
            genomic, sequence tagged site.
ACCESSION BV102520
VERSION BV102520.1 GI:44680182
KEYWORDS STS.
SOURCE Sus scrofa (pig)
ORGANISM Sus scrofa
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
REFERENCE 1 (bases 1 to 523)
AUTHORS Freking,B.A., Nommaman,D.P., Rohrer,G.A., Fahrenkrug,S.C.,
            Smith,T.P.L. and Keele,J.W.
TITLE Development of a comprehensive SNP-based comparative linkage map
            for pigs
JOURNAL Unpublished (2004)
COMMENT

Contact: Freking BA
USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4278
Fax: 402 762 4173
Email: freking@email.marc.usda.gov
Primer A: AIGCCCTCTTGGAGTGAGA
Primer B: CGCCGCTATGACCATTTAG
STS size: 400
PCR Profile:
    Hotstart: 95 degrees for 15 minutes
    Denature: 95 degrees for 30 seconds
    Anneal: 56 degrees
    Extension: 68 degrees for 2 minutes
    Cycles: 32 to 45
Protocol:
    Template: 50-200 ng genomic DNA
    Primer: each 20 pmoles
    dNTPs: each 88 uM
    Taq Polymerase: 0.25 units (Qiagen HotStar)

Buffer: Commercially supplied Qiagen HotStar buffer

The STS is derived from PCR amplicons generated from genomic DNA,
sequenced from each end using the amplification primers. The
sequence does not necessarily represent the entire amplicon.
Sequence derived from PolyPhred was trimmed from each end of each
unique contig until five consecutive bases exceeded a quality score
threshold of 20, and the next ten bases averaged a quality score of
20 or greater. Amplicon size was estimated by agarose gel
electrophoresis.

FEATURES
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            Location/Qualifiers
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                /mol_type="genomic DNA"
                /strain="white composite, duroc, meishan, minzhu,
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fengjing, crossbreeds"
/db_xref="taxon:9823"
/sex="male and female"
/clone_lib="SCF - porcine spleen"
/dev_stage="adult"
/note="Organ: spleen"
124..523
124..144
complement(504..523)

primer_bind
primer_bind
ORIGIN

Query Match 2.9%; Score 37; DB 11; Length 523;
Best Local Similarity 100.0%; Pred. NO. 1.3e-07;
Matches 37; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 672 TGAAGAGCTCTGTGAGTTTAGGCCCTTATTCCTGTCCG 708
      |||||||
Db 118 TGAAGAGCTCTGTGAGTTTAGGCCCTTATTCCTGTCCG 82

Search completed: April 25, 2005, 02:39:49
Job time : 5791 secs
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